



Full wwPDB EM Validation Report ⓘ

Nov 20, 2022 – 02:55 pm GMT

PDB ID : 2CGT
EMDB ID : EMD-1202
Title : GROEL-ADP-gp31 COMPLEX
Authors : Clare, D.K.; Bakkes, P.J.; van Heerikhuizen, H.; van der Vies, S.M.; Saibil, H.R.
Deposited on : 2006-03-09
Resolution : 8.20 Å (reported)
Based on initial models : 1A0N, 1G31

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

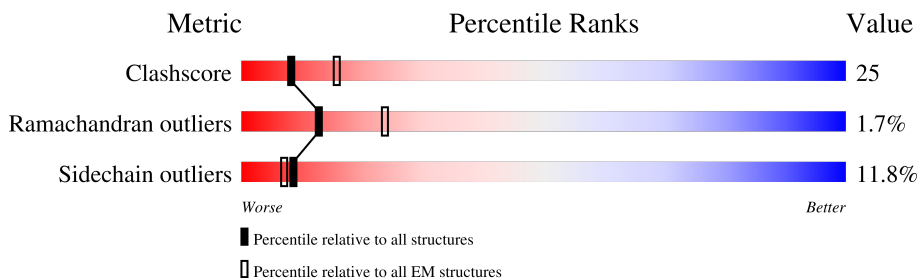
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	547	5% (red), 62% (green), 27% (yellow), 6% (orange), 0% (grey)
1	B	547	7% (red), 62% (green), 27% (yellow), 6% (orange), 0% (grey)
1	C	547	6% (red), 62% (green), 27% (yellow), 6% (orange), 0% (grey)
1	D	547	6% (red), 63% (green), 26% (yellow), 6% (orange), 0% (grey)
1	E	547	5% (red), 62% (green), 27% (yellow), 6% (orange), 0% (grey)
1	F	547	6% (red), 63% (green), 27% (yellow), 6% (orange), 0% (grey)
1	G	547	6% (red), 62% (green), 27% (yellow), 6% (orange), 0% (grey)
1	H	547	12% (red), 56% (green), 32% (yellow), 5% (orange), 6% (grey)

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Mol	Chain	Length	Quality of chain
1	I	547	
1	J	547	
1	K	547	
1	L	547	
1	M	547	
1	N	547	
2	O	111	
2	P	111	
2	Q	111	
2	R	111	
2	S	111	
2	T	111	
2	U	111	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 57953 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 60 KDA GROEL.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	524	3855	2397	665	773	20	0	0
1	B	524	3855	2397	665	773	20	0	0
1	C	524	3855	2397	665	773	20	0	0
1	D	524	3855	2397	665	773	20	0	0
1	E	524	3855	2397	665	773	20	0	0
1	F	524	3855	2397	665	773	20	0	0
1	G	524	3855	2397	665	773	20	0	0
1	H	515	3783	2354	656	753	20	0	0
1	I	515	3783	2354	656	753	20	0	0
1	J	515	3783	2354	656	753	20	0	0
1	K	515	3783	2354	656	753	20	0	0
1	L	515	3783	2354	656	753	20	0	0
1	M	515	3783	2354	656	753	20	0	0
1	N	515	3783	2354	656	753	20	0	0

- Molecule 2 is a protein called CAPSID ASSEMBLY PROTEIN GP31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	O	83	641	417	106	114	4	0	0

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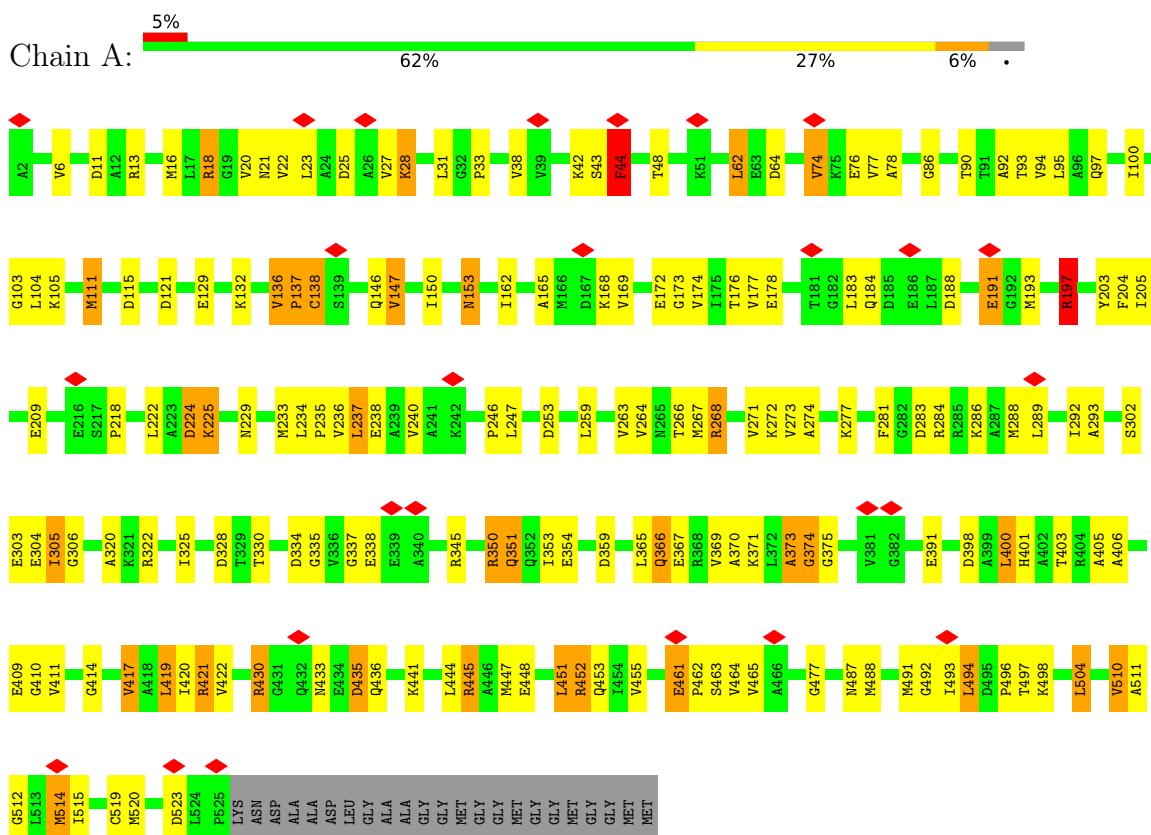
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Mol	Chain	Residues	Atoms					AltConf	Trace
2	P	83	Total 641	C 417	N 106	O 114	S 4	0	0
2	Q	83	Total 641	C 417	N 106	O 114	S 4	0	0
2	R	83	Total 641	C 417	N 106	O 114	S 4	0	0
2	S	83	Total 641	C 417	N 106	O 114	S 4	0	0
2	T	83	Total 641	C 417	N 106	O 114	S 4	0	0
2	U	83	Total 641	C 417	N 106	O 114	S 4	0	0

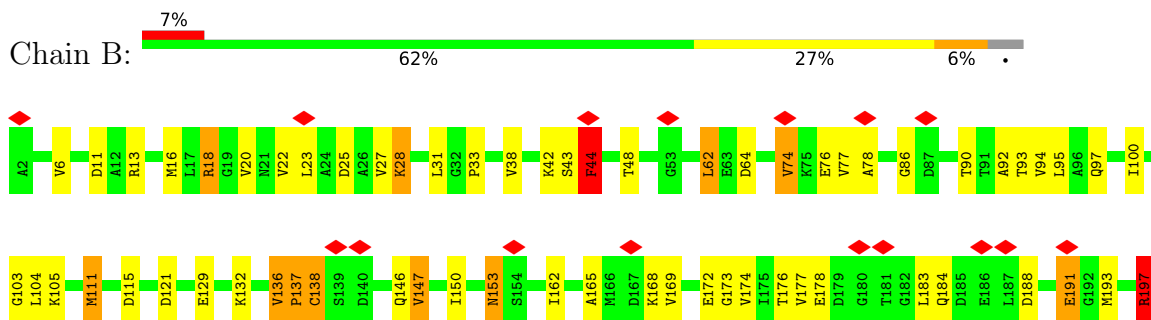
3 Residue-property plots

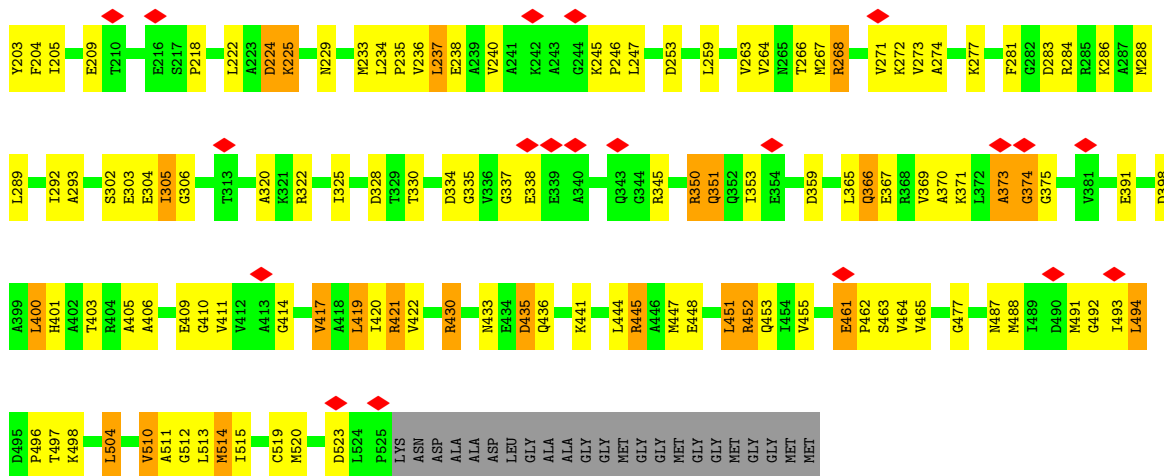
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: 60 KDA GROEL

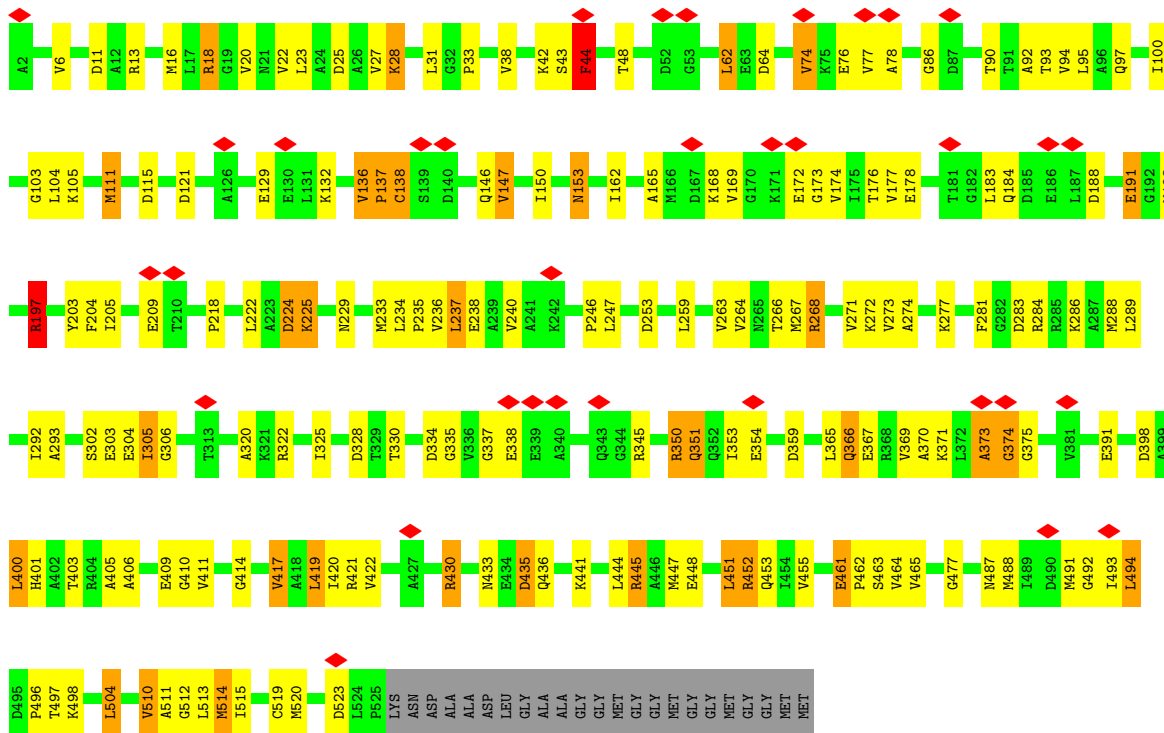


- Molecule 1: 60 KDA GROEL

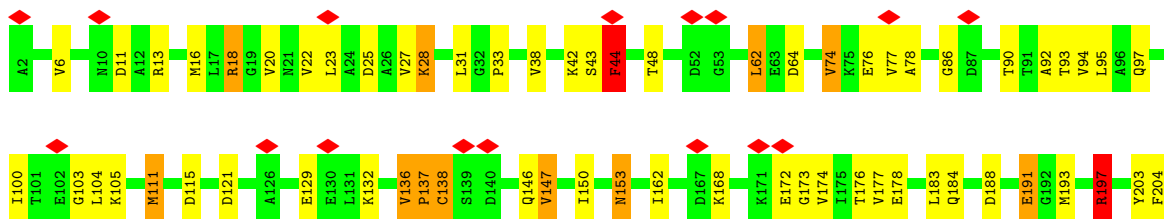


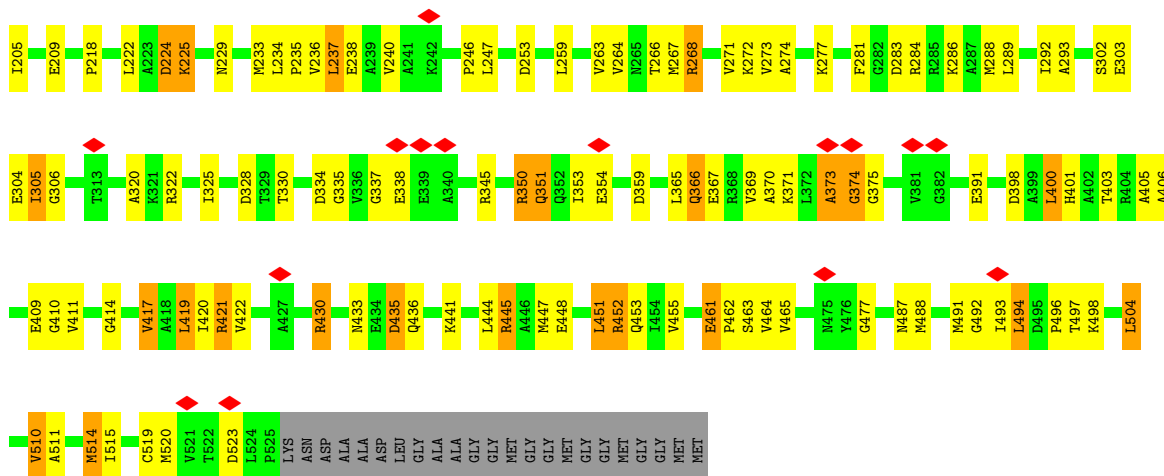


• Molecule 1: 60 KDA GROEL

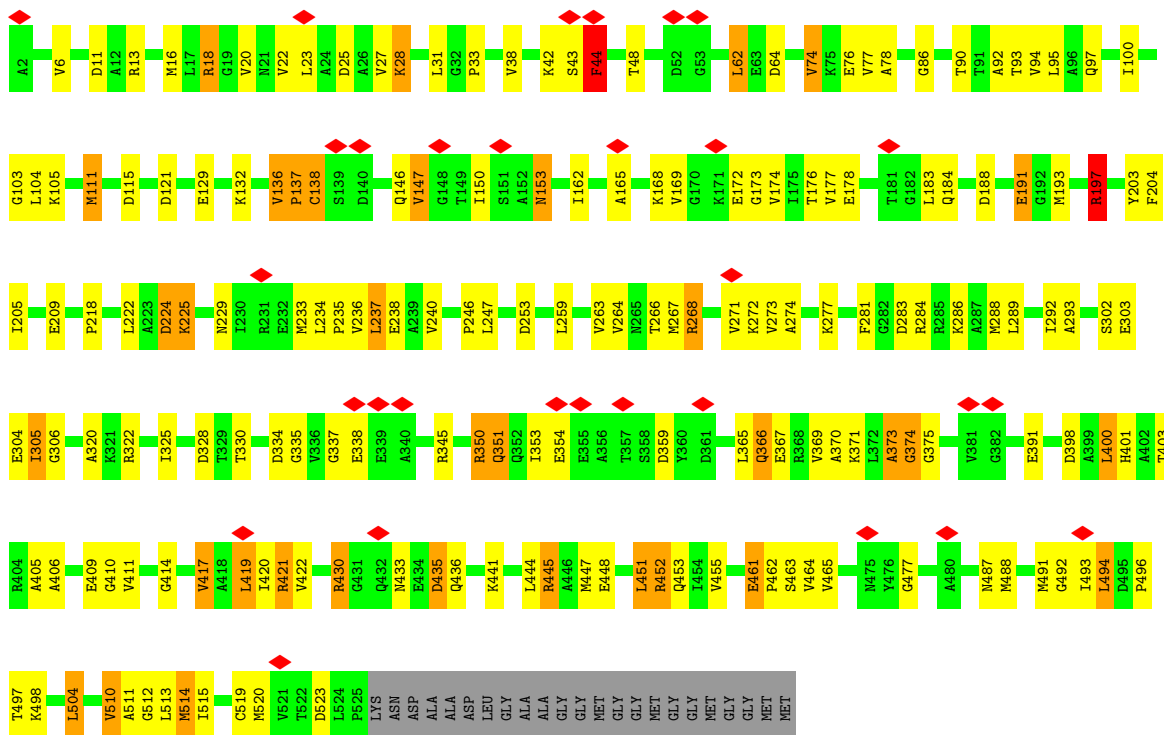


• Molecule 1: 60 KDA GROEL

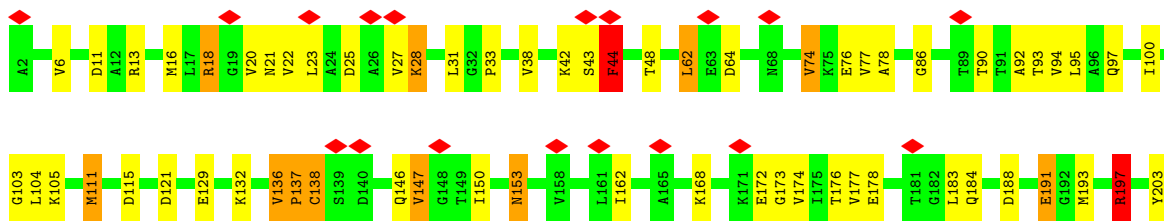


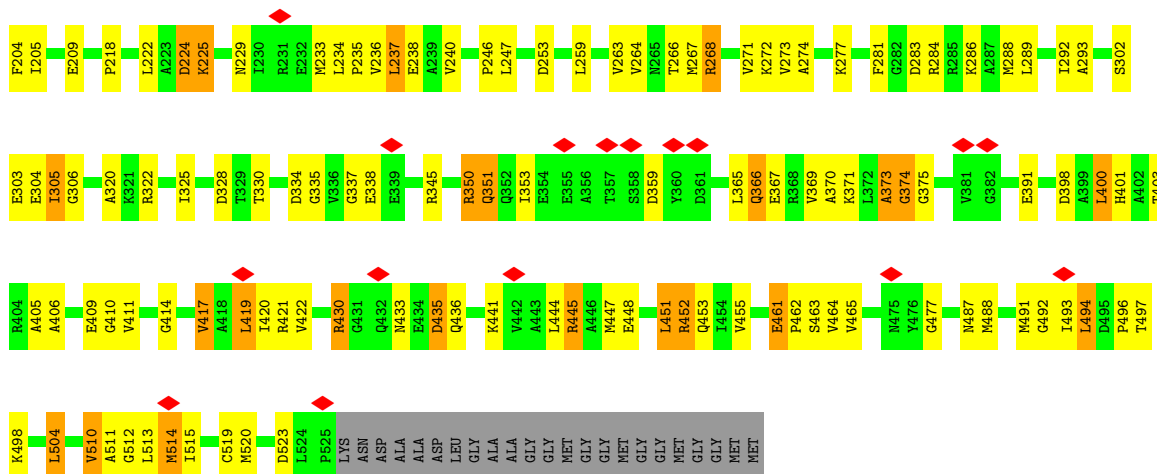


• Molecule 1: 60 KDA GROEL

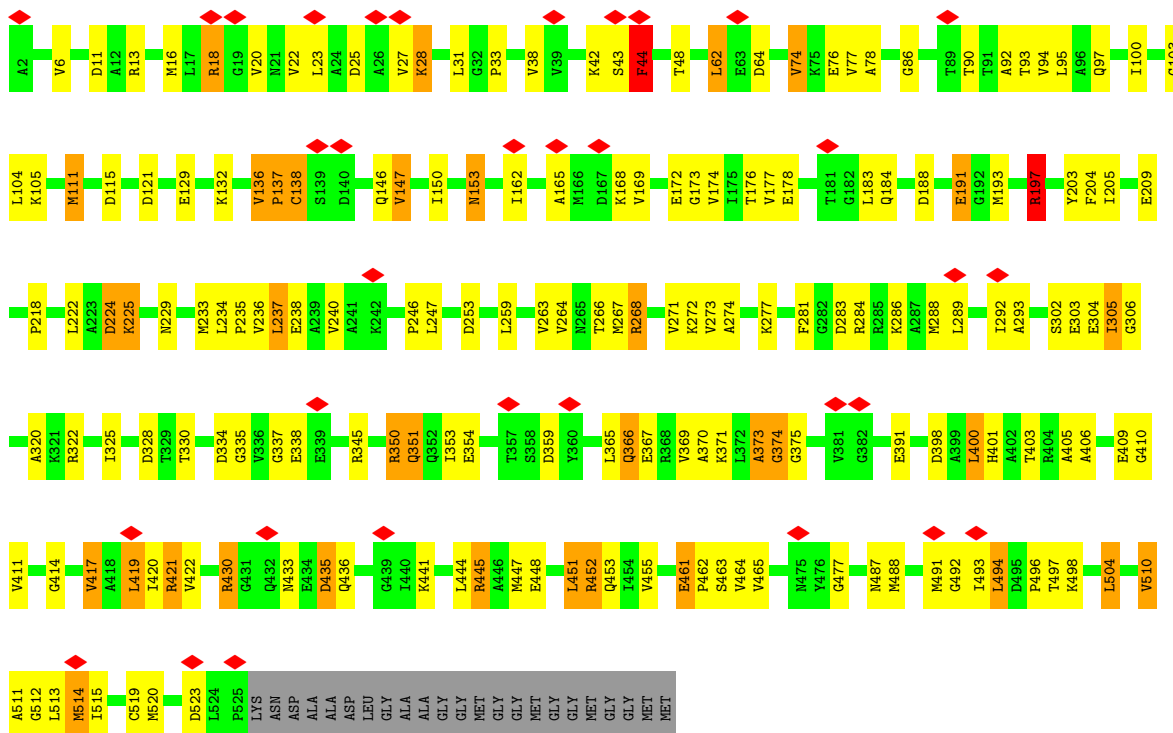


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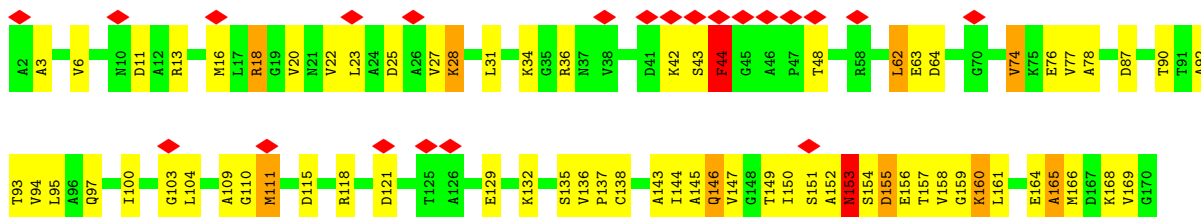


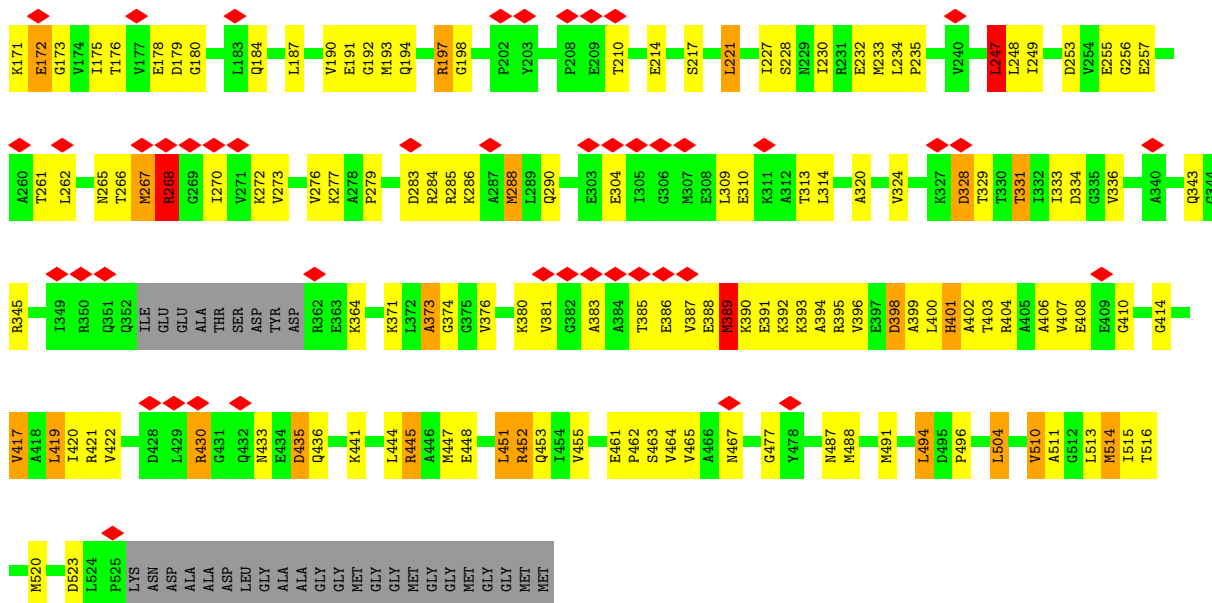


• Molecule 1: 60 KDA GROEL

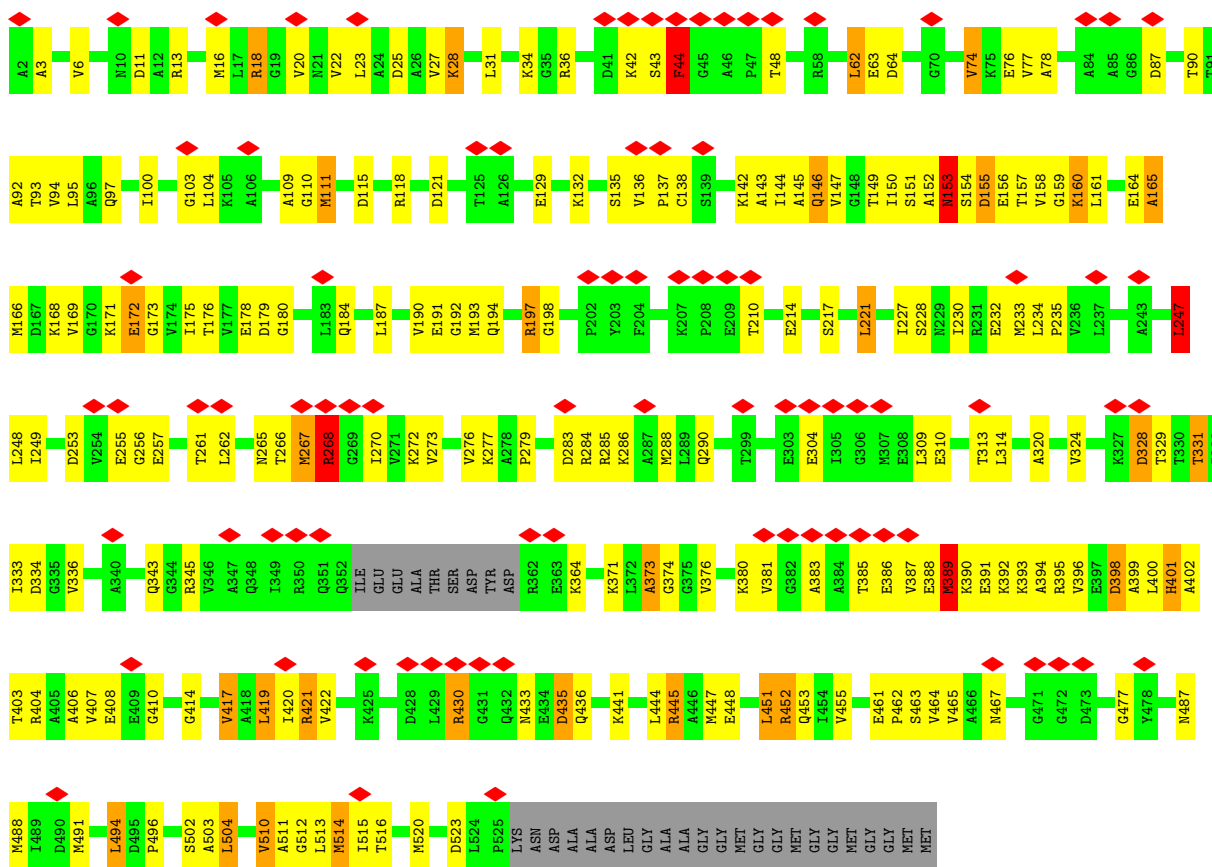


• Molecule 1: 60 KDA GROEL



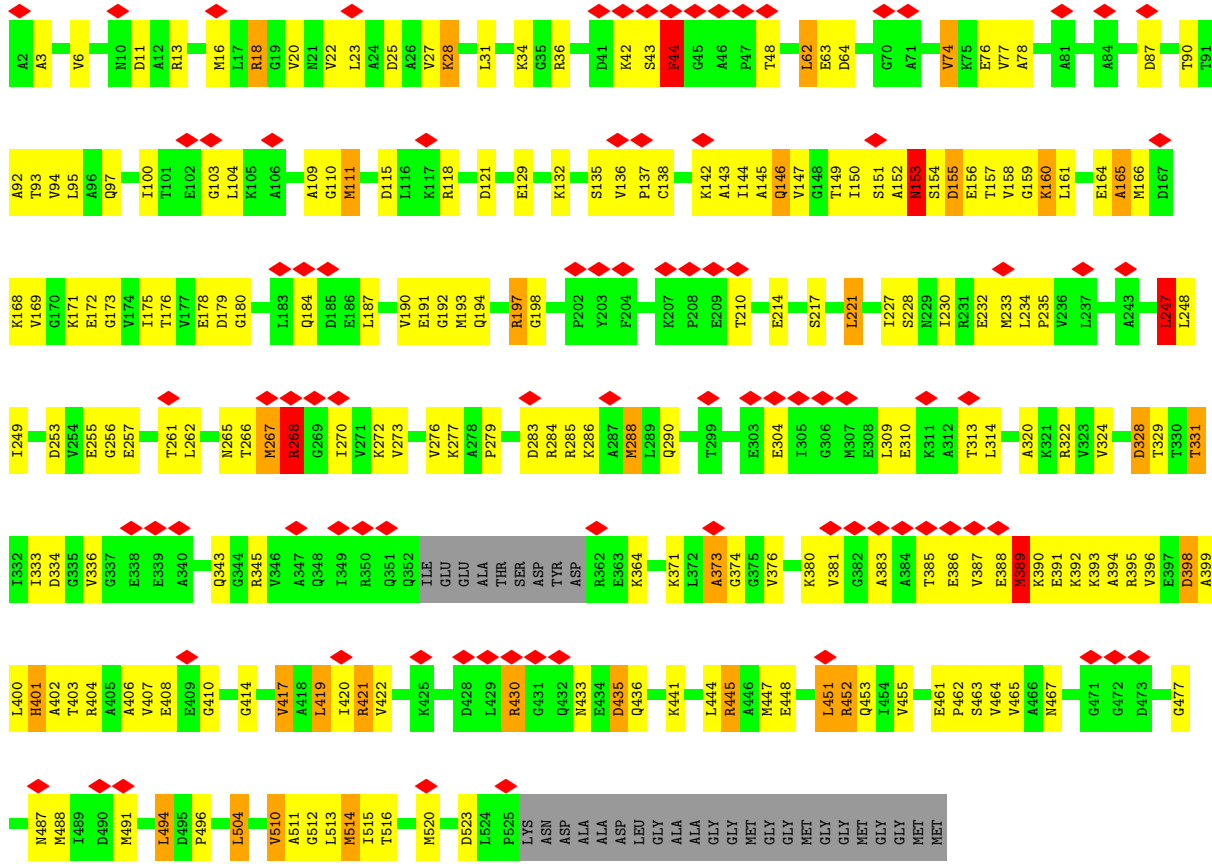


• Molecule 1: 60 KDA GROEL

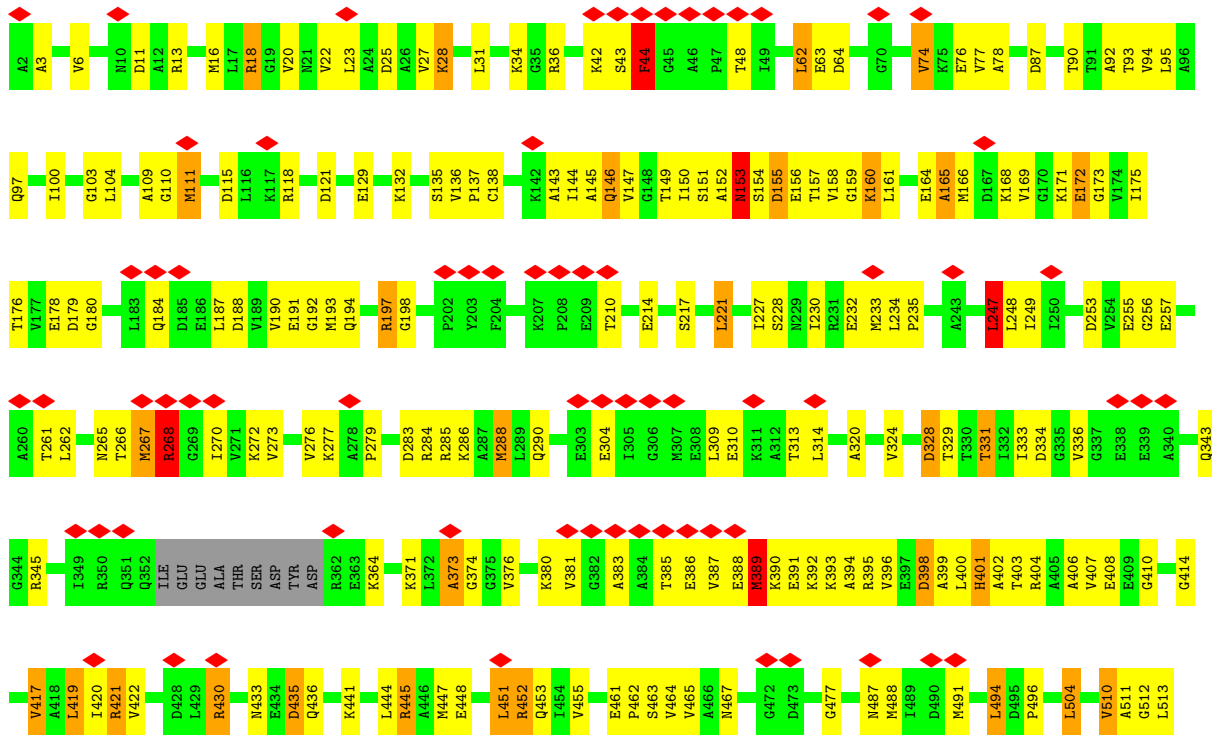


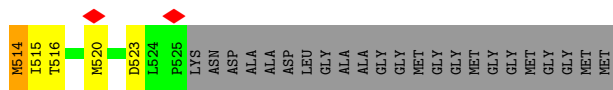
• Molecule 1: 60 KDA GROEL



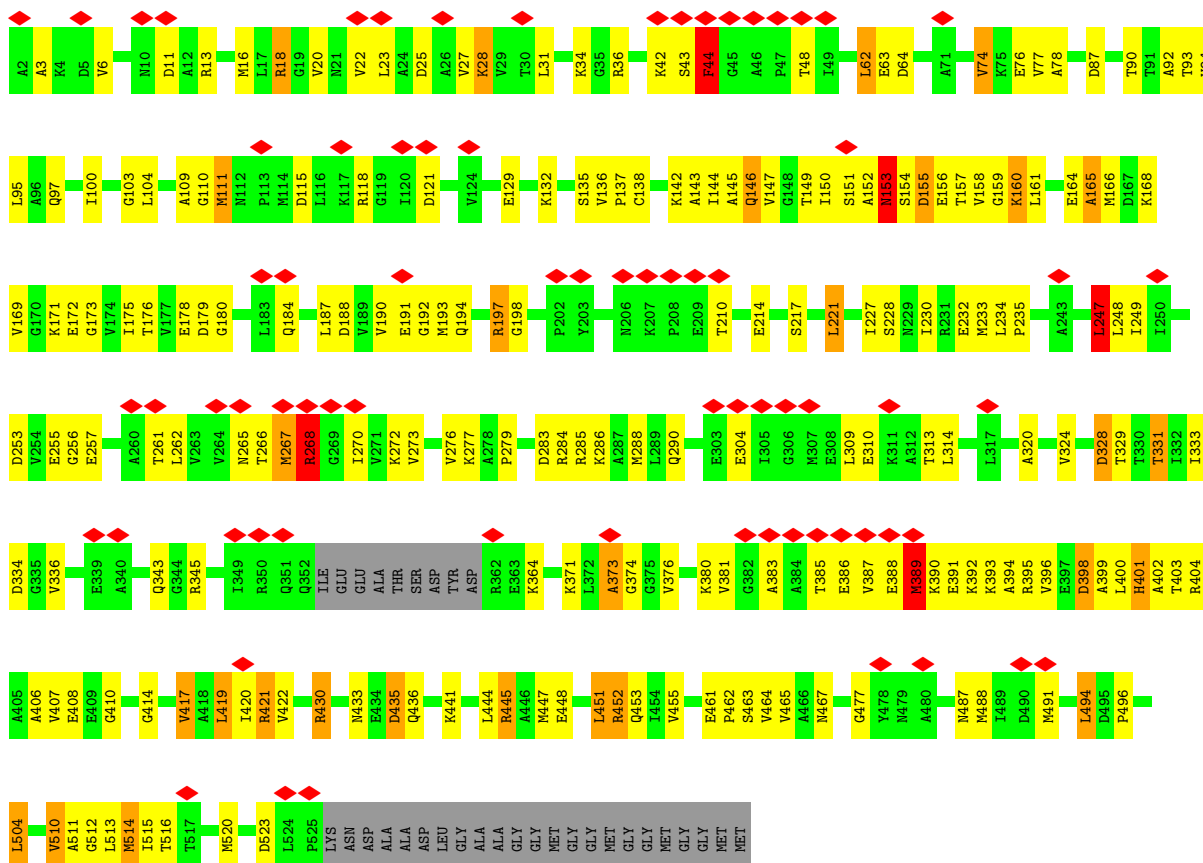


• Molecule 1: 60 KDA GROEL

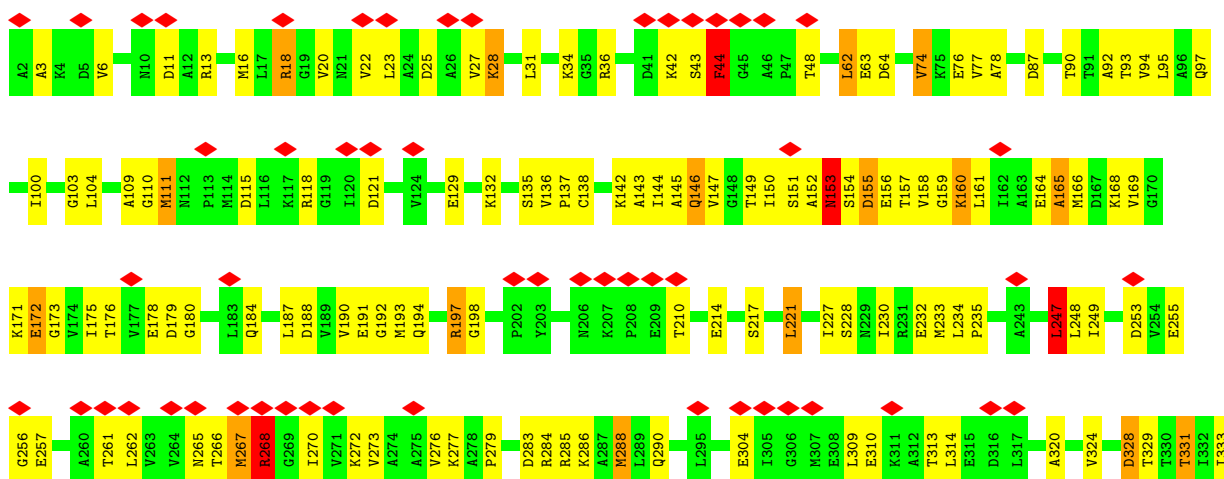


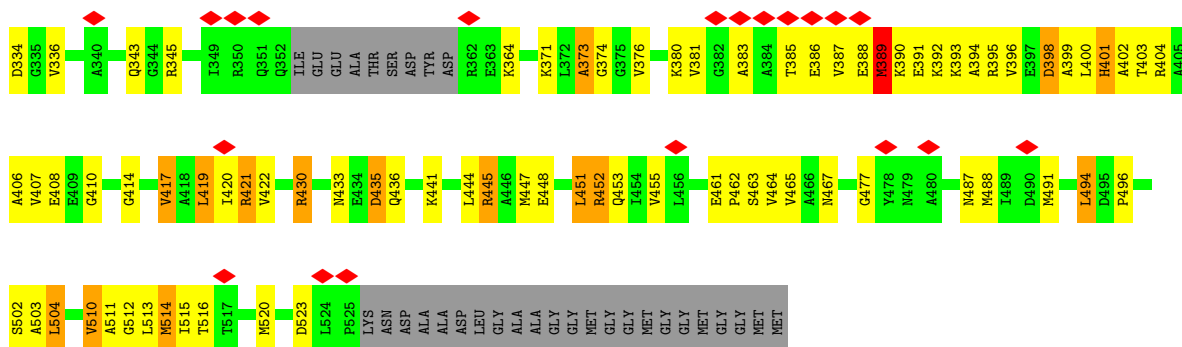


● Molecule 1: 60 KDA GROEL

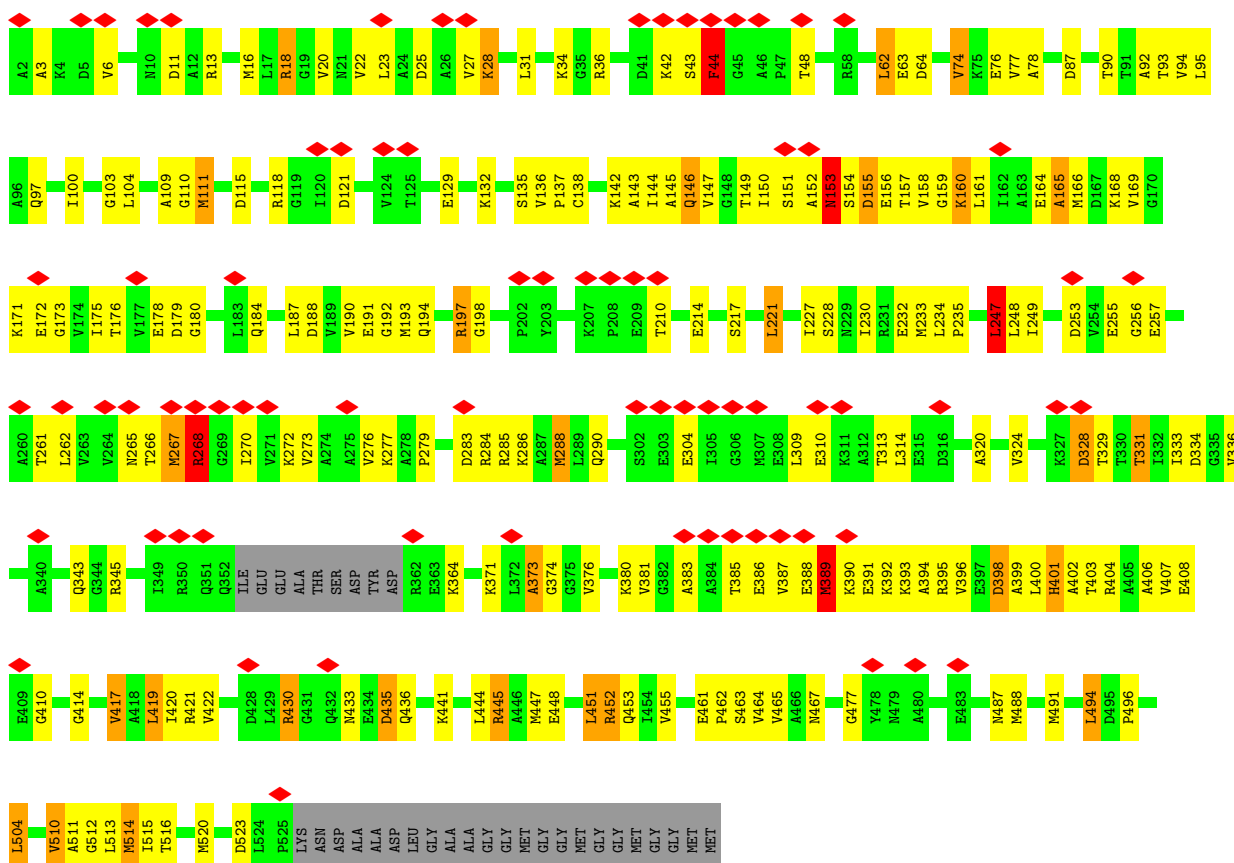


● Molecule 1: 60 KDA GROEL

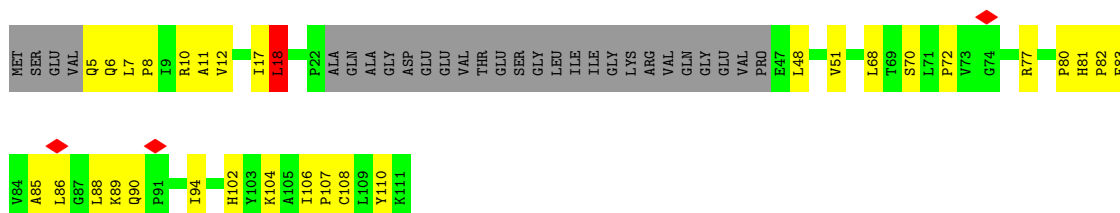




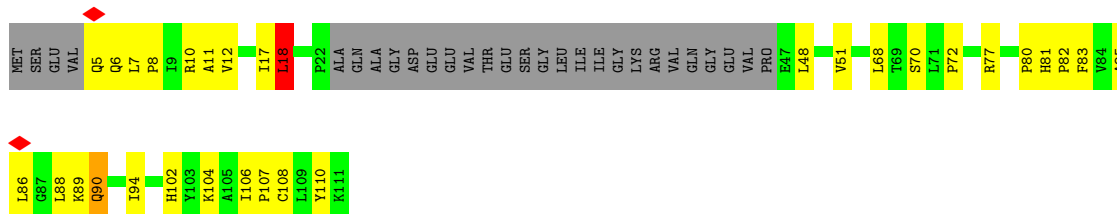
• Molecule 1: 60 KDA GROEL



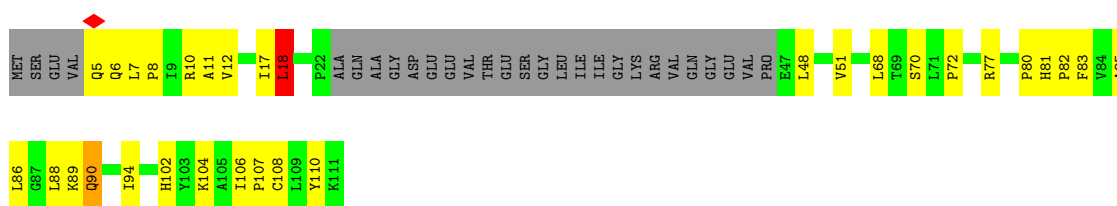
• Molecule 2: CAPSID ASSEMBLY PROTEIN GP31



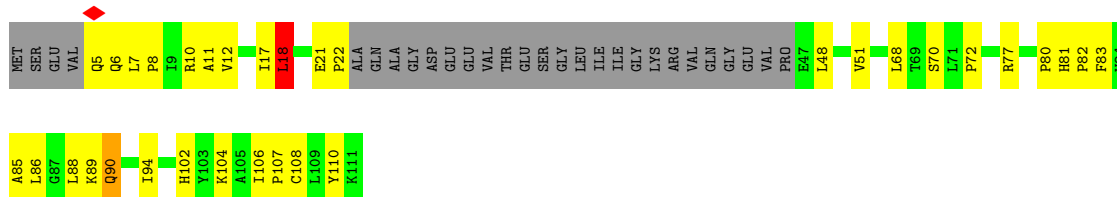
• Molecule 2: CAPSID ASSEMBLY PROTEIN GP31



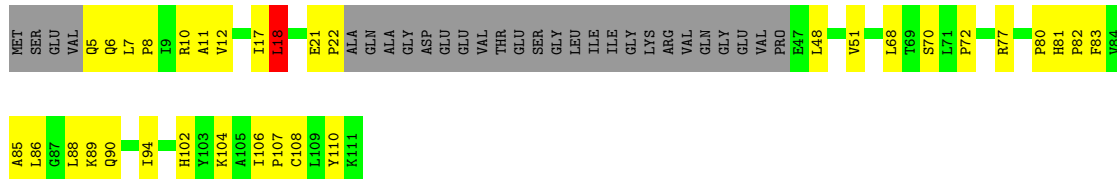
• Molecule 2: CAPSID ASSEMBLY PROTEIN GP31



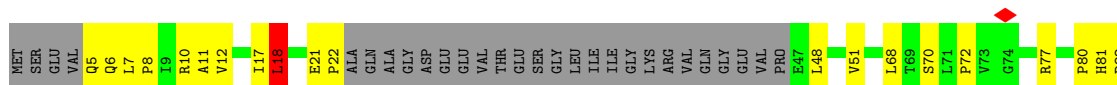
• Molecule 2: CAPSID ASSEMBLY PROTEIN GP31

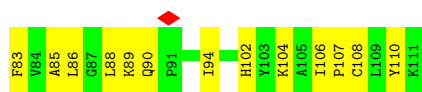


• Molecule 2: CAPSID ASSEMBLY PROTEIN GP31

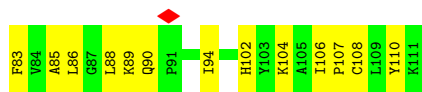
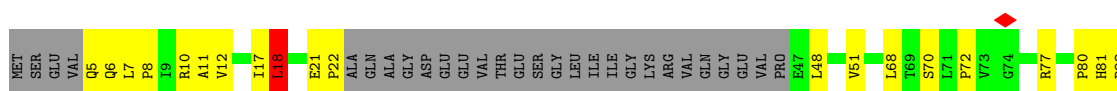


• Molecule 2: CAPSID ASSEMBLY PROTEIN GP31





• Molecule 2: CAPSID ASSEMBLY PROTEIN GP31



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D7	Depositor
Number of particles used	10300	Depositor
Resolution determination method	Not provided	
CTF correction method	FULL CORRECTION ON 2D CLASS AVERAGES	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	15	Depositor
Minimum defocus (nm)	1300	Depositor
Maximum defocus (nm)	3300	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO-163 FILM	Depositor
Maximum map value	3.471	Depositor
Minimum map value	-1.622	Depositor
Average map value	0.053	Depositor
Map value standard deviation	0.232	Depositor
Recommended contour level	0.452	Depositor
Map size (\AA)	268.8, 268.8, 268.8	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing (\AA)	1.4, 1.4, 1.4	Depositor

5 Model quality i

5.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.07	3/3882 (0.1%)	1.23	27/5240 (0.5%)
1	B	1.07	3/3882 (0.1%)	1.23	27/5240 (0.5%)
1	C	1.07	3/3882 (0.1%)	1.23	27/5240 (0.5%)
1	D	1.07	3/3882 (0.1%)	1.23	27/5240 (0.5%)
1	E	1.07	3/3882 (0.1%)	1.23	27/5240 (0.5%)
1	F	1.07	3/3882 (0.1%)	1.23	27/5240 (0.5%)
1	G	1.07	3/3882 (0.1%)	1.23	27/5240 (0.5%)
1	H	0.68	1/3806 (0.0%)	1.04	15/5130 (0.3%)
1	I	0.69	1/3806 (0.0%)	1.04	15/5130 (0.3%)
1	J	0.69	1/3806 (0.0%)	1.04	15/5130 (0.3%)
1	K	0.69	1/3806 (0.0%)	1.04	15/5130 (0.3%)
1	L	0.69	1/3806 (0.0%)	1.04	15/5130 (0.3%)
1	M	0.69	1/3806 (0.0%)	1.04	15/5130 (0.3%)
1	N	0.69	1/3806 (0.0%)	1.04	15/5130 (0.3%)
2	O	0.59	0/657	0.79	1/894 (0.1%)
2	P	0.59	0/657	0.79	1/894 (0.1%)
2	Q	0.59	0/657	0.79	1/894 (0.1%)
2	R	0.59	0/657	0.79	1/894 (0.1%)
2	S	0.59	0/657	0.79	1/894 (0.1%)
2	T	0.59	0/657	0.79	1/894 (0.1%)
2	U	0.59	0/657	0.79	1/894 (0.1%)
All	All	0.88	28/58415 (0.0%)	1.12	301/78848 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
1	J	0	1
1	K	0	1
1	L	0	1
1	M	0	1
1	N	0	1
All	All	0	14

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	191	GLU	C-N	-42.62	0.56	1.33
1	A	191	GLU	C-N	-42.60	0.56	1.33
1	C	191	GLU	C-N	-42.60	0.56	1.33
1	E	191	GLU	C-N	-42.60	0.56	1.33
1	D	191	GLU	C-N	-42.59	0.56	1.33
1	G	191	GLU	C-N	-42.59	0.56	1.33
1	B	191	GLU	C-N	-42.57	0.56	1.33
1	G	136	VAL	C-N	26.70	1.84	1.34
1	C	136	VAL	C-N	26.68	1.84	1.34
1	B	136	VAL	C-N	26.68	1.84	1.34
1	A	136	VAL	C-N	26.67	1.84	1.34
1	E	136	VAL	C-N	26.67	1.84	1.34
1	F	136	VAL	C-N	26.66	1.84	1.34
1	D	136	VAL	C-N	26.66	1.84	1.34
1	M	76	GLU	CD-OE1	5.32	1.31	1.25
1	N	76	GLU	CD-OE1	5.30	1.31	1.25
1	K	76	GLU	CD-OE1	5.29	1.31	1.25
1	H	76	GLU	CD-OE1	5.27	1.31	1.25
1	L	76	GLU	CD-OE1	5.26	1.31	1.25
1	I	76	GLU	CD-OE1	5.26	1.31	1.25
1	J	76	GLU	CD-OE1	5.23	1.31	1.25
1	E	76	GLU	CD-OE1	5.16	1.31	1.25
1	C	76	GLU	CD-OE1	5.16	1.31	1.25
1	A	76	GLU	CD-OE1	5.16	1.31	1.25
1	G	76	GLU	CD-OE1	5.15	1.31	1.25
1	D	76	GLU	CD-OE1	5.13	1.31	1.25
1	B	76	GLU	CD-OE1	5.13	1.31	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	76	GLU	CD-OE1	5.13	1.31	1.25

All (301) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	373	ALA	O-C-N	-33.61	66.06	123.20
1	H	373	ALA	O-C-N	-33.61	66.06	123.20
1	J	373	ALA	O-C-N	-33.61	66.06	123.20
1	K	373	ALA	O-C-N	-33.60	66.07	123.20
1	L	373	ALA	O-C-N	-33.60	66.07	123.20
1	M	373	ALA	O-C-N	-33.60	66.08	123.20
1	I	373	ALA	O-C-N	-33.58	66.11	123.20
1	D	373	ALA	CA-C-N	-26.40	63.40	116.20
1	G	373	ALA	CA-C-N	-26.40	63.40	116.20
1	F	373	ALA	CA-C-N	-26.39	63.41	116.20
1	A	373	ALA	CA-C-N	-26.39	63.42	116.20
1	C	373	ALA	CA-C-N	-26.39	63.42	116.20
1	E	373	ALA	CA-C-N	-26.39	63.42	116.20
1	B	373	ALA	CA-C-N	-26.38	63.44	116.20
1	G	373	ALA	C-N-CA	-25.57	68.61	122.30
1	C	373	ALA	C-N-CA	-25.57	68.61	122.30
1	D	373	ALA	C-N-CA	-25.57	68.61	122.30
1	A	373	ALA	C-N-CA	-25.56	68.62	122.30
1	F	373	ALA	C-N-CA	-25.56	68.62	122.30
1	E	373	ALA	C-N-CA	-25.55	68.64	122.30
1	B	373	ALA	C-N-CA	-25.55	68.64	122.30
1	E	373	ALA	O-C-N	23.38	162.94	123.20
1	F	373	ALA	O-C-N	23.36	162.91	123.20
1	A	373	ALA	O-C-N	23.36	162.91	123.20
1	G	373	ALA	O-C-N	23.35	162.90	123.20
1	D	373	ALA	O-C-N	23.35	162.90	123.20
1	C	373	ALA	O-C-N	23.35	162.89	123.20
1	B	373	ALA	O-C-N	23.33	162.87	123.20
1	F	191	GLU	C-N-CA	-22.34	75.38	122.30
1	D	191	GLU	C-N-CA	-22.34	75.39	122.30
1	A	191	GLU	C-N-CA	-22.33	75.40	122.30
1	B	191	GLU	C-N-CA	-22.33	75.41	122.30
1	E	191	GLU	C-N-CA	-22.33	75.41	122.30
1	C	191	GLU	C-N-CA	-22.33	75.41	122.30
1	G	191	GLU	C-N-CA	-22.33	75.41	122.30
1	M	373	ALA	C-N-CA	-21.43	77.30	122.30
1	L	373	ALA	C-N-CA	-21.43	77.31	122.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	373	ALA	C-N-CA	-21.42	77.31	122.30
1	H	373	ALA	C-N-CA	-21.42	77.32	122.30
1	K	373	ALA	C-N-CA	-21.42	77.32	122.30
1	J	373	ALA	C-N-CA	-21.41	77.33	122.30
1	N	373	ALA	C-N-CA	-21.41	77.33	122.30
1	C	191	GLU	CA-C-N	-20.16	75.89	116.20
1	F	191	GLU	CA-C-N	-20.15	75.89	116.20
1	D	191	GLU	CA-C-N	-20.15	75.90	116.20
1	A	191	GLU	CA-C-N	-20.14	75.91	116.20
1	E	191	GLU	CA-C-N	-20.14	75.92	116.20
1	G	191	GLU	CA-C-N	-20.14	75.92	116.20
1	B	191	GLU	CA-C-N	-20.12	75.95	116.20
1	B	191	GLU	O-C-N	-19.28	90.42	123.20
1	D	191	GLU	O-C-N	-19.28	90.43	123.20
1	G	191	GLU	O-C-N	-19.27	90.45	123.20
1	C	191	GLU	O-C-N	-19.26	90.46	123.20
1	E	191	GLU	O-C-N	-19.25	90.47	123.20
1	A	191	GLU	O-C-N	-19.25	90.47	123.20
1	F	191	GLU	O-C-N	-19.22	90.52	123.20
1	D	268	ARG	NE-CZ-NH2	-11.96	114.32	120.30
1	C	268	ARG	NE-CZ-NH2	-11.95	114.33	120.30
1	E	268	ARG	NE-CZ-NH2	-11.94	114.33	120.30
1	F	268	ARG	NE-CZ-NH2	-11.93	114.34	120.30
1	A	268	ARG	NE-CZ-NH2	-11.92	114.34	120.30
1	B	268	ARG	NE-CZ-NH2	-11.91	114.35	120.30
1	G	268	ARG	NE-CZ-NH2	-11.90	114.35	120.30
1	E	268	ARG	NE-CZ-NH1	11.82	126.21	120.30
1	D	268	ARG	NE-CZ-NH1	11.78	126.19	120.30
1	G	268	ARG	NE-CZ-NH1	11.78	126.19	120.30
1	C	268	ARG	NE-CZ-NH1	11.77	126.18	120.30
1	A	268	ARG	NE-CZ-NH1	11.77	126.18	120.30
1	F	268	ARG	NE-CZ-NH1	11.74	126.17	120.30
1	B	268	ARG	NE-CZ-NH1	11.70	126.15	120.30
1	C	136	VAL	CA-C-N	-11.26	85.57	117.10
1	G	136	VAL	CA-C-N	-11.26	85.56	117.10
1	F	136	VAL	CA-C-N	-11.26	85.58	117.10
1	A	136	VAL	CA-C-N	-11.25	85.59	117.10
1	D	136	VAL	CA-C-N	-11.25	85.60	117.10
1	K	373	ALA	CA-C-N	-11.25	93.70	116.20
1	E	136	VAL	CA-C-N	-11.25	85.61	117.10
1	B	136	VAL	CA-C-N	-11.24	85.61	117.10
1	H	373	ALA	CA-C-N	-11.24	93.72	116.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	373	ALA	CA-C-N	-11.24	93.73	116.20
1	J	373	ALA	CA-C-N	-11.23	93.73	116.20
1	L	373	ALA	CA-C-N	-11.23	93.73	116.20
1	N	373	ALA	CA-C-N	-11.23	93.74	116.20
1	M	373	ALA	CA-C-N	-11.22	93.76	116.20
1	J	523	ASP	CB-CG-OD2	8.99	126.39	118.30
1	K	523	ASP	CB-CG-OD2	8.99	126.39	118.30
1	G	136	VAL	C-N-CA	-8.98	84.28	122.00
1	C	136	VAL	C-N-CA	-8.98	84.30	122.00
1	A	136	VAL	C-N-CA	-8.97	84.31	122.00
1	B	136	VAL	C-N-CA	-8.97	84.31	122.00
1	D	136	VAL	C-N-CA	-8.97	84.31	122.00
1	F	136	VAL	C-N-CA	-8.97	84.31	122.00
1	E	136	VAL	C-N-CA	-8.97	84.32	122.00
1	I	523	ASP	CB-CG-OD2	8.97	126.37	118.30
1	N	523	ASP	CB-CG-OD2	8.95	126.35	118.30
1	H	523	ASP	CB-CG-OD2	8.94	126.35	118.30
1	L	523	ASP	CB-CG-OD2	8.93	126.34	118.30
1	M	523	ASP	CB-CG-OD2	8.92	126.33	118.30
1	F	523	ASP	CB-CG-OD2	8.79	126.21	118.30
1	A	523	ASP	CB-CG-OD2	8.78	126.20	118.30
1	G	523	ASP	CB-CG-OD2	8.77	126.20	118.30
1	D	523	ASP	CB-CG-OD2	8.75	126.18	118.30
1	C	523	ASP	CB-CG-OD2	8.75	126.17	118.30
1	B	523	ASP	CB-CG-OD2	8.74	126.17	118.30
1	E	523	ASP	CB-CG-OD2	8.74	126.16	118.30
1	B	197	ARG	NE-CZ-NH2	-8.72	115.94	120.30
1	G	197	ARG	NE-CZ-NH2	-8.72	115.94	120.30
1	D	197	ARG	NE-CZ-NH2	-8.67	115.97	120.30
1	F	197	ARG	NE-CZ-NH2	-8.64	115.98	120.30
1	A	197	ARG	NE-CZ-NH2	-8.61	116.00	120.30
1	E	197	ARG	NE-CZ-NH2	-8.57	116.01	120.30
1	C	197	ARG	NE-CZ-NH2	-8.55	116.02	120.30
1	G	197	ARG	NE-CZ-NH1	7.60	124.10	120.30
1	B	197	ARG	NE-CZ-NH1	7.60	124.10	120.30
1	D	197	ARG	NE-CZ-NH1	7.54	124.07	120.30
1	A	197	ARG	NE-CZ-NH1	7.54	124.07	120.30
1	F	197	ARG	NE-CZ-NH1	7.54	124.07	120.30
1	E	197	ARG	NE-CZ-NH1	7.51	124.06	120.30
1	C	197	ARG	NE-CZ-NH1	7.49	124.04	120.30
1	M	11	ASP	CB-CG-OD2	7.15	124.74	118.30
1	J	11	ASP	CB-CG-OD2	7.14	124.72	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	11	ASP	CB-CG-OD2	7.13	124.72	118.30
1	H	11	ASP	CB-CG-OD2	7.13	124.72	118.30
1	D	11	ASP	CB-CG-OD2	7.12	124.71	118.30
1	N	11	ASP	CB-CG-OD2	7.12	124.71	118.30
1	F	11	ASP	CB-CG-OD2	7.11	124.70	118.30
1	K	11	ASP	CB-CG-OD2	7.10	124.69	118.30
1	I	11	ASP	CB-CG-OD2	7.10	124.69	118.30
1	B	11	ASP	CB-CG-OD2	7.08	124.67	118.30
1	E	11	ASP	CB-CG-OD2	7.08	124.67	118.30
1	A	11	ASP	CB-CG-OD2	7.07	124.66	118.30
1	C	11	ASP	CB-CG-OD2	7.07	124.66	118.30
1	G	11	ASP	CB-CG-OD2	7.07	124.66	118.30
1	E	115	ASP	CB-CG-OD2	6.85	124.46	118.30
1	C	115	ASP	CB-CG-OD2	6.85	124.46	118.30
1	G	115	ASP	CB-CG-OD2	6.83	124.45	118.30
1	A	115	ASP	CB-CG-OD2	6.83	124.44	118.30
1	B	115	ASP	CB-CG-OD2	6.82	124.44	118.30
1	F	115	ASP	CB-CG-OD2	6.82	124.43	118.30
1	D	115	ASP	CB-CG-OD2	6.81	124.43	118.30
1	I	115	ASP	CB-CG-OD2	6.76	124.38	118.30
1	L	115	ASP	CB-CG-OD2	6.75	124.38	118.30
1	J	115	ASP	CB-CG-OD2	6.74	124.37	118.30
1	K	115	ASP	CB-CG-OD2	6.74	124.37	118.30
1	H	115	ASP	CB-CG-OD2	6.73	124.36	118.30
1	M	115	ASP	CB-CG-OD2	6.71	124.34	118.30
1	N	115	ASP	CB-CG-OD2	6.71	124.34	118.30
1	I	64	ASP	CB-CG-OD2	6.67	124.31	118.30
1	J	64	ASP	CB-CG-OD2	6.66	124.29	118.30
1	L	64	ASP	CB-CG-OD2	6.66	124.29	118.30
1	N	64	ASP	CB-CG-OD2	6.66	124.29	118.30
1	H	64	ASP	CB-CG-OD2	6.65	124.29	118.30
1	M	64	ASP	CB-CG-OD2	6.65	124.29	118.30
1	B	64	ASP	CB-CG-OD2	6.65	124.28	118.30
1	D	64	ASP	CB-CG-OD2	6.64	124.28	118.30
1	E	64	ASP	CB-CG-OD2	6.64	124.28	118.30
1	A	64	ASP	CB-CG-OD2	6.64	124.27	118.30
1	K	64	ASP	CB-CG-OD2	6.64	124.27	118.30
1	F	64	ASP	CB-CG-OD2	6.63	124.27	118.30
1	G	64	ASP	CB-CG-OD2	6.62	124.26	118.30
1	C	64	ASP	CB-CG-OD2	6.61	124.25	118.30
1	E	121	ASP	CB-CG-OD1	6.54	124.19	118.30
1	J	121	ASP	CB-CG-OD1	6.53	124.18	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	435	ASP	CB-CG-OD2	6.51	124.16	118.30
1	N	121	ASP	CB-CG-OD1	6.50	124.15	118.30
1	K	435	ASP	CB-CG-OD2	6.50	124.15	118.30
1	J	435	ASP	CB-CG-OD2	6.50	124.15	118.30
1	I	435	ASP	CB-CG-OD2	6.50	124.15	118.30
1	K	121	ASP	CB-CG-OD1	6.50	124.15	118.30
1	A	435	ASP	CB-CG-OD2	6.49	124.14	118.30
1	E	435	ASP	CB-CG-OD2	6.49	124.14	118.30
1	F	121	ASP	CB-CG-OD1	6.49	124.14	118.30
1	H	435	ASP	CB-CG-OD2	6.49	124.14	118.30
1	L	435	ASP	CB-CG-OD2	6.49	124.14	118.30
1	D	121	ASP	CB-CG-OD1	6.49	124.14	118.30
1	F	435	ASP	CB-CG-OD2	6.49	124.14	118.30
1	D	435	ASP	CB-CG-OD2	6.48	124.13	118.30
1	N	435	ASP	CB-CG-OD2	6.48	124.14	118.30
1	C	435	ASP	CB-CG-OD2	6.48	124.13	118.30
1	G	435	ASP	CB-CG-OD2	6.48	124.13	118.30
1	L	121	ASP	CB-CG-OD1	6.48	124.13	118.30
1	H	121	ASP	CB-CG-OD1	6.48	124.13	118.30
1	G	121	ASP	CB-CG-OD1	6.47	124.12	118.30
1	A	121	ASP	CB-CG-OD1	6.47	124.12	118.30
1	M	435	ASP	CB-CG-OD2	6.47	124.12	118.30
1	B	121	ASP	CB-CG-OD1	6.45	124.10	118.30
1	C	121	ASP	CB-CG-OD1	6.45	124.10	118.30
1	I	268	ARG	NE-CZ-NH1	-6.44	117.08	120.30
1	K	268	ARG	NE-CZ-NH1	-6.44	117.08	120.30
1	M	121	ASP	CB-CG-OD1	6.43	124.09	118.30
1	I	121	ASP	CB-CG-OD1	6.42	124.08	118.30
1	L	268	ARG	NE-CZ-NH1	-6.42	117.09	120.30
1	N	268	ARG	NE-CZ-NH1	-6.38	117.11	120.30
1	J	268	ARG	NE-CZ-NH1	-6.38	117.11	120.30
1	H	268	ARG	NE-CZ-NH1	-6.37	117.11	120.30
1	F	334	ASP	CB-CG-OD2	6.33	124.00	118.30
1	G	334	ASP	CB-CG-OD2	6.33	124.00	118.30
1	N	268	ARG	NE-CZ-NH2	6.33	123.47	120.30
1	M	268	ARG	NE-CZ-NH2	6.33	123.46	120.30
1	E	334	ASP	CB-CG-OD2	6.31	123.98	118.30
1	L	268	ARG	NE-CZ-NH2	6.30	123.45	120.30
1	A	334	ASP	CB-CG-OD2	6.30	123.97	118.30
1	M	268	ARG	NE-CZ-NH1	-6.28	117.16	120.30
1	K	268	ARG	NE-CZ-NH2	6.27	123.44	120.30
1	D	334	ASP	CB-CG-OD2	6.27	123.94	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	334	ASP	CB-CG-OD2	6.27	123.94	118.30
1	H	268	ARG	NE-CZ-NH2	6.27	123.43	120.30
1	I	268	ARG	NE-CZ-NH2	6.26	123.43	120.30
1	B	334	ASP	CB-CG-OD2	6.26	123.93	118.30
1	J	268	ARG	NE-CZ-NH2	6.23	123.41	120.30
1	G	283	ASP	CB-CG-OD2	5.93	123.64	118.30
1	E	283	ASP	CB-CG-OD2	5.92	123.63	118.30
1	D	283	ASP	CB-CG-OD2	5.90	123.61	118.30
1	A	283	ASP	CB-CG-OD2	5.90	123.61	118.30
1	B	283	ASP	CB-CG-OD2	5.89	123.60	118.30
1	C	283	ASP	CB-CG-OD2	5.87	123.59	118.30
1	F	283	ASP	CB-CG-OD2	5.86	123.57	118.30
1	C	136	VAL	O-C-N	-5.55	110.56	121.10
1	E	136	VAL	O-C-N	-5.55	110.56	121.10
1	G	136	VAL	O-C-N	-5.54	110.57	121.10
1	D	136	VAL	O-C-N	-5.54	110.58	121.10
1	A	136	VAL	O-C-N	-5.54	110.58	121.10
1	F	136	VAL	O-C-N	-5.53	110.59	121.10
1	B	136	VAL	O-C-N	-5.53	110.59	121.10
1	F	188	ASP	CB-CG-OD2	5.53	123.28	118.30
1	D	188	ASP	CB-CG-OD2	5.52	123.27	118.30
1	E	188	ASP	CB-CG-OD2	5.52	123.27	118.30
1	F	268	ARG	CD-NE-CZ	5.52	131.32	123.60
1	B	268	ARG	CD-NE-CZ	5.51	131.32	123.60
1	G	268	ARG	CD-NE-CZ	5.51	131.31	123.60
1	C	268	ARG	CD-NE-CZ	5.51	131.31	123.60
1	B	188	ASP	CB-CG-OD2	5.50	123.25	118.30
1	A	268	ARG	CD-NE-CZ	5.50	131.29	123.60
1	G	188	ASP	CB-CG-OD2	5.49	123.24	118.30
1	D	268	ARG	CD-NE-CZ	5.49	131.28	123.60
1	A	188	ASP	CB-CG-OD2	5.48	123.23	118.30
1	N	253	ASP	CB-CG-OD2	5.48	123.23	118.30
1	E	268	ARG	CD-NE-CZ	5.47	131.26	123.60
1	C	188	ASP	CB-CG-OD2	5.47	123.22	118.30
1	F	328	ASP	CB-CG-OD2	5.46	123.22	118.30
1	J	253	ASP	CB-CG-OD2	5.46	123.21	118.30
1	M	253	ASP	CB-CG-OD2	5.46	123.21	118.30
1	L	253	ASP	CB-CG-OD2	5.45	123.20	118.30
1	I	253	ASP	CB-CG-OD2	5.44	123.20	118.30
1	H	253	ASP	CB-CG-OD2	5.44	123.19	118.30
1	K	253	ASP	CB-CG-OD2	5.43	123.19	118.30
1	L	247	LEU	CA-CB-CG	5.42	127.76	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	328	ASP	CB-CG-OD2	5.40	123.16	118.30
1	I	247	LEU	CA-CB-CG	5.40	127.72	115.30
1	A	328	ASP	CB-CG-OD2	5.40	123.16	118.30
1	G	328	ASP	CB-CG-OD2	5.40	123.16	118.30
1	K	247	LEU	CA-CB-CG	5.40	127.71	115.30
1	H	247	LEU	CA-CB-CG	5.39	127.70	115.30
1	M	247	LEU	CA-CB-CG	5.39	127.70	115.30
1	N	247	LEU	CA-CB-CG	5.39	127.70	115.30
1	J	247	LEU	CA-CB-CG	5.39	127.70	115.30
1	C	328	ASP	CB-CG-OD2	5.38	123.14	118.30
1	E	328	ASP	CB-CG-OD2	5.38	123.14	118.30
1	B	328	ASP	CB-CG-OD2	5.37	123.13	118.30
1	K	328	ASP	CB-CG-OD2	5.30	123.07	118.30
1	M	328	ASP	CB-CG-OD2	5.30	123.07	118.30
1	N	328	ASP	CB-CG-OD2	5.30	123.07	118.30
1	H	283	ASP	CB-CG-OD2	5.30	123.07	118.30
1	L	328	ASP	CB-CG-OD2	5.30	123.07	118.30
1	D	224	ASP	CB-CG-OD2	5.29	123.06	118.30
1	C	224	ASP	CB-CG-OD2	5.29	123.06	118.30
1	K	283	ASP	CB-CG-OD2	5.28	123.05	118.30
1	L	283	ASP	CB-CG-OD2	5.28	123.05	118.30
1	A	224	ASP	CB-CG-OD2	5.28	123.05	118.30
1	J	283	ASP	CB-CG-OD2	5.28	123.05	118.30
1	H	328	ASP	CB-CG-OD2	5.27	123.05	118.30
1	E	224	ASP	CB-CG-OD2	5.27	123.04	118.30
1	M	283	ASP	CB-CG-OD2	5.27	123.04	118.30
1	I	283	ASP	CB-CG-OD2	5.27	123.04	118.30
1	J	328	ASP	CB-CG-OD2	5.26	123.03	118.30
1	N	283	ASP	CB-CG-OD2	5.26	123.03	118.30
1	F	224	ASP	CB-CG-OD2	5.24	123.02	118.30
1	I	328	ASP	CB-CG-OD2	5.24	123.01	118.30
2	R	18	LEU	CA-CB-CG	5.23	127.33	115.30
2	P	18	LEU	CA-CB-CG	5.23	127.33	115.30
2	S	18	LEU	CA-CB-CG	5.23	127.33	115.30
2	Q	18	LEU	CA-CB-CG	5.23	127.32	115.30
2	O	18	LEU	CA-CB-CG	5.22	127.32	115.30
2	T	18	LEU	CA-CB-CG	5.22	127.31	115.30
1	B	224	ASP	CB-CG-OD2	5.22	123.00	118.30
1	G	224	ASP	CB-CG-OD2	5.22	122.99	118.30
2	U	18	LEU	CA-CB-CG	5.22	127.30	115.30
1	B	253	ASP	CB-CG-OD2	5.16	122.94	118.30
1	F	253	ASP	CB-CG-OD2	5.15	122.94	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	253	ASP	CB-CG-OD2	5.14	122.93	118.30
1	C	253	ASP	CB-CG-OD2	5.14	122.93	118.30
1	A	253	ASP	CB-CG-OD2	5.12	122.91	118.30
1	G	253	ASP	CB-CG-OD2	5.12	122.90	118.30
1	D	253	ASP	CB-CG-OD2	5.10	122.89	118.30
1	G	359	ASP	CB-CG-OD2	5.10	122.89	118.30
1	B	359	ASP	CB-CG-OD2	5.09	122.88	118.30
1	C	359	ASP	CB-CG-OD2	5.09	122.88	118.30
1	A	359	ASP	CB-CG-OD2	5.07	122.86	118.30
1	D	359	ASP	CB-CG-OD2	5.06	122.86	118.30
1	F	359	ASP	CB-CG-OD2	5.05	122.85	118.30
1	E	359	ASP	CB-CG-OD2	5.04	122.83	118.30

There are no chirality outliers.

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	191	GLU	Mainchain
1	B	191	GLU	Mainchain
1	C	191	GLU	Mainchain
1	D	191	GLU	Mainchain
1	E	191	GLU	Mainchain
1	F	191	GLU	Mainchain
1	G	191	GLU	Mainchain
1	H	373	ALA	Mainchain
1	I	373	ALA	Mainchain
1	J	373	ALA	Mainchain
1	K	373	ALA	Mainchain
1	L	373	ALA	Mainchain
1	M	373	ALA	Mainchain
1	N	373	ALA	Mainchain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3855	0	3971	193	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3855	0	3971	194	0
1	C	3855	0	3971	197	0
1	D	3855	0	3971	189	0
1	E	3855	0	3971	199	0
1	F	3855	0	3971	196	0
1	G	3855	0	3971	198	0
1	H	3783	0	3916	226	0
1	I	3783	0	3916	233	0
1	J	3783	0	3916	229	0
1	K	3783	0	3916	234	0
1	L	3783	0	3916	228	0
1	M	3783	0	3916	236	0
1	N	3783	0	3916	234	0
2	O	641	0	652	60	0
2	P	641	0	652	61	0
2	Q	641	0	652	61	0
2	R	641	0	652	61	0
2	S	641	0	652	60	0
2	T	641	0	652	60	0
2	U	641	0	652	61	0
All	All	57953	0	59773	2885	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 25.

All (2885) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:138:CYS:CB	1:L:410:GLY:HA2	1.38	1.52
1:K:138:CYS:CB	1:K:410:GLY:HA2	1.38	1.51
1:N:138:CYS:CB	1:N:410:GLY:HA2	1.38	1.51
1:M:138:CYS:CB	1:M:410:GLY:HA2	1.38	1.50
1:H:138:CYS:CB	1:H:410:GLY:HA2	1.38	1.49
1:I:138:CYS:CB	1:I:410:GLY:HA2	1.38	1.49
1:L:135:SER:HG	1:L:137:PRO:N	1.11	1.49
1:K:135:SER:HG	1:K:137:PRO:N	1.11	1.48
1:E:464:VAL:HG21	1:L:467:ASN:ND2	1.18	1.48
1:L:138:CYS:HB2	1:L:410:GLY:CA	1.42	1.48
1:C:464:VAL:CG2	1:J:467:ASN:HD22	1.27	1.48
1:N:138:CYS:HB2	1:N:410:GLY:CA	1.42	1.48
1:A:464:VAL:CG2	1:H:467:ASN:HD22	1.27	1.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:138:CYS:CB	1:J:410:GLY:HA2	1.38	1.47
1:F:464:VAL:CG2	1:M:467:ASN:HD22	1.27	1.47
1:D:464:VAL:HG21	1:K:467:ASN:ND2	1.18	1.46
1:G:146:GLN:NE2	1:G:494:LEU:HD11	1.30	1.46
1:A:146:GLN:NE2	1:A:494:LEU:HD11	1.30	1.46
1:H:135:SER:HG	1:H:137:PRO:N	1.13	1.46
1:H:138:CYS:HB2	1:H:410:GLY:CA	1.42	1.46
1:I:138:CYS:HB2	1:I:410:GLY:CA	1.42	1.46
1:E:464:VAL:CG2	1:L:467:ASN:HD22	1.27	1.46
1:J:138:CYS:HB2	1:J:410:GLY:CA	1.42	1.46
1:M:138:CYS:HB2	1:M:410:GLY:CA	1.42	1.46
1:D:464:VAL:CG2	1:K:467:ASN:HD22	1.27	1.45
1:G:464:VAL:CB	1:N:467:ASN:HD22	1.29	1.45
1:C:464:VAL:CB	1:J:467:ASN:HD22	1.29	1.45
1:I:135:SER:HG	1:I:137:PRO:N	1.12	1.45
1:A:464:VAL:CB	1:H:467:ASN:HD22	1.29	1.45
1:C:464:VAL:HG21	1:J:467:ASN:ND2	1.18	1.45
1:G:464:VAL:CG2	1:N:467:ASN:ND2	1.80	1.45
1:M:135:SER:HG	1:M:137:PRO:N	1.13	1.45
1:C:464:VAL:CG2	1:J:467:ASN:ND2	1.80	1.45
1:F:464:VAL:HG21	1:M:467:ASN:ND2	1.18	1.45
1:K:138:CYS:HB2	1:K:410:GLY:CA	1.42	1.44
1:B:146:GLN:NE2	1:B:494:LEU:HD11	1.30	1.44
1:G:464:VAL:CG2	1:N:467:ASN:HD22	1.27	1.44
1:B:464:VAL:CG2	1:I:467:ASN:HD22	1.27	1.44
1:B:464:VAL:CB	1:I:467:ASN:HD22	1.29	1.43
1:D:464:VAL:CG2	1:K:467:ASN:ND2	1.80	1.43
1:F:146:GLN:NE2	1:F:494:LEU:HD11	1.30	1.43
1:E:464:VAL:CB	1:L:467:ASN:HD22	1.29	1.43
1:A:464:VAL:CG2	1:H:467:ASN:ND2	1.80	1.43
1:C:146:GLN:NE2	1:C:494:LEU:HD11	1.30	1.42
1:G:464:VAL:HG21	1:N:467:ASN:ND2	1.18	1.42
1:D:464:VAL:CB	1:K:467:ASN:HD22	1.29	1.42
1:J:135:SER:HG	1:J:137:PRO:N	1.11	1.42
1:A:464:VAL:HG21	1:H:467:ASN:ND2	1.18	1.41
1:B:464:VAL:HG21	1:I:467:ASN:ND2	1.18	1.41
1:F:464:VAL:CB	1:M:467:ASN:HD22	1.29	1.41
1:E:146:GLN:NE2	1:E:494:LEU:HD11	1.30	1.40
1:E:464:VAL:CG2	1:L:467:ASN:ND2	1.80	1.40
1:N:135:SER:HG	1:N:137:PRO:N	1.14	1.40
1:B:464:VAL:CG2	1:I:467:ASN:ND2	1.80	1.39

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:146:GLN:NE2	1:D:494:LEU:HD11	1.30	1.39
1:N:150:ILE:CD1	1:N:494:LEU:O	1.71	1.38
1:H:150:ILE:CD1	1:H:494:LEU:O	1.71	1.38
1:M:150:ILE:CD1	1:M:494:LEU:O	1.71	1.37
1:F:464:VAL:CG2	1:M:467:ASN:ND2	1.80	1.37
1:K:150:ILE:CD1	1:K:494:LEU:O	1.71	1.36
1:I:150:ILE:CD1	1:I:494:LEU:O	1.71	1.35
1:J:150:ILE:CD1	1:J:494:LEU:O	1.71	1.35
1:L:150:ILE:CD1	1:L:494:LEU:O	1.71	1.34
1:I:136:VAL:CA	1:I:137:PRO:HD2	1.59	1.32
1:H:136:VAL:CA	1:H:137:PRO:HD2	1.59	1.32
1:E:136:VAL:C	1:E:137:PRO:N	1.84	1.31
1:D:136:VAL:C	1:D:137:PRO:N	1.84	1.30
1:N:136:VAL:CA	1:N:137:PRO:HD2	1.59	1.30
1:F:136:VAL:C	1:F:137:PRO:N	1.84	1.30
1:D:464:VAL:HG21	1:K:467:ASN:CG	1.50	1.30
1:E:464:VAL:HG21	1:L:467:ASN:CG	1.50	1.30
1:C:136:VAL:C	1:C:137:PRO:N	1.84	1.29
1:A:464:VAL:HG21	1:H:467:ASN:CG	1.50	1.28
1:F:464:VAL:HG21	1:M:467:ASN:CG	1.50	1.28
1:G:464:VAL:HG21	1:N:467:ASN:CG	1.50	1.28
1:M:136:VAL:CA	1:M:137:PRO:HD2	1.59	1.28
1:B:464:VAL:HG21	1:I:467:ASN:CG	1.50	1.28
1:G:136:VAL:C	1:G:137:PRO:N	1.85	1.28
1:D:203:TYR:OH	1:E:286:LYS:HD3	1.31	1.27
1:B:203:TYR:OH	1:C:286:LYS:HD3	1.31	1.27
1:L:136:VAL:CA	1:L:137:PRO:HD2	1.59	1.26
1:A:286:LYS:HD3	1:G:203:TYR:OH	1.31	1.26
1:C:464:VAL:HG21	1:J:467:ASN:CG	1.50	1.26
1:F:203:TYR:OH	1:G:286:LYS:HD3	1.31	1.26
1:B:136:VAL:C	1:B:137:PRO:N	1.84	1.25
1:I:191:GLU:O	1:I:334:ASP:HA	1.09	1.25
1:K:136:VAL:CA	1:K:137:PRO:HD2	1.59	1.25
1:A:136:VAL:C	1:A:137:PRO:N	1.84	1.24
1:C:464:VAL:CB	1:J:467:ASN:ND2	1.98	1.24
1:F:464:VAL:CB	1:M:467:ASN:ND2	1.98	1.24
1:A:203:TYR:OH	1:B:286:LYS:HD3	1.31	1.24
1:C:203:TYR:OH	1:D:286:LYS:HD3	1.31	1.24
1:H:191:GLU:O	1:H:334:ASP:HA	1.09	1.24
1:J:191:GLU:O	1:J:334:ASP:HA	1.09	1.23
1:E:203:TYR:OH	1:F:286:LYS:HD3	1.31	1.22

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:136:VAL:CA	1:J:137:PRO:HD2	1.59	1.22
1:K:136:VAL:HA	1:K:137:PRO:CD	1.68	1.22
1:L:136:VAL:HA	1:L:137:PRO:CD	1.68	1.22
1:M:191:GLU:O	1:M:334:ASP:HA	1.09	1.22
1:N:191:GLU:O	1:N:334:ASP:HA	1.09	1.22
1:J:136:VAL:HA	1:J:137:PRO:CD	1.68	1.22
1:G:464:VAL:CB	1:N:467:ASN:ND2	1.98	1.21
1:H:136:VAL:HA	1:H:137:PRO:CD	1.68	1.21
1:I:136:VAL:HA	1:I:137:PRO:CD	1.68	1.21
1:K:191:GLU:O	1:K:334:ASP:HA	1.09	1.21
1:L:191:GLU:O	1:L:334:ASP:HA	1.09	1.21
1:M:136:VAL:HA	1:M:137:PRO:CD	1.68	1.21
1:D:464:VAL:CB	1:K:467:ASN:ND2	1.98	1.20
1:N:136:VAL:HA	1:N:137:PRO:CD	1.68	1.20
1:L:18:ARG:HH11	1:L:18:ARG:CB	1.55	1.20
1:E:464:VAL:CB	1:L:467:ASN:ND2	1.98	1.19
1:J:138:CYS:CB	1:J:410:GLY:CA	2.08	1.19
1:N:18:ARG:HH11	1:N:18:ARG:CB	1.55	1.19
1:E:18:ARG:HH11	1:E:18:ARG:CB	1.55	1.19
1:I:147:VAL:HG23	1:I:496:PRO:HG3	1.21	1.19
1:K:18:ARG:HH11	1:K:18:ARG:CB	1.55	1.19
1:C:18:ARG:HH11	1:C:18:ARG:CB	1.55	1.18
1:I:18:ARG:HH11	1:I:18:ARG:CB	1.55	1.18
1:J:18:ARG:HH11	1:J:18:ARG:CB	1.55	1.18
1:H:147:VAL:HG23	1:H:496:PRO:HG3	1.21	1.18
1:E:172:GLU:OE2	1:E:350:ARG:HG3	1.44	1.18
1:B:18:ARG:HH11	1:B:18:ARG:CB	1.55	1.18
1:G:18:ARG:HH11	1:G:18:ARG:CB	1.55	1.18
1:H:138:CYS:CB	1:H:410:GLY:CA	2.08	1.18
1:M:18:ARG:HH11	1:M:18:ARG:CB	1.55	1.18
1:L:147:VAL:HG23	1:L:496:PRO:HG3	1.21	1.17
1:M:138:CYS:CB	1:M:410:GLY:CA	2.08	1.17
1:D:18:ARG:HH11	1:D:18:ARG:CB	1.55	1.17
1:J:516:THR:O	1:K:36:ARG:NH1	1.78	1.17
1:A:464:VAL:CG1	1:H:467:ASN:HD22	1.58	1.17
1:C:464:VAL:CG1	1:J:467:ASN:HD22	1.58	1.17
1:E:464:VAL:CG1	1:L:467:ASN:HD22	1.58	1.17
1:F:18:ARG:HH11	1:F:18:ARG:CB	1.55	1.17
1:H:36:ARG:NH1	1:N:516:THR:O	1.78	1.17
1:H:516:THR:O	1:I:36:ARG:NH1	1.78	1.17
1:I:516:THR:O	1:J:36:ARG:NH1	1.78	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:172:GLU:OE2	1:F:350:ARG:HG3	1.44	1.17
1:H:18:ARG:HH11	1:H:18:ARG:CB	1.55	1.17
1:A:18:ARG:HH11	1:A:18:ARG:CB	1.55	1.17
1:G:464:VAL:CG1	1:N:467:ASN:HD22	1.58	1.17
1:D:464:VAL:CG1	1:K:467:ASN:HD22	1.58	1.16
1:G:172:GLU:OE2	1:G:350:ARG:HG3	1.44	1.16
1:K:516:THR:O	1:L:36:ARG:NH1	1.78	1.16
1:L:138:CYS:CB	1:L:410:GLY:CA	2.08	1.16
1:B:464:VAL:CG1	1:I:467:ASN:HD22	1.58	1.16
1:M:516:THR:O	1:N:36:ARG:NH1	1.78	1.16
1:D:172:GLU:OE2	1:D:350:ARG:HG3	1.44	1.15
1:F:464:VAL:CG1	1:M:467:ASN:HD22	1.58	1.15
1:M:147:VAL:HG23	1:M:496:PRO:HG3	1.21	1.15
1:I:138:CYS:CB	1:I:410:GLY:CA	2.08	1.14
1:I:138:CYS:HB3	1:I:410:GLY:N	1.63	1.14
1:J:138:CYS:HB3	1:J:410:GLY:N	1.63	1.14
1:K:138:CYS:HB3	1:K:410:GLY:N	1.63	1.14
1:L:138:CYS:HB3	1:L:410:GLY:N	1.63	1.14
1:N:147:VAL:HG23	1:N:496:PRO:HG3	1.21	1.14
1:A:172:GLU:OE2	1:A:350:ARG:HG3	1.44	1.14
1:K:138:CYS:CB	1:K:410:GLY:CA	2.08	1.14
1:L:516:THR:O	1:M:36:ARG:NH1	1.78	1.14
1:K:147:VAL:HG23	1:K:496:PRO:HG3	1.21	1.13
1:M:138:CYS:HB3	1:M:410:GLY:N	1.63	1.13
1:A:464:VAL:CB	1:H:467:ASN:ND2	1.98	1.13
1:C:172:GLU:OE2	1:C:350:ARG:HG3	1.44	1.13
1:H:138:CYS:HB3	1:H:410:GLY:N	1.63	1.13
1:F:197:ARG:HD3	1:F:277:LYS:HB2	1.30	1.13
1:G:197:ARG:HD3	1:G:277:LYS:HB2	1.30	1.13
1:N:138:CYS:CB	1:N:410:GLY:CA	2.08	1.13
1:B:172:GLU:OE2	1:B:350:ARG:HG3	1.44	1.13
1:K:191:GLU:O	1:K:334:ASP:CA	1.98	1.12
1:L:191:GLU:O	1:L:334:ASP:CA	1.98	1.12
1:M:191:GLU:O	1:M:334:ASP:CA	1.98	1.12
1:J:191:GLU:O	1:J:334:ASP:CA	1.98	1.11
1:B:464:VAL:CB	1:I:467:ASN:ND2	1.98	1.11
1:J:147:VAL:HG23	1:J:496:PRO:HG3	1.20	1.11
1:N:138:CYS:HB3	1:N:410:GLY:N	1.63	1.11
1:I:191:GLU:O	1:I:334:ASP:CA	1.98	1.11
1:N:191:GLU:O	1:N:334:ASP:CA	1.98	1.11
1:H:191:GLU:O	1:H:334:ASP:CA	1.98	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:ARG:HD3	1:A:277:LYS:HB2	1.30	1.10
1:E:197:ARG:HD3	1:E:277:LYS:HB2	1.30	1.10
1:J:136:VAL:CA	1:J:137:PRO:CD	2.28	1.09
1:C:18:ARG:HB3	1:C:18:ARG:NH1	1.68	1.09
1:E:18:ARG:HB3	1:E:18:ARG:NH1	1.68	1.08
1:F:18:ARG:HB3	1:F:18:ARG:NH1	1.68	1.08
1:N:136:VAL:CA	1:N:137:PRO:CD	2.28	1.08
1:N:18:ARG:HB3	1:N:18:ARG:NH1	1.68	1.08
1:A:18:ARG:NH1	1:A:18:ARG:HB3	1.68	1.08
1:M:18:ARG:HB3	1:M:18:ARG:NH1	1.68	1.08
1:C:172:GLU:OE2	1:C:350:ARG:CG	2.03	1.07
1:G:172:GLU:OE2	1:G:350:ARG:CG	2.03	1.07
1:H:18:ARG:HB3	1:H:18:ARG:NH1	1.68	1.07
1:B:197:ARG:HD3	1:B:277:LYS:HB2	1.30	1.07
1:B:204:PHE:HE2	1:B:266:THR:HG21	1.20	1.07
1:F:464:VAL:HG11	1:M:467:ASN:ND2	1.70	1.07
1:G:18:ARG:NH1	1:G:18:ARG:HB3	1.68	1.07
1:I:18:ARG:NH1	1:I:18:ARG:HB3	1.68	1.07
1:L:18:ARG:NH1	1:L:18:ARG:HB3	1.68	1.07
1:A:172:GLU:OE2	1:A:350:ARG:CG	2.03	1.07
1:C:204:PHE:HE2	1:C:266:THR:HG21	1.20	1.07
1:D:18:ARG:NH1	1:D:18:ARG:HB3	1.68	1.07
1:D:197:ARG:HD3	1:D:277:LYS:HB2	1.30	1.07
1:J:18:ARG:NH1	1:J:18:ARG:HB3	1.68	1.07
1:L:136:VAL:CA	1:L:137:PRO:CD	2.28	1.07
1:B:18:ARG:NH1	1:B:18:ARG:HB3	1.68	1.06
1:B:172:GLU:OE2	1:B:350:ARG:CG	2.03	1.06
1:D:172:GLU:OE2	1:D:350:ARG:CG	2.03	1.06
1:G:464:VAL:HG11	1:N:467:ASN:ND2	1.70	1.06
1:K:18:ARG:HB3	1:K:18:ARG:NH1	1.68	1.06
1:A:464:VAL:HG11	1:H:467:ASN:ND2	1.70	1.06
1:F:172:GLU:OE2	1:F:350:ARG:CG	2.03	1.06
1:I:136:VAL:CA	1:I:137:PRO:CD	2.28	1.06
1:K:147:VAL:HG23	1:K:496:PRO:CG	1.86	1.06
1:B:146:GLN:HE21	1:B:494:LEU:CD1	1.69	1.06
1:E:464:VAL:HG11	1:L:467:ASN:ND2	1.70	1.06
1:F:204:PHE:HE2	1:F:266:THR:HG21	1.20	1.06
1:L:147:VAL:HG23	1:L:496:PRO:CG	1.86	1.06
1:D:464:VAL:HG11	1:K:467:ASN:ND2	1.70	1.06
1:G:204:PHE:HE2	1:G:266:THR:HG21	1.20	1.06
1:I:147:VAL:HG23	1:I:496:PRO:CG	1.86	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:18:ARG:HH11	1:K:18:ARG:HB3	0.89	1.06
1:K:136:VAL:CA	1:K:137:PRO:CD	2.28	1.06
1:A:204:PHE:HE2	1:A:266:THR:HG21	1.20	1.06
1:G:146:GLN:HE21	1:G:494:LEU:CD1	1.69	1.06
1:J:18:ARG:HH11	1:J:18:ARG:HB3	0.89	1.06
1:A:172:GLU:OE2	1:A:350:ARG:CD	2.04	1.05
1:D:172:GLU:OE2	1:D:350:ARG:CD	2.04	1.05
1:H:147:VAL:HG23	1:H:496:PRO:CG	1.86	1.05
1:L:18:ARG:HH11	1:L:18:ARG:HB3	0.89	1.05
1:N:147:VAL:HG23	1:N:496:PRO:CG	1.86	1.05
1:C:197:ARG:HD3	1:C:277:LYS:HB2	1.30	1.05
1:C:464:VAL:HG11	1:J:467:ASN:ND2	1.70	1.05
1:D:146:GLN:HE21	1:D:494:LEU:CD1	1.69	1.05
1:F:464:VAL:CG1	1:M:467:ASN:ND2	2.18	1.05
1:G:172:GLU:OE2	1:G:350:ARG:CD	2.04	1.05
1:J:147:VAL:HG23	1:J:496:PRO:CG	1.86	1.05
1:M:147:VAL:HG23	1:M:496:PRO:CG	1.86	1.05
1:C:172:GLU:OE2	1:C:350:ARG:CD	2.04	1.05
1:E:172:GLU:OE2	1:E:350:ARG:CG	2.03	1.05
1:B:464:VAL:HG11	1:I:467:ASN:ND2	1.70	1.05
1:F:172:GLU:OE2	1:F:350:ARG:CD	2.04	1.05
1:I:18:ARG:HH11	1:I:18:ARG:HB3	0.89	1.05
1:M:18:ARG:HH11	1:M:18:ARG:HB3	0.89	1.05
1:A:18:ARG:HH11	1:A:18:ARG:HB3	0.89	1.04
1:A:146:GLN:HE21	1:A:494:LEU:CD1	1.69	1.04
1:E:461:GLU:OE1	1:L:463:SER:HB2	1.57	1.04
1:G:18:ARG:HH11	1:G:18:ARG:HB3	0.89	1.04
1:H:136:VAL:CA	1:H:137:PRO:CD	2.28	1.04
1:D:461:GLU:OE1	1:K:463:SER:HB2	1.57	1.04
1:F:146:GLN:HE21	1:F:494:LEU:CD1	1.69	1.04
1:C:146:GLN:HE21	1:C:494:LEU:CD1	1.69	1.04
1:E:146:GLN:HE21	1:E:494:LEU:CD1	1.69	1.04
1:A:461:GLU:OE1	1:H:463:SER:HB2	1.57	1.04
1:B:172:GLU:OE2	1:B:350:ARG:CD	2.04	1.04
1:E:172:GLU:OE2	1:E:350:ARG:CD	2.04	1.04
1:G:461:GLU:OE1	1:N:463:SER:HB2	1.57	1.04
1:N:18:ARG:HH11	1:N:18:ARG:HB3	0.89	1.04
1:B:18:ARG:HH11	1:B:18:ARG:HB3	0.89	1.03
1:F:461:GLU:OE1	1:M:463:SER:HB2	1.57	1.03
1:H:18:ARG:HH11	1:H:18:ARG:HB3	0.89	1.03
1:D:204:PHE:HE2	1:D:266:THR:HG21	1.20	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:204:PHE:HE2	1:E:266:THR:HG21	1.20	1.03
1:C:172:GLU:OE2	1:C:350:ARG:HD2	1.59	1.03
1:F:172:GLU:OE2	1:F:350:ARG:HD2	1.59	1.03
1:F:18:ARG:HH11	1:F:18:ARG:HB3	0.89	1.03
1:G:464:VAL:CG1	1:N:467:ASN:ND2	2.18	1.03
1:C:18:ARG:HH11	1:C:18:ARG:HB3	0.89	1.02
1:E:172:GLU:OE2	1:E:350:ARG:HD2	1.59	1.02
1:H:135:SER:OG	1:H:137:PRO:N	1.92	1.02
1:C:461:GLU:OE1	1:J:463:SER:HB2	1.57	1.02
1:N:135:SER:OG	1:N:137:PRO:N	1.92	1.02
1:B:461:GLU:OE1	1:I:463:SER:HB2	1.57	1.02
1:G:172:GLU:OE2	1:G:350:ARG:HD2	1.59	1.02
1:M:135:SER:OG	1:M:137:PRO:N	1.92	1.02
1:B:172:GLU:OE2	1:B:350:ARG:HD2	1.59	1.02
1:B:464:VAL:HG21	1:I:467:ASN:CB	1.89	1.02
1:C:464:VAL:HG21	1:J:467:ASN:CB	1.89	1.02
1:E:464:VAL:HG21	1:L:467:ASN:CB	1.89	1.02
1:G:464:VAL:HG21	1:N:467:ASN:CB	1.89	1.02
1:J:138:CYS:CA	1:J:410:GLY:HA2	1.90	1.02
1:I:138:CYS:CA	1:I:410:GLY:HA2	1.90	1.01
1:K:138:CYS:CA	1:K:410:GLY:HA2	1.90	1.01
1:M:136:VAL:CA	1:M:137:PRO:CD	2.28	1.01
1:B:406:ALA:HB2	1:B:496:PRO:HB3	1.40	1.01
1:E:18:ARG:HH11	1:E:18:ARG:HB3	0.89	1.01
1:F:406:ALA:O	1:F:410:GLY:N	1.93	1.01
1:F:464:VAL:HG21	1:M:467:ASN:CB	1.89	1.01
1:I:135:SER:OG	1:I:137:PRO:N	1.92	1.01
1:L:135:SER:OG	1:L:137:PRO:N	1.92	1.01
1:A:406:ALA:O	1:A:410:GLY:N	1.93	1.01
1:A:464:VAL:HG21	1:H:467:ASN:CB	1.89	1.01
1:D:18:ARG:HH11	1:D:18:ARG:HB3	0.89	1.01
1:D:406:ALA:O	1:D:410:GLY:N	1.94	1.01
1:H:138:CYS:CA	1:H:410:GLY:HA2	1.90	1.01
1:F:406:ALA:HB2	1:F:496:PRO:HB3	1.40	1.01
1:C:406:ALA:HB2	1:C:496:PRO:HB3	1.40	1.01
1:D:464:VAL:HG21	1:K:467:ASN:CB	1.89	1.01
1:E:406:ALA:HB2	1:E:496:PRO:HB3	1.40	1.01
1:J:138:CYS:CB	1:J:410:GLY:N	2.23	1.01
1:L:138:CYS:CA	1:L:410:GLY:HA2	1.90	1.00
1:E:406:ALA:O	1:E:410:GLY:N	1.94	1.00
1:N:138:CYS:CA	1:N:410:GLY:HA2	1.90	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:406:ALA:HB2	1:A:496:PRO:HB3	1.40	1.00
1:B:406:ALA:O	1:B:410:GLY:N	1.94	1.00
1:G:406:ALA:O	1:G:410:GLY:N	1.93	1.00
1:B:464:VAL:CG1	1:I:467:ASN:ND2	2.18	1.00
1:D:464:VAL:CG1	1:K:467:ASN:ND2	2.18	1.00
1:J:135:SER:OG	1:J:137:PRO:N	1.92	1.00
1:K:138:CYS:CB	1:K:410:GLY:N	2.23	1.00
1:A:464:VAL:CG1	1:H:467:ASN:ND2	2.18	1.00
1:B:146:GLN:NE2	1:B:494:LEU:CD1	2.25	1.00
1:A:172:GLU:OE2	1:A:350:ARG:HD2	1.59	1.00
1:C:146:GLN:NE2	1:C:494:LEU:CD1	2.25	1.00
1:E:464:VAL:CG1	1:L:467:ASN:ND2	2.18	1.00
1:G:105:LYS:HG2	1:M:109:ALA:O	1.62	1.00
1:K:135:SER:OG	1:K:137:PRO:N	1.92	1.00
1:M:138:CYS:CA	1:M:410:GLY:HA2	1.90	0.99
1:A:105:LYS:HG2	1:N:109:ALA:O	1.62	0.99
1:C:406:ALA:O	1:C:410:GLY:N	1.93	0.99
1:G:406:ALA:HB2	1:G:496:PRO:HB3	1.40	0.99
1:D:172:GLU:OE2	1:D:350:ARG:HD2	1.59	0.99
1:E:138:CYS:HB3	1:E:410:GLY:HA2	1.45	0.99
1:F:105:LYS:HG2	1:L:109:ALA:O	1.62	0.99
1:D:406:ALA:HB2	1:D:496:PRO:HB3	1.40	0.99
1:A:463:SER:OG	1:H:464:VAL:HG23	1.63	0.99
1:F:138:CYS:HB3	1:F:410:GLY:HA2	1.45	0.99
1:D:138:CYS:HB3	1:D:410:GLY:HA2	1.45	0.99
1:D:463:SER:OG	1:K:464:VAL:HG23	1.63	0.99
1:E:463:SER:OG	1:L:464:VAL:HG23	1.63	0.99
1:G:146:GLN:NE2	1:G:494:LEU:CD1	2.25	0.98
1:C:463:SER:OG	1:J:464:VAL:HG23	1.63	0.98
1:C:138:CYS:HB3	1:C:410:GLY:HA2	1.45	0.98
1:A:146:GLN:NE2	1:A:494:LEU:CD1	2.25	0.98
1:B:105:LYS:HG2	1:H:109:ALA:O	1.62	0.98
1:L:138:CYS:CB	1:L:410:GLY:N	2.23	0.98
1:D:105:LYS:HG2	1:J:109:ALA:O	1.62	0.98
1:B:138:CYS:HB3	1:B:410:GLY:HA2	1.45	0.98
1:B:203:TYR:HH	1:C:286:LYS:HD3	1.26	0.98
1:G:463:SER:OG	1:N:464:VAL:HG23	1.63	0.98
1:D:146:GLN:NE2	1:D:494:LEU:CD1	2.25	0.97
1:C:105:LYS:HG2	1:I:109:ALA:O	1.62	0.97
1:C:464:VAL:CG1	1:J:467:ASN:ND2	2.18	0.97
1:F:146:GLN:NE2	1:F:494:LEU:CD1	2.25	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:138:CYS:HB3	1:G:410:GLY:HA2	1.45	0.97
1:H:138:CYS:CB	1:H:410:GLY:N	2.22	0.97
1:A:138:CYS:HB3	1:A:410:GLY:HA2	1.45	0.97
1:N:138:CYS:CB	1:N:410:GLY:N	2.22	0.97
1:B:463:SER:OG	1:I:464:VAL:HG23	1.63	0.97
1:E:105:LYS:HG2	1:K:109:ALA:O	1.62	0.97
1:E:146:GLN:NE2	1:E:494:LEU:CD1	2.25	0.96
1:F:463:SER:OG	1:M:464:VAL:HG23	1.63	0.96
1:N:150:ILE:HD13	1:N:494:LEU:O	0.78	0.95
1:F:204:PHE:CE2	1:F:266:THR:HG21	2.02	0.95
1:H:150:ILE:HD13	1:H:494:LEU:O	0.78	0.95
1:C:204:PHE:CE2	1:C:266:THR:HG21	2.02	0.95
1:D:204:PHE:CE2	1:D:266:THR:HG21	2.01	0.95
1:F:136:VAL:CA	1:F:137:PRO:N	2.30	0.95
1:E:204:PHE:CE2	1:E:266:THR:HG21	2.02	0.95
1:M:150:ILE:HD13	1:M:494:LEU:O	0.78	0.95
1:I:150:ILE:HD13	1:I:494:LEU:O	0.78	0.95
1:K:150:ILE:HD13	1:K:494:LEU:O	0.78	0.95
1:J:150:ILE:HD13	1:J:494:LEU:O	0.78	0.94
1:M:381:VAL:HG21	1:M:393:LYS:HA	1.48	0.94
1:N:381:VAL:HG21	1:N:393:LYS:HA	1.48	0.94
1:L:150:ILE:HD13	1:L:494:LEU:O	0.78	0.94
1:A:203:TYR:HH	1:B:286:LYS:HD3	1.26	0.94
1:D:136:VAL:CA	1:D:137:PRO:N	2.30	0.94
1:E:136:VAL:CA	1:E:137:PRO:N	2.30	0.94
1:B:204:PHE:CE2	1:B:266:THR:HG21	2.01	0.94
1:I:138:CYS:CB	1:I:410:GLY:N	2.23	0.94
1:L:381:VAL:HG21	1:L:393:LYS:HA	1.48	0.94
1:C:136:VAL:CA	1:C:137:PRO:N	2.30	0.94
1:G:204:PHE:CE2	1:G:266:THR:HG21	2.01	0.94
1:H:381:VAL:HG21	1:H:393:LYS:HA	1.48	0.94
1:A:136:VAL:CA	1:A:137:PRO:N	2.30	0.94
1:A:204:PHE:CE2	1:A:266:THR:HG21	2.01	0.94
1:B:136:VAL:CA	1:B:137:PRO:N	2.30	0.93
1:M:138:CYS:CB	1:M:410:GLY:N	2.22	0.93
1:G:136:VAL:CA	1:G:137:PRO:N	2.30	0.93
2:O:70:SER:OG	2:U:80:PRO:HG2	1.69	0.93
2:P:80:PRO:HG2	2:Q:70:SER:OG	1.69	0.93
2:Q:80:PRO:HG2	2:R:70:SER:OG	1.69	0.93
1:K:381:VAL:HG21	1:K:393:LYS:HA	1.48	0.93
1:I:381:VAL:HG21	1:I:393:LYS:HA	1.48	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:80:PRO:HG2	2:S:70:SER:OG	1.69	0.93
1:F:203:TYR:HH	1:G:286:LYS:HD3	1.20	0.93
1:A:286:LYS:HD3	1:G:203:TYR:HH	1.12	0.93
1:J:381:VAL:HG21	1:J:393:LYS:HA	1.48	0.93
2:O:80:PRO:HG2	2:P:70:SER:OG	1.69	0.92
1:E:463:SER:HB2	1:L:464:VAL:HG21	1.51	0.92
1:G:463:SER:HB2	1:N:464:VAL:HG21	1.51	0.92
2:T:80:PRO:HG2	2:U:70:SER:OG	1.69	0.92
1:A:463:SER:HB2	1:H:464:VAL:HG21	1.51	0.92
1:F:463:SER:HB2	1:M:464:VAL:HG21	1.51	0.92
1:D:463:SER:HB2	1:K:464:VAL:HG21	1.51	0.92
2:S:80:PRO:HG2	2:T:70:SER:OG	1.69	0.92
2:S:17:ILE:HD11	2:T:108:CYS:HB3	1.52	0.91
2:R:17:ILE:HD11	2:S:108:CYS:HB3	1.52	0.91
2:T:17:ILE:HD11	2:U:108:CYS:HB3	1.52	0.91
1:D:203:TYR:HH	1:E:286:LYS:HD3	1.17	0.91
1:E:203:TYR:HH	1:F:286:LYS:HD3	1.09	0.91
2:Q:17:ILE:HD11	2:R:108:CYS:HB3	1.52	0.91
1:J:190:VAL:HG21	1:J:334:ASP:OD2	1.71	0.91
1:C:463:SER:HB2	1:J:464:VAL:HG21	1.51	0.90
1:D:146:GLN:HB3	1:D:494:LEU:HG	1.54	0.90
1:B:463:SER:HB2	1:I:464:VAL:HG21	1.51	0.90
1:H:190:VAL:HG21	1:H:334:ASP:OD2	1.71	0.90
1:I:190:VAL:HG21	1:I:334:ASP:OD2	1.71	0.90
1:E:146:GLN:HB3	1:E:494:LEU:HG	1.54	0.89
1:C:146:GLN:HB3	1:C:494:LEU:HG	1.54	0.89
1:N:190:VAL:HG21	1:N:334:ASP:OD2	1.71	0.89
2:P:17:ILE:HD11	2:Q:108:CYS:HB3	1.52	0.89
1:M:190:VAL:HG21	1:M:334:ASP:OD2	1.71	0.89
2:O:108:CYS:HB3	2:U:17:ILE:HD11	1.52	0.89
1:H:150:ILE:HD13	1:H:494:LEU:C	1.93	0.89
1:J:150:ILE:HD13	1:J:494:LEU:C	1.93	0.89
1:K:190:VAL:HG21	1:K:334:ASP:OD2	1.71	0.89
1:L:190:VAL:HG21	1:L:334:ASP:OD2	1.71	0.89
1:J:143:ALA:O	1:J:146:GLN:HB3	1.73	0.89
2:O:17:ILE:HD11	2:P:108:CYS:HB3	1.52	0.89
1:I:143:ALA:O	1:I:146:GLN:HB3	1.73	0.89
1:M:150:ILE:HD13	1:M:494:LEU:C	1.93	0.88
1:F:146:GLN:HB3	1:F:494:LEU:HG	1.54	0.88
1:N:143:ALA:O	1:N:146:GLN:HB3	1.73	0.88
1:H:143:ALA:O	1:H:146:GLN:HB3	1.73	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:143:ALA:O	1:K:146:GLN:HB3	1.73	0.88
1:M:143:ALA:O	1:M:146:GLN:HB3	1.73	0.88
1:D:463:SER:HB2	1:K:464:VAL:CG2	2.04	0.88
1:B:146:GLN:HB3	1:B:494:LEU:HG	1.54	0.88
1:M:166:MET:HE2	1:M:171:LYS:HA	1.55	0.88
1:C:463:SER:HB2	1:J:464:VAL:CG2	2.04	0.88
2:S:82:PRO:HA	2:T:110:TYR:CE1	2.09	0.88
1:A:463:SER:HB2	1:H:464:VAL:CG2	2.04	0.88
1:E:463:SER:HB2	1:L:464:VAL:CG2	2.04	0.87
2:O:82:PRO:HA	2:P:110:TYR:CE1	2.09	0.87
1:A:146:GLN:HB3	1:A:494:LEU:HG	1.54	0.87
1:C:267:MET:SD	1:D:305:ILE:HD12	2.15	0.87
1:G:463:SER:HB2	1:N:464:VAL:CG2	2.04	0.87
2:O:110:TYR:CE1	2:U:82:PRO:HA	2.09	0.87
1:E:267:MET:SD	1:F:305:ILE:HD12	2.15	0.87
1:F:267:MET:SD	1:G:305:ILE:HD12	2.15	0.87
1:N:166:MET:HE2	1:N:171:LYS:HA	1.55	0.87
2:Q:82:PRO:HA	2:R:110:TYR:CE1	2.09	0.87
1:A:203:TYR:CE2	1:B:304:GLU:OE2	2.28	0.87
1:A:267:MET:SD	1:B:305:ILE:HD12	2.15	0.87
1:A:304:GLU:OE2	1:G:203:TYR:CE2	2.28	0.87
1:B:267:MET:SD	1:C:305:ILE:HD12	2.14	0.87
1:D:203:TYR:CE2	1:E:304:GLU:OE2	2.28	0.87
2:R:82:PRO:HA	2:S:110:TYR:CE1	2.09	0.87
1:A:305:ILE:HD12	1:G:267:MET:SD	2.15	0.87
1:F:463:SER:HB2	1:M:464:VAL:CG2	2.04	0.87
1:I:166:MET:HE2	1:I:171:LYS:HA	1.55	0.87
1:L:166:MET:HE2	1:L:171:LYS:HA	1.56	0.87
1:N:150:ILE:HD13	1:N:494:LEU:C	1.93	0.87
2:T:82:PRO:HA	2:U:110:TYR:CE1	2.09	0.87
1:G:146:GLN:HB3	1:G:494:LEU:HG	1.54	0.87
2:P:82:PRO:HA	2:Q:110:TYR:CE1	2.09	0.87
1:K:150:ILE:HD13	1:K:494:LEU:C	1.93	0.87
1:B:463:SER:HB2	1:I:464:VAL:CG2	2.04	0.86
1:F:203:TYR:CE2	1:G:304:GLU:OE2	2.28	0.86
1:I:150:ILE:HD13	1:I:494:LEU:C	1.93	0.86
1:L:143:ALA:O	1:L:146:GLN:HB3	1.73	0.86
1:B:203:TYR:CE2	1:C:304:GLU:OE2	2.28	0.86
1:C:203:TYR:CE2	1:D:304:GLU:OE2	2.28	0.86
1:E:203:TYR:CE2	1:F:304:GLU:OE2	2.28	0.86
1:A:461:GLU:OE1	1:H:463:SER:CB	2.24	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:461:GLU:OE1	1:J:463:SER:CB	2.24	0.86
1:D:267:MET:SD	1:E:305:ILE:HD12	2.15	0.86
1:B:461:GLU:OE1	1:I:463:SER:CB	2.24	0.86
1:F:461:GLU:OE1	1:M:463:SER:CB	2.24	0.86
1:G:461:GLU:OE1	1:N:463:SER:CB	2.24	0.86
1:D:461:GLU:OE1	1:K:463:SER:CB	2.24	0.86
1:L:150:ILE:HD13	1:L:494:LEU:C	1.93	0.86
1:F:174:VAL:HG21	1:F:367:GLU:HA	1.58	0.85
1:E:174:VAL:HG21	1:E:367:GLU:HA	1.58	0.85
1:J:166:MET:HE2	1:J:171:LYS:HA	1.55	0.85
1:B:90:THR:O	1:B:94:VAL:HG23	1.77	0.85
1:H:166:MET:HE2	1:H:171:LYS:HA	1.55	0.85
1:J:90:THR:O	1:J:94:VAL:HG23	1.77	0.85
1:M:90:THR:O	1:M:94:VAL:HG23	1.77	0.85
1:K:90:THR:O	1:K:94:VAL:HG23	1.77	0.85
1:L:90:THR:O	1:L:94:VAL:HG23	1.77	0.85
1:I:90:THR:O	1:I:94:VAL:HG23	1.77	0.85
1:N:90:THR:O	1:N:94:VAL:HG23	1.77	0.85
1:C:90:THR:O	1:C:94:VAL:HG23	1.77	0.85
1:K:166:MET:HE2	1:K:171:LYS:HA	1.55	0.84
1:A:90:THR:O	1:A:94:VAL:HG23	1.77	0.84
1:E:90:THR:O	1:E:94:VAL:HG23	1.77	0.84
1:B:174:VAL:HG21	1:B:367:GLU:HA	1.58	0.84
1:E:461:GLU:OE1	1:L:463:SER:CB	2.24	0.84
1:G:174:VAL:HG21	1:G:367:GLU:HA	1.58	0.84
1:A:174:VAL:HG21	1:A:367:GLU:HA	1.58	0.84
1:D:90:THR:O	1:D:94:VAL:HG23	1.77	0.84
1:G:138:CYS:HB2	1:G:411:VAL:HG13	1.59	0.84
1:C:174:VAL:HG21	1:C:367:GLU:HA	1.58	0.84
1:F:90:THR:O	1:F:94:VAL:HG23	1.77	0.83
1:D:138:CYS:HB2	1:D:411:VAL:HG13	1.59	0.83
1:A:138:CYS:HB2	1:A:411:VAL:HG13	1.59	0.83
1:D:174:VAL:HG21	1:D:367:GLU:HA	1.58	0.83
1:G:90:THR:O	1:G:94:VAL:HG23	1.77	0.83
1:G:463:SER:CB	1:N:464:VAL:CG2	2.57	0.83
1:F:138:CYS:HB2	1:F:411:VAL:HG13	1.59	0.83
1:D:463:SER:CB	1:K:464:VAL:CG2	2.57	0.83
1:E:138:CYS:HB2	1:E:411:VAL:HG13	1.59	0.83
1:B:463:SER:CB	1:I:464:VAL:CG2	2.57	0.83
1:E:197:ARG:HD3	1:E:277:LYS:CB	2.09	0.83
1:F:463:SER:CB	1:M:464:VAL:CG2	2.57	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:90:THR:O	1:H:94:VAL:HG23	1.77	0.83
1:F:197:ARG:HD3	1:F:277:LYS:CB	2.09	0.82
1:A:463:SER:CB	1:H:464:VAL:CG2	2.57	0.82
1:E:463:SER:CB	1:L:464:VAL:CG2	2.57	0.82
1:N:149:THR:HG23	1:N:159:GLY:HA3	1.61	0.82
1:H:149:THR:HG23	1:H:159:GLY:HA3	1.61	0.82
1:M:149:THR:HG23	1:M:159:GLY:HA3	1.61	0.82
1:A:197:ARG:HD3	1:A:277:LYS:CB	2.09	0.82
1:D:197:ARG:HD3	1:D:277:LYS:CB	2.09	0.82
1:B:197:ARG:HD3	1:B:277:LYS:CB	2.09	0.82
1:C:138:CYS:HB2	1:C:411:VAL:HG13	1.59	0.82
1:B:138:CYS:HB2	1:B:411:VAL:HG13	1.59	0.82
1:C:463:SER:CB	1:J:464:VAL:CG2	2.57	0.82
1:E:172:GLU:CD	1:E:350:ARG:HG3	2.01	0.81
1:L:149:THR:HG23	1:L:159:GLY:HA3	1.61	0.81
1:C:197:ARG:HD3	1:C:277:LYS:CB	2.09	0.81
1:F:172:GLU:CD	1:F:350:ARG:HG3	2.01	0.81
1:C:464:VAL:CG2	1:J:467:ASN:CB	2.59	0.81
1:J:143:ALA:O	1:J:147:VAL:HG12	1.81	0.81
1:K:143:ALA:O	1:K:147:VAL:HG12	1.81	0.81
1:J:138:CYS:HB2	1:J:410:GLY:HA2	0.81	0.81
1:J:406:ALA:O	1:J:410:GLY:N	2.14	0.81
1:L:406:ALA:O	1:L:410:GLY:N	2.14	0.81
1:B:414:GLY:O	1:B:417:VAL:HG12	1.81	0.81
1:E:464:VAL:HB	1:L:467:ASN:ND2	1.96	0.81
1:H:143:ALA:O	1:H:147:VAL:HG12	1.81	0.81
1:I:143:ALA:O	1:I:147:VAL:HG12	1.81	0.81
1:I:149:THR:HG23	1:I:159:GLY:HA3	1.61	0.81
1:K:149:THR:HG23	1:K:159:GLY:HA3	1.61	0.81
1:L:414:GLY:O	1:L:417:VAL:HG12	1.81	0.81
1:D:464:VAL:CG2	1:K:467:ASN:CB	2.59	0.81
1:H:136:VAL:CA	1:H:137:PRO:N	2.44	0.81
1:M:136:VAL:CA	1:M:137:PRO:N	2.44	0.81
1:M:143:ALA:O	1:M:147:VAL:HG12	1.81	0.81
1:M:406:ALA:O	1:M:410:GLY:N	2.14	0.81
1:N:414:GLY:O	1:N:417:VAL:HG12	1.81	0.81
1:G:414:GLY:O	1:G:417:VAL:HG12	1.81	0.81
1:K:138:CYS:HB2	1:K:410:GLY:HA2	0.81	0.81
1:L:143:ALA:O	1:L:147:VAL:HG12	1.81	0.81
1:N:143:ALA:O	1:N:147:VAL:HG12	1.81	0.81
1:I:136:VAL:CA	1:I:137:PRO:N	2.44	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:406:ALA:O	1:K:410:GLY:N	2.14	0.81
1:N:136:VAL:CA	1:N:137:PRO:N	2.44	0.81
1:N:138:CYS:HB2	1:N:410:GLY:HA2	0.81	0.81
1:H:138:CYS:HB2	1:H:410:GLY:HA2	0.81	0.80
1:B:172:GLU:CD	1:B:350:ARG:HG3	2.01	0.80
1:C:414:GLY:O	1:C:417:VAL:HG12	1.81	0.80
1:D:172:GLU:CD	1:D:350:ARG:HG3	2.01	0.80
1:I:406:ALA:O	1:I:410:GLY:N	2.14	0.80
1:M:138:CYS:HB2	1:M:410:GLY:HA2	0.81	0.80
1:F:414:GLY:O	1:F:417:VAL:HG12	1.81	0.80
1:J:414:GLY:O	1:J:417:VAL:HG12	1.81	0.80
1:K:136:VAL:CA	1:K:137:PRO:N	2.44	0.80
1:J:149:THR:HG23	1:J:159:GLY:HA3	1.61	0.80
1:L:136:VAL:CA	1:L:137:PRO:N	2.44	0.80
1:N:406:ALA:O	1:N:410:GLY:N	2.14	0.80
1:D:464:VAL:HB	1:K:467:ASN:ND2	1.96	0.80
1:E:464:VAL:CG2	1:L:467:ASN:CB	2.59	0.80
1:G:172:GLU:CD	1:G:350:ARG:HG3	2.01	0.80
1:G:373:ALA:O	1:G:374:GLY:O	1.85	0.80
1:A:172:GLU:CD	1:A:350:ARG:HG3	2.01	0.80
1:J:136:VAL:CA	1:J:137:PRO:N	2.44	0.80
1:G:464:VAL:CG2	1:N:467:ASN:CB	2.59	0.80
1:K:414:GLY:O	1:K:417:VAL:HG12	1.81	0.80
1:D:414:GLY:O	1:D:417:VAL:HG12	1.81	0.80
1:I:414:GLY:O	1:I:417:VAL:HG12	1.81	0.80
1:F:464:VAL:CG2	1:M:467:ASN:CB	2.59	0.79
1:H:406:ALA:O	1:H:410:GLY:N	2.14	0.79
1:A:414:GLY:O	1:A:417:VAL:HG12	1.81	0.79
1:F:373:ALA:O	1:F:374:GLY:O	1.84	0.79
1:H:414:GLY:O	1:H:417:VAL:HG12	1.81	0.79
1:A:373:ALA:O	1:A:374:GLY:O	1.84	0.79
1:A:464:VAL:CG2	1:H:467:ASN:CB	2.59	0.79
1:G:197:ARG:HD3	1:G:277:LYS:CB	2.09	0.79
1:C:172:GLU:CD	1:C:350:ARG:HG3	2.01	0.79
1:E:414:GLY:O	1:E:417:VAL:HG12	1.81	0.79
1:M:414:GLY:O	1:M:417:VAL:HG12	1.81	0.79
1:I:138:CYS:HB2	1:I:410:GLY:HA2	0.81	0.79
1:C:463:SER:OG	1:J:464:VAL:CG2	2.31	0.79
1:H:63:GLU:HB2	1:N:3:ALA:CB	2.13	0.79
1:L:169:VAL:HG13	1:L:173:GLY:HA3	1.65	0.79
1:A:306:GLY:HA3	1:G:264:VAL:CG1	2.13	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:430:ARG:HG2	1:B:430:ARG:HH11	1.48	0.79
1:B:463:SER:OG	1:I:464:VAL:CG2	2.31	0.79
1:J:169:VAL:HG13	1:J:173:GLY:HA3	1.65	0.79
1:M:3:ALA:CB	1:N:63:GLU:HB2	2.13	0.79
1:M:169:VAL:HG13	1:M:173:GLY:HA3	1.65	0.79
1:A:264:VAL:CG1	1:B:306:GLY:HA3	2.13	0.79
1:F:264:VAL:CG1	1:G:306:GLY:HA3	2.13	0.79
1:K:169:VAL:HG13	1:K:173:GLY:HA3	1.65	0.79
1:A:464:VAL:HB	1:H:467:ASN:ND2	1.96	0.79
1:G:464:VAL:HB	1:N:467:ASN:ND2	1.96	0.79
1:L:3:ALA:CB	1:M:63:GLU:HB2	2.13	0.79
1:I:136:VAL:N	1:I:137:PRO:N	2.25	0.78
1:I:169:VAL:HG13	1:I:173:GLY:HA3	1.65	0.78
1:K:430:ARG:HG2	1:K:430:ARG:HH11	1.48	0.78
1:L:430:ARG:HG2	1:L:430:ARG:HH11	1.48	0.78
1:B:264:VAL:CG1	1:C:306:GLY:HA3	2.13	0.78
1:D:463:SER:OG	1:K:464:VAL:CG2	2.31	0.78
1:H:192:GLY:CA	1:H:376:VAL:HG23	2.14	0.78
1:J:3:ALA:CB	1:K:63:GLU:HB2	2.13	0.78
1:J:137:PRO:C	1:J:410:GLY:HA3	2.04	0.78
1:F:430:ARG:HG2	1:F:430:ARG:HH11	1.48	0.78
1:K:192:GLY:CA	1:K:376:VAL:HG23	2.14	0.78
1:L:192:GLY:CA	1:L:376:VAL:HG23	2.14	0.78
1:A:463:SER:OG	1:H:464:VAL:CG2	2.31	0.78
1:E:264:VAL:CG1	1:F:306:GLY:HA3	2.13	0.78
1:H:3:ALA:CB	1:I:63:GLU:HB2	2.13	0.78
1:J:192:GLY:CA	1:J:376:VAL:HG23	2.14	0.78
1:A:430:ARG:HG2	1:A:430:ARG:HH11	1.48	0.78
1:E:373:ALA:O	1:E:374:GLY:O	1.84	0.78
1:G:430:ARG:HG2	1:G:430:ARG:HH11	1.48	0.78
1:I:3:ALA:CB	1:J:63:GLU:HB2	2.13	0.78
1:L:138:CYS:HB2	1:L:410:GLY:HA2	0.81	0.78
1:B:464:VAL:HB	1:I:467:ASN:ND2	1.96	0.78
1:H:169:VAL:HG13	1:H:173:GLY:HA3	1.65	0.78
1:B:464:VAL:CG2	1:I:467:ASN:CB	2.59	0.78
1:D:430:ARG:HG2	1:D:430:ARG:HH11	1.48	0.78
1:H:137:PRO:C	1:H:410:GLY:HA3	2.04	0.78
1:H:430:ARG:HG2	1:H:430:ARG:HH11	1.48	0.78
1:K:137:PRO:C	1:K:410:GLY:HA3	2.04	0.78
1:N:169:VAL:HG13	1:N:173:GLY:HA3	1.65	0.78
1:N:192:GLY:CA	1:N:376:VAL:HG23	2.14	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:463:SER:OG	1:M:464:VAL:CG2	2.31	0.78
1:I:137:PRO:C	1:I:410:GLY:HA3	2.04	0.78
1:K:3:ALA:CB	1:L:63:GLU:HB2	2.13	0.78
1:C:373:ALA:O	1:C:374:GLY:O	1.84	0.78
1:E:463:SER:OG	1:L:464:VAL:CG2	2.31	0.78
1:L:137:PRO:C	1:L:410:GLY:HA3	2.04	0.78
1:M:192:GLY:CA	1:M:376:VAL:HG23	2.14	0.78
1:M:430:ARG:HG2	1:M:430:ARG:HH11	1.48	0.78
1:A:264:VAL:HG11	1:B:306:GLY:HA3	1.67	0.77
1:A:306:GLY:HA3	1:G:264:VAL:HG11	1.67	0.77
1:F:264:VAL:HG11	1:G:306:GLY:HA3	1.67	0.77
1:G:463:SER:OG	1:N:464:VAL:CG2	2.31	0.77
1:I:192:GLY:CA	1:I:376:VAL:HG23	2.14	0.77
1:E:264:VAL:HG11	1:F:306:GLY:HA3	1.67	0.77
1:J:430:ARG:HG2	1:J:430:ARG:HH11	1.48	0.77
1:C:264:VAL:CG1	1:D:306:GLY:HA3	2.13	0.77
1:D:264:VAL:CG1	1:E:306:GLY:HA3	2.13	0.77
1:B:264:VAL:HG11	1:C:306:GLY:HA3	1.67	0.77
1:M:137:PRO:C	1:M:410:GLY:HA3	2.04	0.77
1:F:464:VAL:HB	1:M:467:ASN:ND2	1.96	0.77
1:L:136:VAL:N	1:L:137:PRO:N	2.25	0.77
1:C:138:CYS:CB	1:C:411:VAL:HG13	2.14	0.77
1:G:138:CYS:CB	1:G:411:VAL:HG13	2.14	0.77
1:N:137:PRO:C	1:N:410:GLY:HA3	2.04	0.77
1:A:138:CYS:CB	1:A:411:VAL:HG13	2.14	0.76
1:B:138:CYS:CB	1:B:411:VAL:HG13	2.14	0.76
1:D:264:VAL:HG11	1:E:306:GLY:HA3	1.67	0.76
1:E:430:ARG:HH11	1:E:430:ARG:HG2	1.48	0.76
1:A:138:CYS:CB	1:A:410:GLY:HA2	2.15	0.76
1:C:430:ARG:HG2	1:C:430:ARG:HH11	1.48	0.76
1:A:464:VAL:CG2	1:H:467:ASN:HB2	2.16	0.76
1:C:264:VAL:HG11	1:D:306:GLY:HA3	1.67	0.76
1:C:464:VAL:CG2	1:J:467:ASN:HB2	2.16	0.76
1:D:138:CYS:CB	1:D:411:VAL:HG13	2.14	0.76
1:E:138:CYS:CB	1:E:410:GLY:HA2	2.15	0.76
1:G:138:CYS:CB	1:G:410:GLY:HA2	2.15	0.76
1:G:464:VAL:CG2	1:N:467:ASN:HB2	2.16	0.76
1:C:464:VAL:HB	1:J:467:ASN:ND2	1.96	0.76
1:F:138:CYS:CB	1:F:411:VAL:HG13	2.14	0.76
1:N:430:ARG:HG2	1:N:430:ARG:HH11	1.48	0.76
1:D:203:TYR:OH	1:E:286:LYS:CD	2.25	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:138:CYS:CB	1:F:410:GLY:HA2	2.15	0.76
1:H:136:VAL:N	1:H:137:PRO:N	2.25	0.76
1:B:172:GLU:O	1:B:369:VAL:HG23	1.86	0.76
1:E:138:CYS:CB	1:E:411:VAL:HG13	2.14	0.76
1:F:463:SER:HG	1:M:464:VAL:HG23	1.48	0.76
1:B:138:CYS:CB	1:B:410:GLY:HA2	2.15	0.75
1:B:203:TYR:OH	1:C:286:LYS:CD	2.25	0.75
1:I:430:ARG:HG2	1:I:430:ARG:HH11	1.48	0.75
1:D:138:CYS:CB	1:D:410:GLY:HA2	2.15	0.75
1:D:464:VAL:CG2	1:K:467:ASN:HB2	2.16	0.75
1:G:172:GLU:O	1:G:369:VAL:HG23	1.86	0.75
1:B:373:ALA:O	1:B:374:GLY:O	1.84	0.75
1:B:464:VAL:CG2	1:I:467:ASN:HB2	2.16	0.75
1:F:464:VAL:CG2	1:M:467:ASN:HB2	2.16	0.75
1:N:149:THR:CG2	1:N:156:GLU:HA	2.17	0.75
1:J:149:THR:CG2	1:J:156:GLU:HA	2.17	0.75
1:K:136:VAL:N	1:K:137:PRO:N	2.25	0.75
1:E:464:VAL:CG2	1:L:467:ASN:HB2	2.16	0.75
1:C:203:TYR:OH	1:D:286:LYS:CD	2.26	0.75
1:D:172:GLU:O	1:D:369:VAL:HG23	1.86	0.75
1:K:136:VAL:C	1:K:137:PRO:N	2.40	0.75
1:C:172:GLU:O	1:C:369:VAL:HG23	1.86	0.75
1:A:172:GLU:O	1:A:369:VAL:HG23	1.86	0.74
1:F:172:GLU:O	1:F:369:VAL:HG23	1.86	0.74
1:K:149:THR:CG2	1:K:156:GLU:HA	2.17	0.74
1:L:136:VAL:C	1:L:137:PRO:N	2.40	0.74
1:H:136:VAL:C	1:H:137:PRO:N	2.40	0.74
1:H:149:THR:CG2	1:H:156:GLU:HA	2.17	0.74
1:L:149:THR:CG2	1:L:156:GLU:HA	2.17	0.74
1:D:146:GLN:OE1	1:D:492:GLY:HA2	1.88	0.74
1:I:149:THR:CG2	1:I:156:GLU:HA	2.17	0.74
1:N:136:VAL:N	1:N:137:PRO:N	2.25	0.74
1:B:105:LYS:HD3	1:H:110:GLY:HA3	1.69	0.74
1:C:105:LYS:HD3	1:I:110:GLY:HA3	1.69	0.74
1:G:146:GLN:OE1	1:G:492:GLY:HA2	1.88	0.74
1:M:149:THR:CG2	1:M:156:GLU:HA	2.17	0.74
1:B:136:VAL:HA	1:B:137:PRO:CD	2.18	0.74
1:E:146:GLN:OE1	1:E:492:GLY:HA2	1.88	0.74
1:G:136:VAL:HA	1:G:137:PRO:CD	2.18	0.74
1:C:138:CYS:CB	1:C:410:GLY:HA2	2.15	0.74
1:D:105:LYS:HD3	1:J:110:GLY:HA3	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:136:VAL:HA	1:F:137:PRO:CD	2.18	0.74
1:J:136:VAL:HA	1:J:137:PRO:HD2	0.77	0.74
1:J:136:VAL:C	1:J:137:PRO:N	2.40	0.74
1:C:146:GLN:OE1	1:C:492:GLY:HA2	1.88	0.74
1:E:136:VAL:HA	1:E:137:PRO:CD	2.18	0.74
1:E:172:GLU:O	1:E:369:VAL:HG23	1.86	0.74
1:I:136:VAL:C	1:I:137:PRO:N	2.40	0.74
1:A:105:LYS:HD3	1:N:110:GLY:HA3	1.69	0.74
1:A:136:VAL:HA	1:A:137:PRO:CD	2.18	0.74
1:D:136:VAL:HA	1:D:137:PRO:CD	2.18	0.74
1:N:136:VAL:C	1:N:137:PRO:N	2.40	0.74
1:D:138:CYS:SG	1:D:411:VAL:HG13	2.28	0.73
1:B:146:GLN:OE1	1:B:492:GLY:HA2	1.88	0.73
1:C:136:VAL:HA	1:C:137:PRO:CD	2.18	0.73
1:F:138:CYS:SG	1:F:411:VAL:HG13	2.28	0.73
1:G:138:CYS:SG	1:G:411:VAL:HG13	2.28	0.73
1:G:136:VAL:HA	1:G:137:PRO:HD2	1.70	0.73
1:A:136:VAL:HA	1:A:137:PRO:HD2	1.70	0.73
1:A:146:GLN:OE1	1:A:492:GLY:HA2	1.88	0.73
1:A:138:CYS:SG	1:A:411:VAL:HG13	2.28	0.73
1:E:105:LYS:HD3	1:K:110:GLY:HA3	1.69	0.73
1:F:146:GLN:OE1	1:F:492:GLY:HA2	1.88	0.73
1:F:203:TYR:OH	1:G:286:LYS:CD	2.25	0.73
1:B:138:CYS:SG	1:B:411:VAL:HG13	2.28	0.73
1:D:464:VAL:HG21	1:K:467:ASN:HB2	1.71	0.73
1:C:138:CYS:SG	1:C:411:VAL:HG13	2.28	0.73
1:I:136:VAL:HA	1:I:137:PRO:HD2	0.77	0.72
1:B:136:VAL:HA	1:B:137:PRO:HD2	1.70	0.72
1:E:138:CYS:SG	1:E:411:VAL:HG13	2.28	0.72
1:M:136:VAL:C	1:M:137:PRO:N	2.40	0.72
1:A:286:LYS:CD	1:G:203:TYR:OH	2.25	0.72
1:G:173:GLY:HA2	1:G:370:ALA:HB2	1.71	0.72
1:C:464:VAL:HG21	1:J:467:ASN:HB2	1.71	0.72
1:F:173:GLY:HA2	1:F:370:ALA:HB2	1.71	0.72
1:E:136:VAL:HA	1:E:137:PRO:HD2	1.70	0.72
1:M:136:VAL:N	1:M:137:PRO:N	2.25	0.72
1:C:136:VAL:HA	1:C:137:PRO:HD2	1.70	0.72
1:C:173:GLY:HA2	1:C:370:ALA:HB2	1.71	0.72
1:F:136:VAL:HA	1:F:137:PRO:HD2	1.70	0.72
2:O:80:PRO:O	2:P:110:TYR:OH	2.08	0.71
1:G:105:LYS:HD3	1:M:110:GLY:HA3	1.69	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:105:LYS:HD3	1:L:110:GLY:HA3	1.69	0.71
1:G:464:VAL:HG21	1:N:467:ASN:HB2	1.71	0.71
1:H:136:VAL:HA	1:H:137:PRO:HD2	0.77	0.71
1:A:173:GLY:HA2	1:A:370:ALA:HB2	1.71	0.71
1:D:173:GLY:HA2	1:D:370:ALA:HB2	1.71	0.71
2:P:102:HIS:HD2	2:P:104:LYS:H	1.38	0.71
1:B:173:GLY:HA2	1:B:370:ALA:HB2	1.71	0.71
2:S:102:HIS:HD2	2:S:104:LYS:H	1.38	0.71
2:R:102:HIS:HD2	2:R:104:LYS:H	1.38	0.71
1:M:18:ARG:CB	1:M:18:ARG:NH1	2.41	0.71
2:Q:80:PRO:O	2:R:110:TYR:OH	2.08	0.71
2:T:80:PRO:O	2:U:110:TYR:OH	2.08	0.71
1:A:464:VAL:HG21	1:H:467:ASN:HB2	1.71	0.71
1:D:373:ALA:O	1:D:374:GLY:O	1.84	0.71
1:H:18:ARG:CB	1:H:18:ARG:NH1	2.41	0.71
1:J:136:VAL:N	1:J:137:PRO:N	2.25	0.71
2:Q:102:HIS:HD2	2:Q:104:LYS:H	1.38	0.71
1:D:136:VAL:HA	1:D:137:PRO:HD2	1.70	0.71
1:E:203:TYR:OH	1:F:286:LYS:CD	2.26	0.71
2:R:80:PRO:O	2:S:110:TYR:OH	2.08	0.71
1:A:203:TYR:OH	1:B:286:LYS:CD	2.25	0.70
1:F:18:ARG:CB	1:F:18:ARG:NH1	2.41	0.70
2:U:102:HIS:HD2	2:U:104:LYS:H	1.38	0.70
1:J:398:ASP:O	1:J:401:HIS:HB2	1.92	0.70
1:K:398:ASP:O	1:K:401:HIS:HB2	1.92	0.70
1:N:136:VAL:HA	1:N:137:PRO:HD2	0.77	0.70
1:N:398:ASP:O	1:N:401:HIS:HB2	1.92	0.70
2:S:77:ARG:HD3	2:T:72:PRO:CG	2.22	0.70
1:D:18:ARG:CB	1:D:18:ARG:NH1	2.41	0.70
1:E:173:GLY:HA2	1:E:370:ALA:HB2	1.71	0.70
1:L:398:ASP:O	1:L:401:HIS:HB2	1.92	0.70
1:M:398:ASP:O	1:M:401:HIS:HB2	1.92	0.70
1:H:398:ASP:O	1:H:401:HIS:HB2	1.92	0.70
2:S:80:PRO:O	2:T:110:TYR:OH	2.08	0.70
1:F:464:VAL:HG21	1:M:467:ASN:HB2	1.71	0.70
2:R:77:ARG:HD3	2:S:72:PRO:CG	2.22	0.70
1:I:398:ASP:O	1:I:401:HIS:HB2	1.92	0.70
1:L:192:GLY:HA3	1:L:376:VAL:CG2	2.22	0.70
2:T:102:HIS:HD2	2:T:104:LYS:H	1.38	0.69
1:N:192:GLY:HA3	1:N:376:VAL:CG2	2.22	0.69
2:T:77:ARG:HD3	2:U:72:PRO:CG	2.22	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:138:CYS:HB2	1:I:410:GLY:C	2.13	0.69
2:O:110:TYR:OH	2:U:80:PRO:O	2.08	0.69
2:P:80:PRO:O	2:Q:110:TYR:OH	2.08	0.69
2:R:80:PRO:CG	2:S:70:SER:OG	2.40	0.69
1:K:136:VAL:HA	1:K:137:PRO:HD2	0.77	0.69
1:K:138:CYS:HB2	1:K:410:GLY:C	2.12	0.69
2:O:72:PRO:CG	2:U:77:ARG:HD3	2.22	0.69
2:O:77:ARG:HD3	2:P:72:PRO:CG	2.22	0.69
2:Q:80:PRO:CG	2:R:70:SER:OG	2.40	0.69
1:K:176:THR:HG21	1:K:333:ILE:HD11	1.75	0.69
1:L:176:THR:HG21	1:L:333:ILE:HD11	1.75	0.69
1:N:176:THR:HG21	1:N:333:ILE:HD11	1.75	0.69
1:H:176:THR:HG21	1:H:333:ILE:HD11	1.75	0.69
1:K:192:GLY:HA3	1:K:376:VAL:CG2	2.22	0.69
1:L:138:CYS:HB2	1:L:410:GLY:C	2.13	0.69
1:L:175:ILE:HD12	1:L:175:ILE:N	2.08	0.69
1:M:176:THR:HG21	1:M:333:ILE:HD11	1.75	0.69
1:J:192:GLY:HA3	1:J:376:VAL:CG2	2.22	0.69
1:M:136:VAL:HA	1:M:137:PRO:HD2	0.77	0.69
1:M:157:THR:O	1:M:160:LYS:HB3	1.93	0.69
1:M:414:GLY:O	1:M:417:VAL:CG1	2.41	0.69
1:I:192:GLY:HA3	1:I:376:VAL:CG2	2.22	0.69
1:N:137:PRO:C	1:N:410:GLY:CA	2.62	0.69
2:P:80:PRO:CG	2:Q:70:SER:OG	2.40	0.69
1:B:18:ARG:HH11	1:B:18:ARG:CG	2.06	0.68
1:B:414:GLY:O	1:B:417:VAL:CG1	2.41	0.68
1:H:18:ARG:HH11	1:H:18:ARG:CG	2.06	0.68
1:J:176:THR:HG21	1:J:333:ILE:HD11	1.75	0.68
1:L:157:THR:O	1:L:160:LYS:HB3	1.93	0.68
1:M:137:PRO:C	1:M:410:GLY:CA	2.62	0.68
1:N:157:THR:O	1:N:160:LYS:HB3	1.93	0.68
2:O:102:HIS:HD2	2:O:104:LYS:H	1.38	0.68
1:H:192:GLY:HA3	1:H:376:VAL:CG2	2.22	0.68
1:I:175:ILE:HD12	1:I:175:ILE:N	2.08	0.68
1:L:414:GLY:O	1:L:417:VAL:CG1	2.41	0.68
1:N:192:GLY:C	1:N:376:VAL:HG23	2.14	0.68
2:Q:77:ARG:HD3	2:R:72:PRO:CG	2.22	0.68
1:A:18:ARG:HH11	1:A:18:ARG:CG	2.06	0.68
1:D:414:GLY:O	1:D:417:VAL:CG1	2.41	0.68
1:E:18:ARG:CB	1:E:18:ARG:NH1	2.41	0.68
1:K:137:PRO:C	1:K:410:GLY:CA	2.62	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:157:THR:O	1:K:160:LYS:HB3	1.93	0.68
1:K:175:ILE:N	1:K:175:ILE:HD12	2.08	0.68
1:L:381:VAL:HB	1:L:389:MET:HE3	1.76	0.68
1:N:414:GLY:O	1:N:417:VAL:CG1	2.41	0.68
1:A:414:GLY:O	1:A:417:VAL:CG1	2.41	0.68
1:C:18:ARG:HH11	1:C:18:ARG:CG	2.07	0.68
1:E:414:GLY:O	1:E:417:VAL:CG1	2.41	0.68
1:F:414:GLY:O	1:F:417:VAL:CG1	2.41	0.68
1:I:192:GLY:C	1:I:376:VAL:HG23	2.14	0.68
1:K:381:VAL:HB	1:K:389:MET:HE3	1.76	0.68
1:M:175:ILE:N	1:M:175:ILE:HD12	2.08	0.68
2:P:77:ARG:HD3	2:Q:72:PRO:CG	2.22	0.68
1:C:18:ARG:CB	1:C:18:ARG:NH1	2.41	0.68
1:G:414:GLY:O	1:G:417:VAL:CG1	2.41	0.68
1:I:18:ARG:CB	1:I:18:ARG:NH1	2.41	0.68
1:J:137:PRO:C	1:J:410:GLY:CA	2.62	0.68
1:C:138:CYS:N	1:C:410:GLY:HA2	2.09	0.68
1:G:18:ARG:HH11	1:G:18:ARG:CG	2.06	0.68
1:I:176:THR:HG21	1:I:333:ILE:HD11	1.75	0.68
1:J:18:ARG:HH11	1:J:18:ARG:CG	2.07	0.68
1:J:192:GLY:C	1:J:376:VAL:HG23	2.14	0.68
1:N:381:VAL:HB	1:N:389:MET:HE3	1.76	0.68
1:D:18:ARG:HH11	1:D:18:ARG:CG	2.06	0.68
1:H:137:PRO:C	1:H:410:GLY:CA	2.62	0.68
1:H:157:THR:O	1:H:160:LYS:HB3	1.93	0.68
1:J:157:THR:O	1:J:160:LYS:HB3	1.93	0.68
2:O:80:PRO:CG	2:P:70:SER:OG	2.40	0.68
1:F:18:ARG:HH11	1:F:18:ARG:CG	2.06	0.68
1:I:157:THR:O	1:I:160:LYS:HB3	1.93	0.68
1:M:18:ARG:HH11	1:M:18:ARG:CG	2.06	0.68
1:M:138:CYS:HB2	1:M:410:GLY:C	2.12	0.68
1:E:18:ARG:HH11	1:E:18:ARG:CG	2.06	0.68
1:H:175:ILE:N	1:H:175:ILE:HD12	2.08	0.68
1:I:137:PRO:C	1:I:410:GLY:CA	2.62	0.68
1:L:137:PRO:C	1:L:410:GLY:CA	2.62	0.68
1:K:414:GLY:O	1:K:417:VAL:CG1	2.41	0.68
1:L:192:GLY:C	1:L:376:VAL:HG23	2.14	0.68
1:M:192:GLY:C	1:M:376:VAL:HG23	2.14	0.68
1:M:192:GLY:HA3	1:M:376:VAL:CG2	2.22	0.68
1:H:414:GLY:O	1:H:417:VAL:CG1	2.41	0.67
1:I:404:ARG:O	1:I:408:GLU:HG3	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:70:SER:OG	2:U:80:PRO:CG	2.40	0.67
2:T:80:PRO:CG	2:U:70:SER:OG	2.40	0.67
1:C:414:GLY:O	1:C:417:VAL:CG1	2.41	0.67
1:H:404:ARG:O	1:H:408:GLU:HG3	1.94	0.67
1:I:381:VAL:HB	1:I:389:MET:HE3	1.76	0.67
1:J:381:VAL:HB	1:J:389:MET:HE3	1.76	0.67
1:A:138:CYS:N	1:A:410:GLY:HA2	2.09	0.67
1:E:138:CYS:N	1:E:410:GLY:HA2	2.09	0.67
1:B:138:CYS:N	1:B:410:GLY:HA2	2.09	0.67
1:H:192:GLY:C	1:H:376:VAL:HG23	2.14	0.67
1:I:18:ARG:HH11	1:I:18:ARG:CG	2.07	0.67
1:I:192:GLY:HA3	1:I:376:VAL:HG23	1.76	0.67
1:J:192:GLY:HA3	1:J:376:VAL:HG23	1.76	0.67
1:N:18:ARG:HH11	1:N:18:ARG:CG	2.06	0.67
1:A:304:GLU:OE2	1:G:203:TYR:HE2	1.78	0.67
1:C:209:GLU:O	1:D:351:GLN:NE2	2.28	0.67
1:J:414:GLY:O	1:J:417:VAL:CG1	2.41	0.67
1:K:192:GLY:C	1:K:376:VAL:HG23	2.14	0.67
2:P:82:PRO:CA	2:Q:110:TYR:CE1	2.78	0.67
1:A:351:GLN:NE2	1:G:209:GLU:O	2.28	0.67
1:E:209:GLU:O	1:F:351:GLN:NE2	2.28	0.67
1:F:138:CYS:N	1:F:410:GLY:HA2	2.09	0.67
1:G:138:CYS:N	1:G:410:GLY:HA2	2.09	0.67
1:J:138:CYS:HB2	1:J:410:GLY:C	2.12	0.67
1:J:175:ILE:HD12	1:J:175:ILE:N	2.08	0.67
1:L:136:VAL:HA	1:L:137:PRO:HD2	0.77	0.67
1:L:404:ARG:O	1:L:408:GLU:HG3	1.94	0.67
1:A:203:TYR:HE2	1:B:304:GLU:OE2	1.78	0.67
1:D:138:CYS:N	1:D:410:GLY:HA2	2.09	0.67
1:F:209:GLU:O	1:G:351:GLN:NE2	2.28	0.67
1:I:414:GLY:O	1:I:417:VAL:CG1	2.41	0.67
1:J:404:ARG:O	1:J:408:GLU:HG3	1.94	0.67
1:N:138:CYS:HB2	1:N:410:GLY:C	2.12	0.67
1:N:175:ILE:HD12	1:N:175:ILE:N	2.08	0.67
1:N:404:ARG:O	1:N:408:GLU:HG3	1.94	0.67
1:B:417:VAL:HG11	1:B:488:MET:HG3	1.77	0.67
1:G:13:ARG:HD2	1:G:104:LEU:HD22	1.77	0.67
1:H:381:VAL:HB	1:H:389:MET:HE3	1.76	0.67
1:K:18:ARG:HH11	1:K:18:ARG:CG	2.07	0.67
1:A:13:ARG:HD2	1:A:104:LEU:HD22	1.77	0.67
1:C:13:ARG:HD2	1:C:104:LEU:HD22	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:13:ARG:HD2	1:D:104:LEU:HD22	1.77	0.67
1:F:203:TYR:HE2	1:G:304:GLU:OE2	1.78	0.67
1:G:138:CYS:HB3	1:G:410:GLY:CA	2.22	0.67
1:L:13:ARG:HD2	1:L:104:LEU:HD22	1.77	0.67
2:Q:77:ARG:HD3	2:R:72:PRO:HG2	1.77	0.67
2:R:77:ARG:HD3	2:S:72:PRO:HG2	1.77	0.67
2:R:82:PRO:CA	2:S:110:TYR:CE1	2.78	0.67
1:K:192:GLY:HA3	1:K:376:VAL:HG23	1.76	0.67
2:S:80:PRO:CG	2:T:70:SER:OG	2.40	0.67
1:A:74:VAL:O	1:A:77:VAL:HG13	1.95	0.66
1:A:417:VAL:HG11	1:A:488:MET:HG3	1.77	0.66
1:C:417:VAL:HG11	1:C:488:MET:HG3	1.77	0.66
1:F:74:VAL:O	1:F:77:VAL:HG13	1.96	0.66
1:J:18:ARG:CB	1:J:18:ARG:NH1	2.41	0.66
1:A:209:GLU:O	1:B:351:GLN:NE2	2.28	0.66
1:C:150:ILE:HD11	1:C:493:ILE:HA	1.78	0.66
1:D:150:ILE:HD11	1:D:493:ILE:HA	1.78	0.66
1:G:74:VAL:O	1:G:77:VAL:HG13	1.96	0.66
1:H:74:VAL:O	1:H:77:VAL:HG13	1.95	0.66
1:H:192:GLY:HA3	1:H:376:VAL:HG23	1.76	0.66
1:J:13:ARG:HD2	1:J:104:LEU:HD22	1.77	0.66
1:K:13:ARG:HD2	1:K:104:LEU:HD22	1.77	0.66
1:L:18:ARG:HH11	1:L:18:ARG:CG	2.06	0.66
2:T:82:PRO:CA	2:U:110:TYR:CE1	2.78	0.66
1:A:138:CYS:HB3	1:A:410:GLY:CA	2.22	0.66
1:E:74:VAL:O	1:E:77:VAL:HG13	1.96	0.66
1:F:13:ARG:HD2	1:F:104:LEU:HD22	1.77	0.66
1:F:138:CYS:HB3	1:F:410:GLY:CA	2.22	0.66
1:K:404:ARG:O	1:K:408:GLU:HG3	1.94	0.66
1:L:74:VAL:O	1:L:77:VAL:HG13	1.95	0.66
1:M:381:VAL:HB	1:M:389:MET:HE3	1.76	0.66
2:Q:82:PRO:CA	2:R:110:TYR:CE1	2.78	0.66
2:S:77:ARG:HD3	2:T:72:PRO:HG2	1.77	0.66
1:E:150:ILE:HD11	1:E:493:ILE:HA	1.78	0.66
1:I:13:ARG:HD2	1:I:104:LEU:HD22	1.78	0.66
1:I:74:VAL:O	1:I:77:VAL:HG13	1.95	0.66
2:S:82:PRO:CA	2:T:110:TYR:CE1	2.78	0.66
1:A:18:ARG:CB	1:A:18:ARG:NH1	2.41	0.66
1:E:13:ARG:HD2	1:E:104:LEU:HD22	1.77	0.66
1:L:452:ARG:HG2	1:L:452:ARG:NH1	2.11	0.66
2:T:77:ARG:HD3	2:U:72:PRO:HG2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:13:ARG:HD2	1:B:104:LEU:HD22	1.77	0.66
1:B:209:GLU:O	1:C:351:GLN:NE2	2.28	0.66
1:D:138:CYS:HB3	1:D:410:GLY:CA	2.22	0.66
1:D:209:GLU:O	1:E:351:GLN:NE2	2.28	0.66
1:G:417:VAL:HG11	1:G:488:MET:HG3	1.77	0.66
1:I:452:ARG:HG2	1:I:452:ARG:NH1	2.11	0.66
1:J:417:VAL:HG11	1:J:488:MET:HG3	1.77	0.66
1:M:13:ARG:HD2	1:M:104:LEU:HD22	1.78	0.66
1:N:147:VAL:CG2	1:N:496:PRO:HG3	2.14	0.66
1:B:74:VAL:O	1:B:77:VAL:HG13	1.95	0.66
1:B:138:CYS:HB3	1:B:410:GLY:CA	2.22	0.66
1:B:452:ARG:NH1	1:B:452:ARG:HG2	2.11	0.66
1:K:18:ARG:CB	1:K:18:ARG:NH1	2.41	0.66
2:O:82:PRO:CA	2:P:110:TYR:CE1	2.78	0.66
2:P:77:ARG:HD3	2:Q:72:PRO:HG2	1.77	0.66
1:L:417:VAL:HG11	1:L:488:MET:HG3	1.77	0.66
1:M:74:VAL:O	1:M:77:VAL:HG13	1.95	0.66
1:B:150:ILE:HD11	1:B:493:ILE:HA	1.78	0.66
1:B:203:TYR:HE2	1:C:304:GLU:OE2	1.78	0.66
1:E:138:CYS:HB3	1:E:410:GLY:CA	2.22	0.66
1:I:138:CYS:N	1:I:410:GLY:HA2	2.11	0.66
1:L:192:GLY:HA3	1:L:376:VAL:HG23	1.76	0.66
1:M:417:VAL:HG11	1:M:488:MET:HG3	1.77	0.66
1:H:13:ARG:HD2	1:H:104:LEU:HD22	1.77	0.66
1:I:417:VAL:HG11	1:I:488:MET:HG3	1.77	0.66
1:J:74:VAL:O	1:J:77:VAL:HG13	1.95	0.66
1:L:3:ALA:HB1	1:M:63:GLU:HB2	1.78	0.66
1:A:452:ARG:HG2	1:A:452:ARG:NH1	2.11	0.65
1:C:138:CYS:HB3	1:C:410:GLY:CA	2.22	0.65
1:J:138:CYS:N	1:J:410:GLY:HA2	2.11	0.65
1:K:417:VAL:HG11	1:K:488:MET:HG3	1.77	0.65
1:K:452:ARG:NH1	1:K:452:ARG:HG2	2.11	0.65
1:M:404:ARG:O	1:M:408:GLU:HG3	1.94	0.65
1:D:74:VAL:O	1:D:77:VAL:HG13	1.96	0.65
1:D:417:VAL:HG11	1:D:488:MET:HG3	1.77	0.65
1:E:417:VAL:HG11	1:E:488:MET:HG3	1.77	0.65
1:F:150:ILE:HD11	1:F:493:ILE:HA	1.78	0.65
1:H:138:CYS:N	1:H:410:GLY:HA2	2.11	0.65
1:I:155:ASP:OD1	1:I:158:VAL:HG23	1.97	0.65
1:E:464:VAL:HG21	1:L:467:ASN:HB2	1.71	0.65
1:M:155:ASP:OD1	1:M:158:VAL:HG23	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:102:HIS:CD2	2:P:104:LYS:H	2.15	0.65
1:H:138:CYS:HB2	1:H:410:GLY:C	2.12	0.65
1:K:155:ASP:OD1	1:K:158:VAL:HG23	1.97	0.65
2:O:72:PRO:HG2	2:U:77:ARG:HD3	1.77	0.65
1:E:452:ARG:NH1	1:E:452:ARG:HG2	2.11	0.65
1:H:452:ARG:NH1	1:H:452:ARG:HG2	2.11	0.65
1:J:452:ARG:NH1	1:J:452:ARG:HG2	2.11	0.65
1:K:74:VAL:O	1:K:77:VAL:HG13	1.95	0.65
1:M:452:ARG:NH1	1:M:452:ARG:HG2	2.11	0.65
2:T:102:HIS:CD2	2:T:104:LYS:H	2.15	0.65
1:E:203:TYR:HE2	1:F:304:GLU:OE2	1.78	0.65
1:H:3:ALA:HB1	1:I:63:GLU:HB2	1.78	0.65
1:H:63:GLU:HB2	1:N:3:ALA:HB1	1.78	0.65
1:K:138:CYS:N	1:K:410:GLY:HA2	2.11	0.65
1:K:448:GLU:HB3	1:K:452:ARG:HD2	1.79	0.65
1:N:13:ARG:HD2	1:N:104:LEU:HD22	1.77	0.65
2:O:110:TYR:CE1	2:U:82:PRO:CA	2.78	0.65
1:A:150:ILE:HD11	1:A:493:ILE:HA	1.78	0.65
1:C:448:GLU:HB3	1:C:452:ARG:HD2	1.79	0.65
1:F:417:VAL:HG11	1:F:488:MET:HG3	1.77	0.65
1:J:155:ASP:OD1	1:J:158:VAL:HG23	1.97	0.65
1:L:448:GLU:HB3	1:L:452:ARG:HD2	1.79	0.65
1:N:417:VAL:HG11	1:N:488:MET:HG3	1.77	0.65
2:R:102:HIS:CD2	2:R:104:LYS:H	2.15	0.65
2:U:102:HIS:CD2	2:U:104:LYS:H	2.15	0.65
1:C:74:VAL:O	1:C:77:VAL:HG13	1.96	0.65
1:C:203:TYR:HH	1:D:286:LYS:HD3	1.57	0.65
1:D:448:GLU:HB3	1:D:452:ARG:HD2	1.79	0.65
1:E:448:GLU:HB3	1:E:452:ARG:HD2	1.79	0.65
1:F:146:GLN:HB2	1:F:494:LEU:CD1	2.27	0.65
1:H:417:VAL:HG11	1:H:488:MET:HG3	1.77	0.65
1:J:448:GLU:HB3	1:J:452:ARG:HD2	1.79	0.65
1:M:192:GLY:HA3	1:M:376:VAL:HG23	1.76	0.65
1:N:138:CYS:N	1:N:410:GLY:HA2	2.11	0.65
1:N:155:ASP:OD1	1:N:158:VAL:HG23	1.97	0.65
1:F:448:GLU:HB3	1:F:452:ARG:HD2	1.79	0.65
1:F:452:ARG:NH1	1:F:452:ARG:HG2	2.11	0.65
1:G:146:GLN:HB2	1:G:494:LEU:CD1	2.27	0.65
1:L:18:ARG:CB	1:L:18:ARG:NH1	2.41	0.65
1:M:448:GLU:HB3	1:M:452:ARG:HD2	1.79	0.65
1:N:74:VAL:O	1:N:77:VAL:HG13	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:77:ARG:HD3	2:P:72:PRO:HG2	1.77	0.65
1:B:18:ARG:CB	1:B:18:ARG:NH1	2.41	0.65
1:B:146:GLN:HB2	1:B:494:LEU:CD1	2.27	0.65
1:C:146:GLN:HB2	1:C:494:LEU:CD1	2.27	0.65
1:G:150:ILE:HD11	1:G:493:ILE:HA	1.78	0.65
1:M:147:VAL:CG2	1:M:496:PRO:HG3	2.14	0.65
1:N:192:GLY:HA3	1:N:376:VAL:HG23	1.76	0.65
1:N:448:GLU:HB3	1:N:452:ARG:HD2	1.79	0.65
2:O:102:HIS:CD2	2:O:104:LYS:H	2.15	0.65
1:A:146:GLN:HB2	1:A:494:LEU:CD1	2.27	0.64
1:D:146:GLN:HB2	1:D:494:LEU:CD1	2.27	0.64
1:E:146:GLN:HB2	1:E:494:LEU:CD1	2.27	0.64
1:M:3:ALA:HB1	1:N:63:GLU:HB2	1.78	0.64
1:B:448:GLU:HB3	1:B:452:ARG:HD2	1.79	0.64
1:H:448:GLU:HB3	1:H:452:ARG:HD2	1.79	0.64
1:I:448:GLU:HB3	1:I:452:ARG:HD2	1.79	0.64
1:D:452:ARG:HG2	1:D:452:ARG:NH1	2.11	0.64
1:L:138:CYS:N	1:L:410:GLY:HA2	2.11	0.64
1:I:3:ALA:HB1	1:J:63:GLU:HB2	1.78	0.64
1:M:138:CYS:N	1:M:410:GLY:HA2	2.11	0.64
2:S:102:HIS:CD2	2:S:104:LYS:H	2.15	0.64
1:A:448:GLU:HB3	1:A:452:ARG:HD2	1.79	0.64
1:E:452:ARG:HG2	1:E:452:ARG:HH11	1.63	0.64
1:F:452:ARG:HG2	1:F:452:ARG:HH11	1.63	0.64
1:G:452:ARG:HG2	1:G:452:ARG:NH1	2.11	0.64
1:K:87:ASP:OD2	1:K:151:SER:HA	1.98	0.64
1:K:171:LYS:HD3	1:K:407:VAL:HG11	1.80	0.64
1:M:87:ASP:OD2	1:M:151:SER:HA	1.98	0.64
1:N:452:ARG:NH1	1:N:452:ARG:HG2	2.11	0.64
1:G:448:GLU:HB3	1:G:452:ARG:HD2	1.79	0.64
1:G:452:ARG:HG2	1:G:452:ARG:HH11	1.63	0.64
1:H:155:ASP:OD1	1:H:158:VAL:HG23	1.97	0.64
1:I:87:ASP:OD2	1:I:151:SER:HA	1.98	0.64
1:J:3:ALA:HB1	1:K:63:GLU:HB2	1.78	0.64
1:J:171:LYS:HD3	1:J:407:VAL:HG11	1.80	0.64
1:K:452:ARG:HG2	1:K:452:ARG:HH11	1.63	0.64
1:N:18:ARG:CB	1:N:18:ARG:NH1	2.41	0.64
2:Q:102:HIS:CD2	2:Q:104:LYS:H	2.15	0.64
1:C:452:ARG:NH1	1:C:452:ARG:HG2	2.11	0.64
1:J:452:ARG:HG2	1:J:452:ARG:HH11	1.63	0.64
1:K:25:ASP:HA	1:K:28:LYS:HE2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:452:ARG:HG2	1:L:452:ARG:HH11	1.63	0.64
1:N:87:ASP:OD2	1:N:151:SER:HA	1.98	0.64
1:B:44:PHE:CD1	1:B:44:PHE:N	2.66	0.64
1:C:203:TYR:HE2	1:D:304:GLU:OE2	1.78	0.64
1:G:18:ARG:CB	1:G:18:ARG:NH1	2.41	0.64
1:I:25:ASP:HA	1:I:28:LYS:HE2	1.80	0.64
1:I:452:ARG:HG2	1:I:452:ARG:HH11	1.63	0.64
1:J:25:ASP:HA	1:J:28:LYS:HE2	1.80	0.64
2:R:10:ARG:O	2:S:108:CYS:HA	1.98	0.64
1:A:477:GLY:HA3	1:A:488:MET:SD	2.38	0.64
1:C:44:PHE:CD1	1:C:44:PHE:N	2.66	0.64
1:D:452:ARG:HG2	1:D:452:ARG:HH11	1.63	0.64
1:G:105:LYS:CG	1:M:109:ALA:O	2.45	0.64
1:H:25:ASP:HA	1:H:28:LYS:HE2	1.80	0.64
1:L:25:ASP:HA	1:L:28:LYS:HE2	1.80	0.64
1:L:155:ASP:OD1	1:L:158:VAL:HG23	1.97	0.64
1:I:171:LYS:HD3	1:I:407:VAL:HG11	1.79	0.64
1:M:477:GLY:HA3	1:M:488:MET:SD	2.38	0.64
2:P:10:ARG:O	2:Q:108:CYS:HA	1.98	0.64
1:B:464:VAL:HG21	1:I:467:ASN:HB2	1.71	0.63
1:B:477:GLY:HA3	1:B:488:MET:SD	2.38	0.63
1:G:477:GLY:HA3	1:G:488:MET:SD	2.38	0.63
1:H:87:ASP:OD2	1:H:151:SER:HA	1.98	0.63
1:I:477:GLY:HA3	1:I:488:MET:SD	2.38	0.63
1:L:87:ASP:OD2	1:L:151:SER:HA	1.98	0.63
1:A:452:ARG:HG2	1:A:452:ARG:HH11	1.63	0.63
1:K:477:GLY:HA3	1:K:488:MET:SD	2.38	0.63
1:M:157:THR:O	1:M:161:LEU:HD13	1.98	0.63
1:N:477:GLY:HA3	1:N:488:MET:SD	2.38	0.63
1:A:44:PHE:CD1	1:A:44:PHE:N	2.66	0.63
1:J:477:GLY:HA3	1:J:488:MET:SD	2.39	0.63
1:L:477:GLY:HA3	1:L:488:MET:SD	2.39	0.63
2:Q:10:ARG:O	2:R:108:CYS:HA	1.98	0.63
1:C:452:ARG:HG2	1:C:452:ARG:HH11	1.63	0.63
1:K:3:ALA:HB1	1:L:63:GLU:HB2	1.78	0.63
1:L:171:LYS:HD3	1:L:407:VAL:HG11	1.80	0.63
1:N:452:ARG:HG2	1:N:452:ARG:HH11	1.63	0.63
2:O:108:CYS:HA	2:U:10:ARG:O	1.98	0.63
1:B:452:ARG:HG2	1:B:452:ARG:HH11	1.63	0.63
1:C:477:GLY:HA3	1:C:488:MET:SD	2.38	0.63
1:B:25:ASP:HA	1:B:28:LYS:HE2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:44:PHE:CD1	1:D:44:PHE:N	2.66	0.63
1:M:25:ASP:HA	1:M:28:LYS:HE2	1.80	0.63
1:N:25:ASP:HA	1:N:28:LYS:HE2	1.80	0.63
1:N:171:LYS:HD3	1:N:407:VAL:HG11	1.79	0.63
1:E:44:PHE:CD1	1:E:44:PHE:N	2.66	0.63
1:F:477:GLY:HA3	1:F:488:MET:SD	2.38	0.63
1:H:452:ARG:HG2	1:H:452:ARG:HH11	1.63	0.63
1:N:145:ALA:HA	1:N:159:GLY:O	1.99	0.63
2:O:10:ARG:O	2:P:108:CYS:HA	1.98	0.63
2:T:10:ARG:O	2:U:108:CYS:HA	1.98	0.63
1:A:25:ASP:HA	1:A:28:LYS:HE2	1.80	0.63
1:H:157:THR:O	1:H:161:LEU:HD13	1.98	0.63
1:M:452:ARG:HG2	1:M:452:ARG:HH11	1.63	0.63
1:G:44:PHE:CD1	1:G:44:PHE:N	2.66	0.63
1:M:138:CYS:N	1:M:410:GLY:CA	2.62	0.63
1:M:171:LYS:HD3	1:M:407:VAL:HG11	1.79	0.63
2:S:10:ARG:O	2:T:108:CYS:HA	1.98	0.63
1:C:25:ASP:HA	1:C:28:LYS:HE2	1.80	0.62
1:H:145:ALA:HA	1:H:159:GLY:O	1.99	0.62
1:J:87:ASP:OD2	1:J:151:SER:HA	1.98	0.62
1:J:145:ALA:HA	1:J:159:GLY:O	1.99	0.62
1:J:138:CYS:N	1:J:410:GLY:CA	2.62	0.62
1:L:138:CYS:N	1:L:410:GLY:CA	2.62	0.62
1:I:155:ASP:CG	1:I:158:VAL:HG23	2.20	0.62
1:J:155:ASP:CG	1:J:158:VAL:HG23	2.20	0.62
1:K:155:ASP:CG	1:K:158:VAL:HG23	2.20	0.62
1:H:171:LYS:HD3	1:H:407:VAL:HG11	1.80	0.62
1:H:477:GLY:HA3	1:H:488:MET:SD	2.38	0.62
1:J:157:THR:O	1:J:161:LEU:HD13	1.98	0.62
1:M:145:ALA:HA	1:M:159:GLY:O	1.99	0.62
1:N:138:CYS:N	1:N:410:GLY:CA	2.62	0.62
1:N:155:ASP:CG	1:N:158:VAL:HG23	2.20	0.62
2:O:82:PRO:HB3	2:P:110:TYR:CD1	2.35	0.62
2:T:82:PRO:HB3	2:U:110:TYR:CD1	2.35	0.62
1:D:25:ASP:HA	1:D:28:LYS:HE2	1.80	0.62
1:H:155:ASP:CG	1:H:158:VAL:HG23	2.20	0.62
2:O:110:TYR:CD1	2:U:82:PRO:HB3	2.35	0.62
1:E:263:VAL:CG1	1:F:305:ILE:HG22	2.30	0.62
1:K:157:THR:O	1:K:161:LEU:HD13	1.98	0.62
1:L:155:ASP:CG	1:L:158:VAL:HG23	2.20	0.62
1:N:157:THR:O	1:N:161:LEU:HD13	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:190:VAL:CG2	1:N:334:ASP:OD2	2.47	0.62
1:D:477:GLY:HA3	1:D:488:MET:SD	2.38	0.62
1:H:44:PHE:CD1	1:H:44:PHE:N	2.66	0.62
1:I:138:CYS:N	1:I:410:GLY:CA	2.62	0.62
1:J:235:PRO:HG3	1:J:310:GLU:HA	1.82	0.62
1:K:145:ALA:HA	1:K:159:GLY:O	1.99	0.62
2:P:82:PRO:HB3	2:Q:110:TYR:CD1	2.35	0.62
1:F:263:VAL:CG1	1:G:305:ILE:HG22	2.30	0.62
1:G:25:ASP:HA	1:G:28:LYS:HE2	1.80	0.62
1:H:190:VAL:CG2	1:H:334:ASP:OD2	2.47	0.62
1:I:235:PRO:HG3	1:I:310:GLU:HA	1.82	0.62
1:L:157:THR:O	1:L:161:LEU:HD13	1.98	0.62
1:C:263:VAL:CG1	1:D:305:ILE:HG22	2.30	0.62
1:D:263:VAL:CG1	1:E:305:ILE:HG22	2.30	0.62
1:E:25:ASP:HA	1:E:28:LYS:HE2	1.80	0.62
1:E:477:GLY:HA3	1:E:488:MET:SD	2.38	0.62
1:I:44:PHE:CD1	1:I:44:PHE:N	2.66	0.62
1:K:138:CYS:N	1:K:410:GLY:CA	2.62	0.62
1:M:155:ASP:CG	1:M:158:VAL:HG23	2.20	0.62
1:B:263:VAL:CG1	1:C:305:ILE:HG22	2.30	0.62
1:C:146:GLN:HE21	1:C:494:LEU:HD11	0.77	0.62
1:D:203:TYR:HE2	1:E:304:GLU:OE2	1.78	0.61
1:H:235:PRO:HG3	1:H:310:GLU:HA	1.82	0.61
1:I:157:THR:O	1:I:161:LEU:HD13	1.98	0.61
2:S:82:PRO:HB3	2:T:110:TYR:CD1	2.35	0.61
1:H:169:VAL:HG22	1:H:169:VAL:O	2.01	0.61
1:L:145:ALA:HA	1:L:159:GLY:O	1.99	0.61
1:N:235:PRO:HG3	1:N:310:GLU:HA	1.82	0.61
1:A:105:LYS:CG	1:N:109:ALA:O	2.45	0.61
1:I:145:ALA:HA	1:I:159:GLY:O	1.99	0.61
1:I:169:VAL:O	1:I:169:VAL:HG22	2.01	0.61
1:K:169:VAL:O	1:K:169:VAL:HG22	2.01	0.61
1:A:305:ILE:HG22	1:G:263:VAL:CG1	2.30	0.61
1:F:25:ASP:HA	1:F:28:LYS:HE2	1.80	0.61
1:J:169:VAL:HG22	1:J:169:VAL:O	2.01	0.61
1:K:235:PRO:HG3	1:K:310:GLU:HA	1.82	0.61
1:A:325:ILE:HG12	1:A:330:THR:HG23	1.83	0.61
1:K:190:VAL:CG2	1:K:334:ASP:OD2	2.47	0.61
1:A:263:VAL:CG1	1:B:305:ILE:HG22	2.30	0.61
2:R:82:PRO:HB3	2:S:110:TYR:CD1	2.35	0.61
1:F:105:LYS:CG	1:L:109:ALA:O	2.45	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Q:82:PRO:HB3	2:R:110:TYR:CD1	2.35	0.61
1:G:325:ILE:HG12	1:G:330:THR:HG23	1.83	0.61
1:J:190:VAL:CG2	1:J:334:ASP:OD2	2.47	0.61
1:L:169:VAL:O	1:L:169:VAL:HG22	2.01	0.61
2:O:8:PRO:O	2:P:110:TYR:HA	2.01	0.61
2:P:8:PRO:O	2:Q:110:TYR:HA	2.01	0.61
1:H:138:CYS:N	1:H:410:GLY:CA	2.62	0.61
1:M:190:VAL:CG2	1:M:334:ASP:OD2	2.47	0.61
1:M:235:PRO:HG3	1:M:310:GLU:HA	1.82	0.61
1:A:305:ILE:CD1	1:G:267:MET:SD	2.89	0.61
1:B:325:ILE:HG12	1:B:330:THR:HG23	1.83	0.61
1:M:385:THR:HG23	1:M:388:GLU:HB3	1.83	0.61
2:T:8:PRO:O	2:U:110:TYR:HA	2.01	0.61
1:M:44:PHE:CD1	1:M:44:PHE:N	2.66	0.60
1:N:385:THR:HG23	1:N:388:GLU:HB3	1.83	0.60
2:S:8:PRO:O	2:T:110:TYR:HA	2.01	0.60
1:N:169:VAL:O	1:N:169:VAL:HG22	2.01	0.60
2:O:110:TYR:HA	2:U:8:PRO:O	2.01	0.60
2:Q:8:PRO:O	2:R:110:TYR:HA	2.01	0.60
1:I:190:VAL:CG2	1:I:334:ASP:OD2	2.47	0.60
1:K:430:ARG:HG2	1:K:430:ARG:NH1	2.17	0.60
1:L:385:THR:O	1:L:389:MET:HB2	2.02	0.60
1:F:463:SER:CB	1:M:464:VAL:HG21	2.27	0.60
1:K:385:THR:HG23	1:K:388:GLU:HB3	1.83	0.60
1:L:385:THR:HG23	1:L:388:GLU:HB3	1.83	0.60
1:N:44:PHE:CD1	1:N:44:PHE:N	2.66	0.60
1:E:267:MET:SD	1:F:305:ILE:CD1	2.89	0.60
1:F:267:MET:SD	1:G:305:ILE:CD1	2.89	0.60
1:F:325:ILE:HG12	1:F:330:THR:HG23	1.83	0.60
1:I:400:LEU:HD23	1:I:400:LEU:C	2.22	0.60
1:J:44:PHE:CD1	1:J:44:PHE:N	2.66	0.60
1:L:235:PRO:HG3	1:L:310:GLU:HA	1.82	0.60
1:L:516:THR:C	1:M:36:ARG:NH1	2.55	0.60
1:N:400:LEU:HD23	1:N:400:LEU:C	2.22	0.60
1:B:267:MET:SD	1:C:305:ILE:CD1	2.89	0.60
1:K:516:THR:C	1:L:36:ARG:NH1	2.55	0.60
1:N:385:THR:O	1:N:389:MET:HB2	2.02	0.60
1:N:510:VAL:HG12	1:N:514:MET:CE	2.32	0.60
2:R:8:PRO:O	2:S:110:TYR:HA	2.01	0.60
1:H:385:THR:O	1:H:389:MET:HB2	2.02	0.60
1:L:147:VAL:CG2	1:L:496:PRO:HB3	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:430:ARG:HG2	1:M:430:ARG:NH1	2.17	0.60
1:D:146:GLN:HE21	1:D:494:LEU:HD11	0.77	0.60
1:F:146:GLN:HE21	1:F:494:LEU:HD11	0.77	0.60
1:H:385:THR:HG23	1:H:388:GLU:HB3	1.83	0.60
1:J:400:LEU:HD23	1:J:400:LEU:C	2.22	0.60
1:L:510:VAL:HG12	1:L:514:MET:CE	2.32	0.60
1:M:510:VAL:HG12	1:M:514:MET:CE	2.32	0.60
1:H:400:LEU:C	1:H:400:LEU:HD23	2.22	0.60
1:K:147:VAL:CG2	1:K:496:PRO:HB3	2.32	0.60
1:K:385:THR:O	1:K:389:MET:HB2	2.02	0.60
1:M:169:VAL:HG22	1:M:169:VAL:O	2.01	0.60
1:M:516:THR:C	1:N:36:ARG:NH1	2.55	0.60
1:G:510:VAL:HG12	1:G:514:MET:CE	2.32	0.59
1:J:430:ARG:HG2	1:J:430:ARG:NH1	2.17	0.59
1:M:385:THR:O	1:M:389:MET:HB2	2.02	0.59
1:E:510:VAL:HG12	1:E:514:MET:CE	2.32	0.59
1:F:44:PHE:CD1	1:F:44:PHE:N	2.66	0.59
1:J:385:THR:HG23	1:J:388:GLU:HB3	1.83	0.59
1:C:325:ILE:HG12	1:C:330:THR:HG23	1.83	0.59
1:J:147:VAL:CG2	1:J:496:PRO:HB3	2.32	0.59
1:J:385:THR:O	1:J:389:MET:HB2	2.02	0.59
1:K:400:LEU:HD23	1:K:400:LEU:C	2.22	0.59
1:N:147:VAL:CG2	1:N:496:PRO:HB3	2.32	0.59
1:I:147:VAL:CG2	1:I:496:PRO:HB3	2.32	0.59
1:F:406:ALA:CB	1:F:496:PRO:HB3	2.27	0.59
1:F:510:VAL:HG12	1:F:514:MET:CE	2.32	0.59
1:A:510:VAL:HG12	1:A:514:MET:CE	2.32	0.59
1:H:147:VAL:CG2	1:H:496:PRO:HB3	2.32	0.59
1:K:510:VAL:HG12	1:K:514:MET:CE	2.32	0.59
1:L:430:ARG:HG2	1:L:430:ARG:NH1	2.17	0.59
1:D:510:VAL:HG12	1:D:514:MET:CE	2.32	0.59
1:I:385:THR:HG23	1:I:388:GLU:HB3	1.83	0.59
1:J:516:THR:C	1:K:36:ARG:NH1	2.55	0.59
1:L:400:LEU:HD23	1:L:400:LEU:C	2.22	0.59
1:M:147:VAL:CG2	1:M:496:PRO:HB3	2.32	0.59
1:E:325:ILE:HG12	1:E:330:THR:HG23	1.83	0.59
1:M:400:LEU:C	1:M:400:LEU:HD23	2.22	0.59
1:C:510:VAL:HG12	1:C:514:MET:CE	2.32	0.59
1:J:385:THR:HG23	1:J:388:GLU:H	1.68	0.59
1:A:430:ARG:HG2	1:A:430:ARG:NH1	2.17	0.59
1:D:325:ILE:HG12	1:D:330:THR:HG23	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:146:GLN:HE21	1:G:494:LEU:HD11	0.77	0.59
1:I:510:VAL:HG12	1:I:514:MET:CE	2.32	0.59
1:B:510:VAL:HG12	1:B:514:MET:CE	2.32	0.58
1:F:353:ILE:HG12	1:F:365:LEU:HB3	1.85	0.58
1:I:385:THR:O	1:I:389:MET:HB2	2.02	0.58
1:J:510:VAL:HG12	1:J:514:MET:CE	2.32	0.58
1:B:353:ILE:HG12	1:B:365:LEU:HB3	1.85	0.58
1:E:353:ILE:HG12	1:E:365:LEU:HB3	1.85	0.58
1:H:36:ARG:NH1	1:N:516:THR:C	2.55	0.58
1:M:385:THR:HG23	1:M:388:GLU:H	1.68	0.58
2:R:81:HIS:HD2	2:R:83:PHE:H	1.52	0.58
2:T:11:ALA:HA	2:U:107:PRO:O	2.04	0.58
1:D:224:ASP:HB3	1:D:302:SER:HA	1.86	0.58
1:G:353:ILE:HG12	1:G:365:LEU:HB3	1.85	0.58
2:P:80:PRO:HG2	2:Q:70:SER:HG	1.68	0.58
2:Q:11:ALA:HA	2:R:107:PRO:O	2.04	0.58
1:B:105:LYS:CG	1:H:109:ALA:O	2.45	0.58
1:C:353:ILE:HG12	1:C:365:LEU:HB3	1.85	0.58
1:D:353:ILE:HG12	1:D:365:LEU:HB3	1.85	0.58
1:H:385:THR:HG23	1:H:388:GLU:H	1.68	0.58
1:H:510:VAL:HG12	1:H:514:MET:CE	2.32	0.58
1:L:385:THR:HG23	1:L:388:GLU:H	1.68	0.58
1:A:353:ILE:HG12	1:A:365:LEU:HB3	1.85	0.58
1:A:409:GLU:CB	1:A:498:LYS:HB2	2.34	0.58
1:D:409:GLU:CB	1:D:498:LYS:HB2	2.34	0.58
1:E:105:LYS:CG	1:K:109:ALA:O	2.45	0.58
2:P:11:ALA:HA	2:Q:107:PRO:O	2.04	0.58
2:R:11:ALA:HA	2:S:107:PRO:O	2.04	0.58
1:C:224:ASP:HB3	1:C:302:SER:HA	1.86	0.58
1:F:409:GLU:CB	1:F:498:LYS:HB2	2.34	0.58
2:O:11:ALA:HA	2:P:107:PRO:O	2.04	0.58
2:O:110:TYR:HD1	2:U:82:PRO:HB3	1.69	0.58
1:B:406:ALA:CB	1:B:496:PRO:HB3	2.27	0.58
1:C:430:ARG:HG2	1:C:430:ARG:NH1	2.17	0.58
1:L:190:VAL:CG2	1:L:334:ASP:OD2	2.47	0.58
2:P:82:PRO:HB3	2:Q:110:TYR:HD1	1.69	0.58
1:K:385:THR:HG23	1:K:388:GLU:H	1.68	0.58
1:D:105:LYS:CG	1:J:109:ALA:O	2.45	0.58
1:D:86:GLY:HA3	1:D:401:HIS:HB3	1.86	0.58
1:E:86:GLY:HA3	1:E:401:HIS:HB3	1.86	0.58
1:F:86:GLY:HA3	1:F:401:HIS:HB3	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:86:GLY:HA3	1:G:401:HIS:HB3	1.86	0.58
1:I:279:PRO:O	1:I:285:ARG:HB3	2.04	0.58
1:L:44:PHE:CD1	1:L:44:PHE:N	2.66	0.58
1:M:279:PRO:O	1:M:285:ARG:HB3	2.04	0.58
1:N:279:PRO:O	1:N:285:ARG:HB3	2.04	0.58
1:F:430:ARG:HG2	1:F:430:ARG:NH1	2.17	0.57
1:H:279:PRO:O	1:H:285:ARG:HB3	2.04	0.57
2:O:82:PRO:HB3	2:P:110:TYR:HD1	1.69	0.57
2:S:11:ALA:HA	2:T:107:PRO:O	2.04	0.57
1:E:224:ASP:HB3	1:E:302:SER:HA	1.86	0.57
1:K:44:PHE:CD1	1:K:44:PHE:N	2.66	0.57
1:L:392:LYS:O	1:L:396:VAL:HG23	2.04	0.57
1:N:392:LYS:O	1:N:396:VAL:HG23	2.04	0.57
2:P:81:HIS:HD2	2:P:83:PHE:H	1.52	0.57
2:Q:82:PRO:HB3	2:R:110:TYR:HD1	1.69	0.57
2:T:81:HIS:HD2	2:T:83:PHE:H	1.52	0.57
1:A:86:GLY:HA3	1:A:401:HIS:HB3	1.86	0.57
1:B:409:GLU:CB	1:B:498:LYS:HB2	2.33	0.57
1:D:147:VAL:HB	1:D:496:PRO:HG3	1.87	0.57
1:E:146:GLN:HE21	1:E:494:LEU:HD11	0.77	0.57
1:H:161:LEU:H	1:H:161:LEU:HD12	1.70	0.57
2:S:81:HIS:HD2	2:S:83:PHE:H	1.52	0.57
1:A:146:GLN:HE21	1:A:494:LEU:HD11	0.77	0.57
1:D:16:MET:HG3	1:D:520:MET:HE1	1.87	0.57
1:E:147:VAL:HB	1:E:496:PRO:HG3	1.87	0.57
1:I:385:THR:HG23	1:I:388:GLU:H	1.68	0.57
1:J:279:PRO:O	1:J:285:ARG:HB3	2.04	0.57
1:N:385:THR:HG23	1:N:388:GLU:H	1.68	0.57
2:O:48:LEU:CD2	2:U:85:ALA:HA	2.34	0.57
2:O:85:ALA:HA	2:P:48:LEU:CD2	2.34	0.57
1:F:16:MET:HG3	1:F:520:MET:HE1	1.87	0.57
1:F:147:VAL:HB	1:F:496:PRO:HG3	1.87	0.57
1:H:516:THR:C	1:I:36:ARG:NH1	2.55	0.57
1:L:161:LEU:H	1:L:161:LEU:HD12	1.70	0.57
1:M:16:MET:HG3	1:M:520:MET:HE1	1.87	0.57
2:S:85:ALA:HA	2:T:48:LEU:CD2	2.34	0.57
2:T:82:PRO:HB3	2:U:110:TYR:HD1	1.69	0.57
1:C:409:GLU:CB	1:C:498:LYS:HB2	2.34	0.57
1:E:409:GLU:CB	1:E:498:LYS:HB2	2.34	0.57
1:L:279:PRO:O	1:L:285:ARG:HB3	2.04	0.57
2:O:107:PRO:O	2:U:11:ALA:HA	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:82:PRO:HB3	2:S:110:TYR:HD1	1.69	0.57
2:R:85:ALA:HA	2:S:48:LEU:CD2	2.34	0.57
2:U:81:HIS:HD2	2:U:83:PHE:H	1.51	0.57
1:B:224:ASP:HB3	1:B:302:SER:HA	1.86	0.57
1:G:147:VAL:HB	1:G:496:PRO:HG3	1.87	0.57
1:G:409:GLU:CB	1:G:498:LYS:HB2	2.33	0.57
1:I:16:MET:HG3	1:I:520:MET:HE1	1.87	0.57
1:I:516:THR:C	1:J:36:ARG:NH1	2.55	0.57
2:S:82:PRO:HB3	2:T:110:TYR:HD1	1.69	0.57
1:D:263:VAL:HG11	1:E:305:ILE:HG22	1.87	0.57
1:G:16:MET:HG3	1:G:520:MET:HE1	1.87	0.57
1:K:138:CYS:SG	1:K:144:ILE:HD13	2.45	0.57
1:L:138:CYS:SG	1:L:144:ILE:HD13	2.45	0.57
2:O:70:SER:HG	2:U:80:PRO:HG2	1.70	0.57
2:P:85:ALA:HA	2:Q:48:LEU:CD2	2.34	0.57
1:C:86:GLY:HA3	1:C:401:HIS:HB3	1.86	0.57
1:C:147:VAL:HB	1:C:496:PRO:HG3	1.87	0.57
1:H:16:MET:HG3	1:H:520:MET:HE1	1.87	0.57
1:I:171:LYS:HD3	1:I:407:VAL:CG1	2.35	0.57
1:N:16:MET:HG3	1:N:520:MET:HE3	1.87	0.57
1:B:16:MET:HG3	1:B:520:MET:HE1	1.87	0.57
1:C:263:VAL:HG11	1:D:305:ILE:HG22	1.87	0.57
1:E:263:VAL:HG11	1:F:305:ILE:HG22	1.87	0.57
1:I:392:LYS:O	1:I:396:VAL:HG23	2.05	0.57
1:K:392:LYS:O	1:K:396:VAL:HG23	2.04	0.57
1:M:392:LYS:O	1:M:396:VAL:HG23	2.04	0.57
2:Q:81:HIS:HD2	2:Q:83:PHE:H	1.52	0.57
1:H:171:LYS:HD3	1:H:407:VAL:CG1	2.35	0.56
1:J:16:MET:HG3	1:J:520:MET:HE1	1.87	0.56
1:J:138:CYS:SG	1:J:144:ILE:HD13	2.45	0.56
1:K:16:MET:HG3	1:K:520:MET:HE1	1.87	0.56
1:K:279:PRO:O	1:K:285:ARG:HB3	2.04	0.56
1:L:16:MET:HG3	1:L:520:MET:HE1	1.87	0.56
1:M:138:CYS:SG	1:M:144:ILE:HD13	2.45	0.56
2:Q:85:ALA:HA	2:R:48:LEU:CD2	2.34	0.56
2:T:85:ALA:HA	2:U:48:LEU:CD2	2.34	0.56
1:A:16:MET:HG3	1:A:520:MET:HE1	1.87	0.56
1:D:406:ALA:CB	1:D:496:PRO:HB3	2.27	0.56
1:J:171:LYS:HD3	1:J:407:VAL:CG1	2.35	0.56
1:K:171:LYS:HD3	1:K:407:VAL:CG1	2.35	0.56
1:A:147:VAL:HB	1:A:496:PRO:HG3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:267:MET:SD	1:B:305:ILE:CD1	2.89	0.56
1:C:16:MET:HG3	1:C:520:MET:HE3	1.87	0.56
1:C:105:LYS:CG	1:I:109:ALA:O	2.45	0.56
1:E:16:MET:HG3	1:E:520:MET:HE1	1.87	0.56
1:H:261:THR:O	1:H:265:ASN:HB2	2.05	0.56
1:I:138:CYS:SG	1:I:144:ILE:HD13	2.45	0.56
1:I:261:THR:O	1:I:265:ASN:HB2	2.05	0.56
1:J:161:LEU:HD12	1:J:161:LEU:H	1.69	0.56
1:J:261:THR:O	1:J:265:ASN:HB2	2.05	0.56
1:J:392:LYS:O	1:J:396:VAL:HG23	2.05	0.56
1:L:171:LYS:HD3	1:L:407:VAL:CG1	2.35	0.56
1:N:138:CYS:SG	1:N:144:ILE:HD13	2.45	0.56
1:B:147:VAL:HB	1:B:496:PRO:HG3	1.87	0.56
1:G:204:PHE:HE1	1:G:274:ALA:HB2	1.71	0.56
1:H:392:LYS:O	1:H:396:VAL:HG23	2.05	0.56
1:N:171:LYS:HD3	1:N:407:VAL:CG1	2.35	0.56
1:A:263:VAL:HG11	1:B:305:ILE:HG22	1.87	0.56
1:B:204:PHE:HE1	1:B:274:ALA:HB2	1.71	0.56
1:F:224:ASP:HB3	1:F:302:SER:HA	1.86	0.56
1:M:261:THR:O	1:M:265:ASN:HB2	2.05	0.56
1:N:16:MET:O	1:N:20:VAL:HG23	2.06	0.56
1:N:261:THR:O	1:N:265:ASN:HB2	2.05	0.56
2:O:81:HIS:HD2	2:O:83:PHE:H	1.52	0.56
1:B:86:GLY:HA3	1:B:401:HIS:HB3	1.86	0.56
1:G:224:ASP:HB3	1:G:302:SER:HA	1.86	0.56
1:J:510:VAL:HG12	1:J:514:MET:HE1	1.88	0.56
1:L:261:THR:O	1:L:265:ASN:HB2	2.05	0.56
1:A:16:MET:O	1:A:20:VAL:HG23	2.06	0.56
1:D:16:MET:O	1:D:20:VAL:HG23	2.06	0.56
1:F:16:MET:O	1:F:20:VAL:HG23	2.06	0.56
1:F:263:VAL:HG11	1:G:305:ILE:HG22	1.87	0.56
1:G:463:SER:CB	1:N:464:VAL:HG21	2.27	0.56
1:I:161:LEU:H	1:I:161:LEU:HD12	1.69	0.56
1:J:16:MET:O	1:J:20:VAL:HG23	2.06	0.56
1:K:16:MET:O	1:K:20:VAL:HG23	2.06	0.56
1:M:161:LEU:HD12	1:M:161:LEU:H	1.70	0.56
1:K:161:LEU:H	1:K:161:LEU:HD12	1.70	0.56
1:A:224:ASP:HB3	1:A:302:SER:HA	1.86	0.56
1:B:136:VAL:HA	1:B:137:PRO:N	2.18	0.56
1:C:16:MET:O	1:C:20:VAL:HG23	2.06	0.56
1:E:204:PHE:HE1	1:E:274:ALA:HB2	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:234:LEU:N	1:H:235:PRO:HD2	2.21	0.56
1:B:16:MET:O	1:B:20:VAL:HG23	2.06	0.56
1:G:16:MET:O	1:G:20:VAL:HG23	2.06	0.56
1:H:138:CYS:SG	1:H:144:ILE:HD13	2.45	0.56
1:N:161:LEU:H	1:N:161:LEU:HD12	1.70	0.56
1:B:172:GLU:O	1:B:369:VAL:CG2	2.54	0.55
1:B:263:VAL:HG11	1:C:305:ILE:HG22	1.87	0.55
1:C:172:GLU:O	1:C:369:VAL:CG2	2.54	0.55
1:C:204:PHE:HE1	1:C:274:ALA:HB2	1.71	0.55
1:K:234:LEU:N	1:K:235:PRO:HD2	2.21	0.55
1:A:204:PHE:HE1	1:A:274:ALA:HB2	1.71	0.55
1:G:406:ALA:CB	1:G:496:PRO:HB3	2.27	0.55
1:I:16:MET:O	1:I:20:VAL:HG23	2.06	0.55
1:N:147:VAL:CG2	1:N:496:PRO:CG	2.75	0.55
1:F:204:PHE:HE1	1:F:274:ALA:HB2	1.71	0.55
1:J:419:LEU:HG	1:J:447:MET:HG2	1.89	0.55
1:L:16:MET:O	1:L:20:VAL:HG23	2.06	0.55
1:M:171:LYS:HD3	1:M:407:VAL:CG1	2.35	0.55
2:Q:82:PRO:HA	2:R:110:TYR:CD1	2.42	0.55
1:A:510:VAL:HG12	1:A:514:MET:HE1	1.89	0.55
1:C:33:PRO:HA	1:C:153:ASN:HD21	1.72	0.55
1:G:33:PRO:HA	1:G:153:ASN:HD21	1.72	0.55
1:I:234:LEU:N	1:I:235:PRO:HD2	2.21	0.55
1:A:77:VAL:HG23	1:A:92:ALA:HB1	1.89	0.55
1:E:136:VAL:CA	1:E:137:PRO:CD	2.83	0.55
1:L:419:LEU:HG	1:L:447:MET:HG2	1.89	0.55
1:M:419:LEU:HG	1:M:447:MET:HG2	1.89	0.55
1:D:77:VAL:HG23	1:D:92:ALA:HB1	1.89	0.55
1:E:510:VAL:HG12	1:E:514:MET:HE1	1.89	0.55
1:I:419:LEU:HG	1:I:447:MET:HG2	1.89	0.55
1:K:147:VAL:HG21	1:K:496:PRO:HB3	1.89	0.55
1:K:419:LEU:HG	1:K:447:MET:HG2	1.89	0.55
1:M:234:LEU:N	1:M:235:PRO:HD2	2.21	0.55
1:C:77:VAL:HG23	1:C:92:ALA:HB1	1.89	0.55
1:E:419:LEU:HG	1:E:447:MET:HG2	1.89	0.55
2:R:82:PRO:HA	2:S:110:TYR:CD1	2.42	0.55
1:A:146:GLN:CB	1:A:494:LEU:CD1	2.85	0.55
1:A:305:ILE:HG22	1:G:263:VAL:HG11	1.87	0.55
1:B:77:VAL:HG23	1:B:92:ALA:HB1	1.89	0.55
1:E:16:MET:O	1:E:20:VAL:HG23	2.06	0.55
1:G:510:VAL:HG12	1:G:514:MET:HE1	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:147:VAL:CG2	1:H:496:PRO:CG	2.75	0.55
1:M:16:MET:O	1:M:20:VAL:HG23	2.06	0.55
1:C:510:VAL:HG12	1:C:514:MET:HE1	1.89	0.55
1:E:430:ARG:HG2	1:E:430:ARG:NH1	2.17	0.55
1:F:33:PRO:HA	1:F:153:ASN:HD21	1.72	0.55
1:G:77:VAL:HG23	1:G:92:ALA:HB1	1.89	0.55
1:G:146:GLN:CB	1:G:494:LEU:CD1	2.85	0.55
1:H:510:VAL:HG12	1:H:514:MET:HE1	1.89	0.55
1:L:147:VAL:HG21	1:L:496:PRO:HB3	1.89	0.55
1:L:175:ILE:HD13	1:L:404:ARG:NH2	2.22	0.55
1:M:77:VAL:HG23	1:M:92:ALA:HB1	1.89	0.55
1:N:175:ILE:HD13	1:N:404:ARG:NH2	2.22	0.55
1:B:430:ARG:HG2	1:B:430:ARG:NH1	2.17	0.55
1:B:510:VAL:HG12	1:B:514:MET:HE1	1.89	0.55
1:D:33:PRO:HA	1:D:153:ASN:HD21	1.72	0.55
1:D:146:GLN:CB	1:D:494:LEU:CD1	2.85	0.55
1:D:463:SER:HG	1:K:464:VAL:HG23	1.68	0.55
1:E:146:GLN:CB	1:E:494:LEU:CD1	2.85	0.55
1:H:16:MET:O	1:H:20:VAL:HG23	2.06	0.55
1:H:77:VAL:HG23	1:H:92:ALA:HB1	1.89	0.55
1:H:175:ILE:HD13	1:H:404:ARG:NH2	2.22	0.55
1:J:147:VAL:CG2	1:J:496:PRO:HG3	2.14	0.55
1:K:261:THR:O	1:K:265:ASN:HB2	2.05	0.55
1:L:234:LEU:N	1:L:235:PRO:HD2	2.21	0.55
1:N:77:VAL:HG23	1:N:92:ALA:HB1	1.89	0.55
1:A:172:GLU:O	1:A:369:VAL:CG2	2.54	0.54
1:A:419:LEU:HG	1:A:447:MET:HG2	1.89	0.54
1:B:33:PRO:HA	1:B:153:ASN:HD21	1.72	0.54
1:B:146:GLN:CB	1:B:494:LEU:CD1	2.85	0.54
1:D:204:PHE:HE1	1:D:274:ALA:HB2	1.71	0.54
1:D:419:LEU:HG	1:D:447:MET:HG2	1.89	0.54
1:E:77:VAL:HG23	1:E:92:ALA:HB1	1.89	0.54
1:F:510:VAL:HG12	1:F:514:MET:HE1	1.89	0.54
1:G:172:GLU:O	1:G:369:VAL:CG2	2.54	0.54
1:J:234:LEU:N	1:J:235:PRO:HD2	2.21	0.54
1:K:184:GLN:OE1	1:K:184:GLN:HA	2.07	0.54
1:K:510:VAL:HG12	1:K:514:MET:HE1	1.89	0.54
1:L:510:VAL:HG12	1:L:514:MET:HE1	1.90	0.54
1:M:175:ILE:HD13	1:M:404:ARG:NH2	2.22	0.54
2:P:82:PRO:HA	2:Q:110:TYR:CD1	2.42	0.54
1:D:172:GLU:O	1:D:369:VAL:CG2	2.54	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:419:LEU:HG	1:F:447:MET:HG2	1.89	0.54
1:J:184:GLN:OE1	1:J:184:GLN:HA	2.07	0.54
1:K:175:ILE:HD13	1:K:404:ARG:NH2	2.22	0.54
1:M:147:VAL:HG21	1:M:496:PRO:HB3	1.89	0.54
1:N:234:LEU:N	1:N:235:PRO:HD2	2.21	0.54
2:O:82:PRO:HA	2:P:110:TYR:CD1	2.42	0.54
1:A:33:PRO:HA	1:A:153:ASN:HD21	1.72	0.54
1:D:510:VAL:HG12	1:D:514:MET:HE1	1.89	0.54
1:I:175:ILE:HD13	1:I:404:ARG:NH2	2.22	0.54
1:K:441:LYS:HB3	1:K:445:ARG:HH21	1.73	0.54
1:L:441:LYS:HB3	1:L:445:ARG:HH21	1.73	0.54
1:N:419:LEU:HG	1:N:447:MET:HG2	1.89	0.54
1:B:146:GLN:HE21	1:B:494:LEU:HD11	0.77	0.54
1:B:146:GLN:CB	1:B:494:LEU:HG	2.34	0.54
1:C:441:LYS:HB3	1:C:445:ARG:HH21	1.73	0.54
1:E:33:PRO:HA	1:E:153:ASN:HD21	1.72	0.54
1:I:433:ASN:OD1	1:I:436:GLN:HG3	2.08	0.54
1:I:510:VAL:HG12	1:I:514:MET:HE1	1.89	0.54
1:J:147:VAL:HG21	1:J:496:PRO:HB3	1.89	0.54
1:L:433:ASN:OD1	1:L:436:GLN:HG3	2.08	0.54
2:T:82:PRO:HA	2:U:110:TYR:CD1	2.42	0.54
1:F:146:GLN:CB	1:F:494:LEU:CD1	2.85	0.54
1:F:433:ASN:OD1	1:F:436:GLN:HG3	2.08	0.54
1:G:111:MET:HG3	1:G:435:ASP:OD1	2.08	0.54
1:G:433:ASN:OD1	1:G:436:GLN:HG3	2.08	0.54
1:H:147:VAL:HG21	1:H:496:PRO:HB3	1.89	0.54
1:K:433:ASN:OD1	1:K:436:GLN:HG3	2.08	0.54
1:L:77:VAL:HG23	1:L:92:ALA:HB1	1.89	0.54
1:N:441:LYS:HB3	1:N:445:ARG:HH21	1.73	0.54
1:B:433:ASN:OD1	1:B:436:GLN:HG3	2.08	0.54
1:F:138:CYS:SG	1:F:411:VAL:CG1	2.96	0.54
1:J:111:MET:HG3	1:J:435:ASP:OD1	2.08	0.54
1:N:184:GLN:OE1	1:N:184:GLN:HA	2.07	0.54
2:O:80:PRO:CD	2:P:70:SER:OG	2.56	0.54
2:P:80:PRO:CD	2:Q:70:SER:OG	2.56	0.54
2:T:77:ARG:HD3	2:U:72:PRO:HG3	1.90	0.54
1:A:433:ASN:OD1	1:A:436:GLN:HG3	2.08	0.54
1:F:77:VAL:HG23	1:F:92:ALA:HB1	1.89	0.54
1:G:430:ARG:HG2	1:G:430:ARG:NH1	2.17	0.54
1:J:441:LYS:HB3	1:J:445:ARG:HH21	1.73	0.54
1:L:149:THR:HG22	1:L:156:GLU:HA	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:184:GLN:HA	1:L:184:GLN:OE1	2.07	0.54
2:S:77:ARG:HD3	2:T:72:PRO:HG3	1.90	0.54
2:T:80:PRO:CD	2:U:70:SER:OG	2.56	0.54
1:G:419:LEU:HG	1:G:447:MET:HG2	1.89	0.54
1:H:419:LEU:HG	1:H:447:MET:HG2	1.89	0.54
1:K:18:ARG:NH1	1:K:18:ARG:CG	2.70	0.54
1:M:433:ASN:OD1	1:M:436:GLN:HG3	2.08	0.54
1:M:510:VAL:HG12	1:M:514:MET:HE1	1.89	0.54
2:S:80:PRO:CD	2:T:70:SER:OG	2.56	0.54
1:C:146:GLN:CB	1:C:494:LEU:CD1	2.85	0.54
1:C:267:MET:SD	1:D:305:ILE:CD1	2.89	0.54
1:E:441:LYS:HB3	1:E:445:ARG:HH21	1.73	0.54
1:H:111:MET:HG3	1:H:435:ASP:OD1	2.08	0.54
1:H:441:LYS:HB3	1:H:445:ARG:HH21	1.73	0.54
1:I:111:MET:HG3	1:I:435:ASP:OD1	2.08	0.54
1:J:433:ASN:OD1	1:J:436:GLN:HG3	2.08	0.54
1:K:42:LYS:HG2	1:K:44:PHE:CE2	2.43	0.54
1:L:149:THR:CG2	1:L:159:GLY:HA3	2.37	0.54
1:N:111:MET:HG3	1:N:435:ASP:OD1	2.08	0.54
1:N:433:ASN:OD1	1:N:436:GLN:HG3	2.08	0.54
1:B:111:MET:HG3	1:B:435:ASP:OD1	2.08	0.54
1:B:419:LEU:HG	1:B:447:MET:HG2	1.89	0.54
1:C:18:ARG:NH1	1:C:18:ARG:CG	2.70	0.54
1:C:433:ASN:OD1	1:C:436:GLN:HG3	2.08	0.54
1:D:138:CYS:SG	1:D:411:VAL:CG1	2.96	0.54
1:F:172:GLU:O	1:F:369:VAL:CG2	2.54	0.54
1:H:433:ASN:OD1	1:H:436:GLN:HG3	2.08	0.54
1:I:77:VAL:HG23	1:I:92:ALA:HB1	1.89	0.54
1:I:147:VAL:CG2	1:I:496:PRO:HG3	2.14	0.54
1:I:184:GLN:HA	1:I:184:GLN:OE1	2.07	0.54
1:J:42:LYS:HG2	1:J:44:PHE:CE2	2.43	0.54
1:J:152:ALA:O	1:J:153:ASN:HB3	2.08	0.54
1:J:175:ILE:HD13	1:J:404:ARG:NH2	2.22	0.54
1:K:77:VAL:HG23	1:K:92:ALA:HB1	1.89	0.54
2:Q:80:PRO:CD	2:R:70:SER:OG	2.56	0.54
1:A:441:LYS:HB3	1:A:445:ARG:HH21	1.73	0.53
1:B:138:CYS:SG	1:B:411:VAL:CG1	2.96	0.53
1:D:409:GLU:HB3	1:D:498:LYS:HB2	1.90	0.53
1:D:441:LYS:HB3	1:D:445:ARG:HH21	1.73	0.53
1:F:111:MET:HG3	1:F:435:ASP:OD1	2.08	0.53
1:L:145:ALA:O	1:L:149:THR:HG23	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:145:ALA:O	1:M:149:THR:HG23	2.08	0.53
1:C:111:MET:HG3	1:C:435:ASP:OD1	2.08	0.53
1:C:419:LEU:HG	1:C:447:MET:HG2	1.89	0.53
1:E:172:GLU:O	1:E:369:VAL:CG2	2.54	0.53
1:F:42:LYS:HG2	1:F:44:PHE:CE2	2.43	0.53
1:F:441:LYS:HB3	1:F:445:ARG:HH21	1.73	0.53
1:G:42:LYS:HG2	1:G:44:PHE:CE2	2.43	0.53
1:J:77:VAL:HG23	1:J:92:ALA:HB1	1.89	0.53
1:K:111:MET:HG3	1:K:435:ASP:OD1	2.08	0.53
1:K:147:VAL:CG2	1:K:496:PRO:CG	2.75	0.53
1:M:149:THR:HG22	1:M:156:GLU:HA	1.89	0.53
1:B:42:LYS:HG2	1:B:44:PHE:CE2	2.43	0.53
1:E:433:ASN:OD1	1:E:436:GLN:HG3	2.08	0.53
1:H:152:ALA:O	1:H:153:ASN:HB3	2.08	0.53
1:I:152:ALA:O	1:I:153:ASN:HB3	2.08	0.53
1:I:441:LYS:HB3	1:I:445:ARG:HH21	1.73	0.53
1:J:192:GLY:C	1:J:376:VAL:CG2	2.77	0.53
1:J:386:GLU:HG2	1:J:390:LYS:HE2	1.90	0.53
1:J:402:ALA:O	1:J:406:ALA:N	2.32	0.53
1:K:145:ALA:O	1:K:149:THR:HG23	2.08	0.53
1:M:111:MET:HG3	1:M:435:ASP:OD1	2.08	0.53
1:M:192:GLY:C	1:M:376:VAL:CG2	2.77	0.53
1:N:147:VAL:HG21	1:N:496:PRO:HB3	1.89	0.53
2:O:70:SER:OG	2:U:80:PRO:CD	2.56	0.53
1:C:409:GLU:HB3	1:C:498:LYS:HB2	1.90	0.53
1:I:145:ALA:O	1:I:149:THR:HG23	2.08	0.53
1:I:386:GLU:HG2	1:I:390:LYS:HE2	1.90	0.53
1:N:145:ALA:O	1:N:149:THR:HG23	2.08	0.53
1:N:192:GLY:C	1:N:376:VAL:CG2	2.77	0.53
1:N:510:VAL:HG12	1:N:514:MET:HE1	1.89	0.53
1:E:111:MET:HG3	1:E:435:ASP:OD1	2.08	0.53
1:H:42:LYS:HG2	1:H:44:PHE:CE2	2.43	0.53
1:K:147:VAL:HG23	1:K:496:PRO:CB	2.38	0.53
1:K:386:GLU:HG2	1:K:390:LYS:HE2	1.90	0.53
1:M:42:LYS:HG2	1:M:44:PHE:CE2	2.43	0.53
1:M:441:LYS:HB3	1:M:445:ARG:HH21	1.73	0.53
2:O:72:PRO:HG3	2:U:77:ARG:HD3	1.90	0.53
2:R:77:ARG:HD3	2:S:72:PRO:HG3	1.90	0.53
1:A:111:MET:HG3	1:A:435:ASP:OD1	2.08	0.53
1:C:138:CYS:SG	1:C:411:VAL:CG1	2.96	0.53
1:D:42:LYS:HG2	1:D:44:PHE:CE2	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:42:LYS:HG2	1:E:44:PHE:CE2	2.43	0.53
1:G:136:VAL:CA	1:G:137:PRO:CD	2.83	0.53
1:H:386:GLU:HG2	1:H:390:LYS:HE2	1.90	0.53
1:H:395:ARG:O	1:H:398:ASP:HB2	2.09	0.53
1:I:147:VAL:HG21	1:I:496:PRO:HB3	1.89	0.53
1:L:152:ALA:O	1:L:153:ASN:HB3	2.08	0.53
1:M:147:VAL:HG23	1:M:496:PRO:CB	2.39	0.53
1:M:184:GLN:OE1	1:M:184:GLN:HA	2.07	0.53
1:M:395:ARG:O	1:M:398:ASP:HB2	2.09	0.53
1:N:386:GLU:HG2	1:N:390:LYS:HE2	1.90	0.53
2:S:82:PRO:HA	2:T:110:TYR:CD1	2.42	0.53
1:B:441:LYS:HB3	1:B:445:ARG:HH21	1.73	0.53
1:D:267:MET:SD	1:E:305:ILE:CD1	2.89	0.53
1:H:145:ALA:O	1:H:149:THR:HG23	2.08	0.53
1:I:192:GLY:C	1:I:376:VAL:CG2	2.77	0.53
1:K:149:THR:HG22	1:K:156:GLU:HA	1.90	0.53
1:M:152:ALA:O	1:M:153:ASN:HB3	2.08	0.53
1:M:386:GLU:HG2	1:M:390:LYS:HE2	1.90	0.53
1:N:395:ARG:O	1:N:398:ASP:HB2	2.09	0.53
2:O:110:TYR:CD1	2:U:82:PRO:HA	2.42	0.53
2:S:17:ILE:CD1	2:T:108:CYS:HB3	2.34	0.53
1:C:42:LYS:HG2	1:C:44:PHE:CE2	2.43	0.53
1:E:138:CYS:SG	1:E:411:VAL:CG1	2.96	0.53
1:E:409:GLU:HB3	1:E:498:LYS:HB2	1.90	0.53
1:I:42:LYS:HG2	1:I:44:PHE:CE2	2.43	0.53
1:L:267:MET:O	1:L:268:ARG:HB2	2.09	0.53
1:L:386:GLU:HG2	1:L:390:LYS:HE2	1.90	0.53
1:D:111:MET:HG3	1:D:435:ASP:OD1	2.08	0.53
1:D:433:ASN:OD1	1:D:436:GLN:HG3	2.08	0.53
1:H:184:GLN:OE1	1:H:184:GLN:HA	2.07	0.53
1:I:147:VAL:HG23	1:I:496:PRO:CB	2.39	0.53
1:K:192:GLY:C	1:K:376:VAL:CG2	2.77	0.53
1:N:147:VAL:HG23	1:N:496:PRO:CB	2.39	0.53
2:R:80:PRO:CD	2:S:70:SER:OG	2.56	0.53
1:B:409:GLU:HB3	1:B:498:LYS:HB2	1.90	0.53
1:G:409:GLU:HB3	1:G:498:LYS:HB2	1.90	0.53
1:I:147:VAL:HA	1:I:150:ILE:HD12	1.91	0.53
1:I:395:ARG:O	1:I:398:ASP:HB2	2.09	0.53
1:J:395:ARG:O	1:J:398:ASP:HB2	2.09	0.53
1:K:147:VAL:CG2	1:K:496:PRO:HG3	2.14	0.53
1:M:149:THR:CG2	1:M:159:GLY:HA3	2.36	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:152:ALA:O	1:N:153:ASN:HB3	2.08	0.53
1:C:136:VAL:CA	1:C:137:PRO:CD	2.83	0.52
1:C:146:GLN:CB	1:C:494:LEU:HG	2.34	0.52
1:H:192:GLY:C	1:H:376:VAL:CG2	2.77	0.52
1:L:111:MET:HG3	1:L:435:ASP:OD1	2.08	0.52
1:N:147:VAL:HA	1:N:150:ILE:HD12	1.91	0.52
1:N:430:ARG:HG2	1:N:430:ARG:NH1	2.17	0.52
2:S:5:GLN:HG3	2:S:6:GLN:NE2	2.24	0.52
2:T:5:GLN:HG3	2:T:6:GLN:NE2	2.24	0.52
1:G:138:CYS:SG	1:G:411:VAL:CG1	2.96	0.52
1:K:395:ARG:O	1:K:398:ASP:HB2	2.09	0.52
1:L:18:ARG:NH1	1:L:18:ARG:CG	2.70	0.52
1:N:192:GLY:CA	1:N:376:VAL:CG2	2.83	0.52
1:H:44:PHE:H	1:H:44:PHE:HD1	1.55	0.52
1:K:152:ALA:O	1:K:153:ASN:HB3	2.08	0.52
1:K:403:THR:O	1:K:407:VAL:HG23	2.10	0.52
1:M:267:MET:O	1:M:268:ARG:HB2	2.09	0.52
1:M:385:THR:CG2	1:M:388:GLU:HB3	2.40	0.52
2:O:5:GLN:HG3	2:O:6:GLN:NE2	2.24	0.52
1:A:409:GLU:HB3	1:A:498:LYS:HB2	1.90	0.52
1:J:403:THR:O	1:J:407:VAL:HG23	2.10	0.52
1:K:267:MET:O	1:K:268:ARG:HB2	2.09	0.52
1:L:385:THR:CG2	1:L:388:GLU:HB3	2.40	0.52
2:O:77:ARG:HD3	2:P:72:PRO:HG3	1.90	0.52
1:D:18:ARG:NH1	1:D:18:ARG:CG	2.70	0.52
1:D:430:ARG:HG2	1:D:430:ARG:NH1	2.17	0.52
1:H:430:ARG:HG2	1:H:430:ARG:NH1	2.17	0.52
1:I:403:THR:O	1:I:407:VAL:HG23	2.10	0.52
1:L:42:LYS:HG2	1:L:44:PHE:CE2	2.43	0.52
1:L:161:LEU:H	1:L:161:LEU:CD1	2.23	0.52
1:M:147:VAL:HA	1:M:150:ILE:HD12	1.91	0.52
1:C:455:VAL:HG21	1:C:465:VAL:HG11	1.92	0.52
1:G:405:ALA:HB1	1:G:498:LYS:HB3	1.91	0.52
1:G:441:LYS:HB3	1:G:445:ARG:HH21	1.73	0.52
1:H:147:VAL:HA	1:H:150:ILE:HD12	1.91	0.52
1:N:42:LYS:HG2	1:N:44:PHE:CE2	2.43	0.52
2:Q:5:GLN:HG3	2:Q:6:GLN:NE2	2.24	0.52
2:U:5:GLN:HG3	2:U:6:GLN:NE2	2.24	0.52
1:A:405:ALA:HB1	1:A:498:LYS:HB3	1.91	0.52
1:H:267:MET:O	1:H:268:ARG:HB2	2.09	0.52
1:I:385:THR:CG2	1:I:388:GLU:HB3	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:145:ALA:O	1:J:149:THR:HG23	2.08	0.52
1:K:161:LEU:H	1:K:161:LEU:CD1	2.23	0.52
1:K:455:VAL:HG21	1:K:465:VAL:HG11	1.92	0.52
1:L:403:THR:O	1:L:407:VAL:HG23	2.10	0.52
2:Q:85:ALA:HA	2:R:48:LEU:CD1	2.40	0.52
1:D:455:VAL:HG21	1:D:465:VAL:HG11	1.92	0.52
1:F:264:VAL:HG13	1:G:306:GLY:HA3	1.92	0.52
1:L:192:GLY:C	1:L:376:VAL:CG2	2.77	0.52
1:M:161:LEU:H	1:M:161:LEU:CD1	2.23	0.52
1:N:161:LEU:H	1:N:161:LEU:CD1	2.23	0.52
2:O:48:LEU:CD1	2:U:85:ALA:HA	2.40	0.52
2:O:85:ALA:HA	2:P:48:LEU:CD1	2.40	0.52
2:P:5:GLN:HG3	2:P:6:GLN:NE2	2.24	0.52
2:R:5:GLN:HG3	2:R:6:GLN:NE2	2.24	0.52
1:A:138:CYS:SG	1:A:411:VAL:CG1	2.96	0.52
1:A:464:VAL:HG22	1:H:467:ASN:HB2	1.92	0.52
1:C:405:ALA:HB1	1:C:498:LYS:HB3	1.91	0.52
1:H:403:THR:O	1:H:407:VAL:HG23	2.10	0.52
1:H:455:VAL:HG21	1:H:465:VAL:HG11	1.92	0.52
1:J:455:VAL:HG21	1:J:465:VAL:HG11	1.92	0.52
1:L:455:VAL:HG21	1:L:465:VAL:HG11	1.92	0.52
1:M:455:VAL:HG21	1:M:465:VAL:HG11	1.92	0.52
1:N:149:THR:CG2	1:N:159:GLY:HA3	2.37	0.52
1:N:455:VAL:HG21	1:N:465:VAL:HG11	1.92	0.52
2:P:85:ALA:HA	2:Q:48:LEU:CD1	2.40	0.52
1:A:42:LYS:HG2	1:A:44:PHE:CE2	2.43	0.52
1:B:136:VAL:CA	1:B:137:PRO:CD	2.83	0.52
1:C:146:GLN:HB3	1:C:494:LEU:CG	2.35	0.52
1:D:146:GLN:CB	1:D:494:LEU:HG	2.34	0.52
1:N:149:THR:HG22	1:N:156:GLU:HA	1.90	0.52
1:N:267:MET:O	1:N:268:ARG:HB2	2.09	0.52
2:P:77:ARG:HD3	2:Q:72:PRO:HG3	1.90	0.52
2:R:85:ALA:HA	2:S:48:LEU:CD1	2.40	0.52
2:T:85:ALA:HA	2:U:48:LEU:CD1	2.40	0.52
1:A:18:ARG:NH1	1:A:18:ARG:CG	2.70	0.51
1:A:136:VAL:CA	1:A:137:PRO:CD	2.83	0.51
1:A:306:GLY:HA3	1:G:264:VAL:HG13	1.92	0.51
1:B:455:VAL:HG21	1:B:465:VAL:HG11	1.92	0.51
1:B:464:VAL:HG22	1:I:467:ASN:HB2	1.92	0.51
1:G:487:ASN:O	1:G:491:MET:HG3	2.11	0.51
1:H:192:GLY:CA	1:H:376:VAL:CG2	2.83	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:455:VAL:HG21	1:I:465:VAL:HG11	1.92	0.51
1:J:149:THR:HG22	1:J:156:GLU:HA	1.90	0.51
1:N:385:THR:CG2	1:N:388:GLU:HB3	2.40	0.51
1:D:405:ALA:HB1	1:D:498:LYS:HB3	1.91	0.51
1:E:146:GLN:HB3	1:E:494:LEU:CG	2.35	0.51
1:E:405:ALA:HB1	1:E:498:LYS:HB3	1.91	0.51
1:F:409:GLU:HB3	1:F:498:LYS:HB2	1.90	0.51
1:H:149:THR:HG22	1:H:156:GLU:HA	1.90	0.51
1:H:385:THR:CG2	1:H:388:GLU:HB3	2.40	0.51
1:I:267:MET:O	1:I:268:ARG:HB2	2.09	0.51
1:I:487:ASN:O	1:I:491:MET:HG3	2.10	0.51
1:J:487:ASN:O	1:J:491:MET:HG3	2.10	0.51
1:D:44:PHE:H	1:D:44:PHE:HD1	1.55	0.51
1:E:146:GLN:CB	1:E:494:LEU:HG	2.34	0.51
1:H:487:ASN:O	1:H:491:MET:HG3	2.11	0.51
1:I:161:LEU:H	1:I:161:LEU:CD1	2.23	0.51
1:J:385:THR:CG2	1:J:388:GLU:HB3	2.40	0.51
1:K:385:THR:CG2	1:K:388:GLU:HB3	2.40	0.51
1:L:395:ARG:O	1:L:398:ASP:HB2	2.09	0.51
1:M:143:ALA:C	1:M:146:GLN:HB3	2.31	0.51
1:M:403:THR:O	1:M:407:VAL:HG23	2.10	0.51
1:N:487:ASN:O	1:N:491:MET:HG3	2.10	0.51
1:E:18:ARG:NH1	1:E:18:ARG:CG	2.70	0.51
1:H:149:THR:CG2	1:H:159:GLY:HA3	2.37	0.51
1:H:161:LEU:H	1:H:161:LEU:CD1	2.22	0.51
1:K:143:ALA:C	1:K:146:GLN:HB3	2.31	0.51
1:N:403:THR:O	1:N:407:VAL:HG23	2.10	0.51
1:B:405:ALA:HB1	1:B:498:LYS:HB3	1.91	0.51
1:E:264:VAL:HG13	1:F:306:GLY:HA3	1.92	0.51
1:E:463:SER:HG	1:L:464:VAL:HG23	1.75	0.51
1:H:402:ALA:O	1:H:406:ALA:N	2.32	0.51
1:I:149:THR:HG22	1:I:156:GLU:HA	1.90	0.51
1:J:147:VAL:HA	1:J:150:ILE:HD12	1.91	0.51
2:O:106:ILE:O	2:U:12:VAL:CG2	2.58	0.51
2:R:17:ILE:CD1	2:S:108:CYS:HB3	2.34	0.51
1:A:455:VAL:HG21	1:A:465:VAL:HG11	1.92	0.51
1:D:464:VAL:HG22	1:K:467:ASN:HB2	1.92	0.51
1:F:18:ARG:NH1	1:F:18:ARG:CG	2.70	0.51
1:F:172:GLU:OE1	1:F:350:ARG:HG3	2.11	0.51
1:H:147:VAL:HG23	1:H:496:PRO:CB	2.39	0.51
1:I:149:THR:CG2	1:I:159:GLY:HA3	2.37	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:267:MET:O	1:J:268:ARG:HB2	2.09	0.51
1:K:487:ASN:O	1:K:491:MET:HG3	2.11	0.51
2:O:12:VAL:CG2	2:P:106:ILE:O	2.59	0.51
2:O:17:ILE:CD1	2:P:108:CYS:HB3	2.34	0.51
2:Q:12:VAL:CG2	2:R:106:ILE:O	2.59	0.51
2:S:85:ALA:HA	2:T:48:LEU:CD1	2.40	0.51
1:B:172:GLU:OE1	1:B:350:ARG:HG3	2.11	0.51
1:F:487:ASN:O	1:F:491:MET:HG3	2.11	0.51
1:I:192:GLY:CA	1:I:376:VAL:CG2	2.83	0.51
1:L:194:GLN:HB2	1:L:331:THR:HB	1.93	0.51
2:P:12:VAL:CG2	2:Q:106:ILE:O	2.58	0.51
2:T:17:ILE:CD1	2:U:108:CYS:HB3	2.34	0.51
1:A:172:GLU:OE1	1:A:350:ARG:HG3	2.11	0.51
1:C:44:PHE:H	1:C:44:PHE:HD1	1.55	0.51
1:J:190:VAL:HG22	1:J:191:GLU:N	2.26	0.51
1:M:194:GLN:HB2	1:M:331:THR:HB	1.93	0.51
2:Q:77:ARG:HD3	2:R:72:PRO:HG3	1.90	0.51
1:A:487:ASN:O	1:A:491:MET:HG3	2.11	0.51
1:E:455:VAL:HG21	1:E:465:VAL:HG11	1.92	0.51
1:E:487:ASN:O	1:E:491:MET:HG3	2.11	0.51
1:F:146:GLN:CB	1:F:494:LEU:HG	2.34	0.51
1:F:405:ALA:HB1	1:F:498:LYS:HB3	1.91	0.51
1:G:18:ARG:NH1	1:G:18:ARG:CG	2.70	0.51
1:G:172:GLU:OE1	1:G:350:ARG:HG3	2.11	0.51
1:I:180:GLY:HA2	1:I:380:LYS:HB3	1.93	0.51
1:I:430:ARG:HG2	1:I:430:ARG:NH1	2.17	0.51
1:J:44:PHE:H	1:J:44:PHE:HD1	1.55	0.51
1:J:161:LEU:H	1:J:161:LEU:CD1	2.22	0.51
2:T:12:VAL:CG2	2:U:106:ILE:O	2.58	0.51
1:C:172:GLU:OE1	1:C:350:ARG:HG3	2.11	0.51
1:C:487:ASN:O	1:C:491:MET:HG3	2.11	0.51
1:E:172:GLU:OE1	1:E:350:ARG:HG3	2.11	0.51
1:L:147:VAL:HA	1:L:150:ILE:HD12	1.91	0.51
1:M:18:ARG:NH1	1:M:18:ARG:CG	2.70	0.51
1:M:381:VAL:HB	1:M:389:MET:CE	2.41	0.51
1:A:406:ALA:CB	1:A:496:PRO:HB3	2.27	0.50
1:E:44:PHE:H	1:E:44:PHE:HD1	1.55	0.50
1:I:190:VAL:HG22	1:I:191:GLU:N	2.26	0.50
1:N:18:ARG:NH1	1:N:18:ARG:CG	2.70	0.50
1:N:381:VAL:HB	1:N:389:MET:CE	2.41	0.50
2:O:108:CYS:HB3	2:U:17:ILE:CD1	2.34	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:264:VAL:HG13	1:B:306:GLY:HA3	1.92	0.50
1:B:487:ASN:O	1:B:491:MET:HG3	2.11	0.50
1:G:455:VAL:HG21	1:G:465:VAL:HG11	1.92	0.50
1:L:147:VAL:CG2	1:L:496:PRO:CG	2.75	0.50
1:M:190:VAL:HG22	1:M:191:GLU:N	2.26	0.50
1:M:487:ASN:O	1:M:491:MET:HG3	2.11	0.50
1:D:487:ASN:O	1:D:491:MET:HG3	2.11	0.50
1:F:455:VAL:HG21	1:F:465:VAL:HG11	1.92	0.50
1:H:147:VAL:CG2	1:H:496:PRO:HG3	2.14	0.50
1:H:180:GLY:HA2	1:H:380:LYS:HB3	1.93	0.50
1:I:194:GLN:HB2	1:I:331:THR:HB	1.93	0.50
1:J:147:VAL:CG2	1:J:496:PRO:CG	2.75	0.50
1:J:180:GLY:HA2	1:J:380:LYS:HB3	1.93	0.50
1:M:389:MET:HE1	1:M:389:MET:O	2.12	0.50
2:R:12:VAL:CG2	2:S:106:ILE:O	2.59	0.50
2:S:12:VAL:CG2	2:T:106:ILE:O	2.58	0.50
1:E:464:VAL:HG22	1:L:467:ASN:HB2	1.92	0.50
1:G:464:VAL:HG22	1:N:467:ASN:HB2	1.92	0.50
1:I:143:ALA:C	1:I:146:GLN:HB3	2.31	0.50
1:K:147:VAL:HA	1:K:150:ILE:HD12	1.91	0.50
1:K:391:GLU:O	1:K:394:ALA:HB3	2.12	0.50
1:L:391:GLU:O	1:L:394:ALA:HB3	2.12	0.50
1:N:193:MET:HG3	1:N:371:LYS:HB3	1.93	0.50
1:N:194:GLN:HB2	1:N:331:THR:HB	1.93	0.50
2:T:18:LEU:HD13	2:T:51:VAL:HA	1.93	0.50
1:A:146:GLN:CB	1:A:494:LEU:HG	2.34	0.50
1:D:264:VAL:HG13	1:E:306:GLY:HA3	1.92	0.50
1:H:135:SER:HG	1:H:137:PRO:CA	2.14	0.50
1:H:193:MET:HG3	1:H:371:LYS:HB3	1.93	0.50
1:L:147:VAL:HG23	1:L:496:PRO:CB	2.39	0.50
1:L:487:ASN:O	1:L:491:MET:HG3	2.11	0.50
2:U:18:LEU:HD13	2:U:51:VAL:HA	1.93	0.50
1:H:143:ALA:C	1:H:146:GLN:HB3	2.31	0.50
1:L:44:PHE:H	1:L:44:PHE:HD1	1.55	0.50
1:N:290:GLN:HB3	1:N:345:ARG:HH21	1.77	0.50
1:N:402:ALA:O	1:N:406:ALA:N	2.32	0.50
1:B:146:GLN:HB3	1:B:494:LEU:CG	2.35	0.50
1:H:381:VAL:HB	1:H:389:MET:CE	2.41	0.50
1:J:147:VAL:HG23	1:J:496:PRO:CB	2.39	0.50
1:J:391:GLU:O	1:J:394:ALA:HB3	2.12	0.50
1:L:190:VAL:HG22	1:L:191:GLU:N	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:381:VAL:HB	1:L:389:MET:CE	2.41	0.50
1:M:391:GLU:O	1:M:394:ALA:HB3	2.12	0.50
1:N:391:GLU:O	1:N:394:ALA:HB3	2.12	0.50
1:F:464:VAL:HG22	1:M:467:ASN:HB2	1.92	0.50
1:J:149:THR:CG2	1:J:159:GLY:HA3	2.37	0.50
1:J:194:GLN:HB2	1:J:331:THR:HB	1.93	0.50
1:K:136:VAL:C	1:K:137:PRO:CB	2.79	0.50
2:Q:17:ILE:CD1	2:R:108:CYS:HB3	2.34	0.50
1:C:406:ALA:CB	1:C:496:PRO:HB3	2.27	0.50
1:H:194:GLN:HB2	1:H:331:THR:HB	1.93	0.50
1:I:193:MET:HG3	1:I:371:LYS:HB3	1.93	0.50
1:J:136:VAL:C	1:J:137:PRO:CB	2.79	0.50
1:M:193:MET:HG3	1:M:371:LYS:HB3	1.93	0.50
1:N:190:VAL:HG22	1:N:191:GLU:N	2.26	0.50
1:N:451:LEU:O	1:N:451:LEU:HD22	2.12	0.50
2:S:18:LEU:HD13	2:S:51:VAL:HA	1.94	0.50
1:F:451:LEU:O	1:F:451:LEU:HD22	2.12	0.49
1:H:391:GLU:O	1:H:394:ALA:HB3	2.12	0.49
1:H:451:LEU:O	1:H:451:LEU:HD22	2.12	0.49
1:I:135:SER:HG	1:I:137:PRO:CA	2.14	0.49
1:I:402:ALA:O	1:I:406:ALA:N	2.32	0.49
1:K:194:GLN:HB2	1:K:331:THR:HB	1.93	0.49
1:I:391:GLU:O	1:I:394:ALA:HB3	2.12	0.49
1:J:143:ALA:C	1:J:146:GLN:HB3	2.31	0.49
1:L:143:ALA:C	1:L:146:GLN:HB3	2.31	0.49
1:L:193:MET:HG3	1:L:371:LYS:HB3	1.93	0.49
1:M:451:LEU:O	1:M:451:LEU:HD22	2.12	0.49
1:N:135:SER:HG	1:N:137:PRO:CA	2.15	0.49
1:C:150:ILE:CD1	1:C:493:ILE:HA	2.43	0.49
1:E:406:ALA:CB	1:E:496:PRO:HB3	2.27	0.49
1:G:451:LEU:O	1:G:451:LEU:HD22	2.12	0.49
1:H:190:VAL:HG22	1:H:191:GLU:N	2.26	0.49
1:H:290:GLN:HB3	1:H:345:ARG:HH21	1.77	0.49
1:J:193:MET:HG3	1:J:371:LYS:HB3	1.93	0.49
1:K:95:LEU:HD13	1:K:504:LEU:HD23	1.95	0.49
1:K:180:GLY:HA2	1:K:380:LYS:HB3	1.93	0.49
1:K:193:MET:HG3	1:K:371:LYS:HB3	1.93	0.49
1:L:290:GLN:HB3	1:L:345:ARG:HH21	1.77	0.49
1:M:192:GLY:CA	1:M:376:VAL:CG2	2.83	0.49
1:N:214:GLU:HG2	1:N:324:VAL:HG12	1.95	0.49
1:D:172:GLU:OE1	1:D:350:ARG:HG3	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:95:LEU:HD13	1:E:504:LEU:HD23	1.95	0.49
1:F:44:PHE:H	1:F:44:PHE:HD1	1.55	0.49
1:I:136:VAL:C	1:I:137:PRO:CB	2.79	0.49
1:L:95:LEU:HD13	1:L:504:LEU:HD23	1.95	0.49
1:L:180:GLY:HA2	1:L:380:LYS:HB3	1.93	0.49
1:M:180:GLY:HA2	1:M:380:LYS:HB3	1.93	0.49
1:M:214:GLU:HG2	1:M:324:VAL:HG12	1.95	0.49
1:M:290:GLN:HB3	1:M:345:ARG:HH21	1.77	0.49
2:O:18:LEU:HD13	2:O:51:VAL:HA	1.93	0.49
1:B:44:PHE:H	1:B:44:PHE:HD1	1.55	0.49
1:B:264:VAL:HG13	1:C:306:GLY:HA3	1.92	0.49
1:K:179:ASP:OD2	1:K:390:LYS:HG2	2.13	0.49
1:K:190:VAL:HG22	1:K:191:GLU:N	2.26	0.49
1:K:214:GLU:HG2	1:K:324:VAL:HG12	1.94	0.49
1:L:214:GLU:HG2	1:L:324:VAL:HG12	1.95	0.49
1:B:18:ARG:NH1	1:B:18:ARG:CG	2.70	0.49
1:C:95:LEU:HD13	1:C:504:LEU:HD23	1.95	0.49
1:C:409:GLU:HB2	1:C:498:LYS:HB2	1.94	0.49
1:C:451:LEU:O	1:C:451:LEU:HD22	2.12	0.49
1:D:31:LEU:HD23	1:D:453:GLN:HB3	1.95	0.49
1:D:95:LEU:HD13	1:D:504:LEU:HD23	1.95	0.49
1:E:150:ILE:CD1	1:E:493:ILE:HA	2.43	0.49
1:E:451:LEU:O	1:E:451:LEU:HD22	2.12	0.49
1:F:146:GLN:HB3	1:F:494:LEU:CG	2.35	0.49
1:H:136:VAL:C	1:H:137:PRO:CB	2.79	0.49
1:H:179:ASP:OD2	1:H:390:LYS:HG2	2.13	0.49
1:I:381:VAL:HB	1:I:389:MET:CE	2.41	0.49
1:K:402:ALA:O	1:K:406:ALA:N	2.32	0.49
1:L:451:LEU:O	1:L:451:LEU:HD22	2.12	0.49
1:N:143:ALA:C	1:N:146:GLN:HB3	2.31	0.49
1:F:95:LEU:HD13	1:F:504:LEU:HD23	1.95	0.49
1:J:95:LEU:HD13	1:J:504:LEU:HD23	1.95	0.49
1:J:381:VAL:HB	1:J:389:MET:CE	2.41	0.49
1:K:381:VAL:HB	1:K:389:MET:CE	2.41	0.49
1:B:95:LEU:HD13	1:B:504:LEU:HD23	1.95	0.49
1:C:464:VAL:HG22	1:J:467:ASN:HB2	1.92	0.49
1:H:214:GLU:HG2	1:H:324:VAL:HG12	1.95	0.49
1:I:451:LEU:O	1:I:451:LEU:HD22	2.12	0.49
1:J:179:ASP:OD2	1:J:390:LYS:HG2	2.13	0.49
1:J:214:GLU:HG2	1:J:324:VAL:HG12	1.95	0.49
1:J:399:ALA:O	1:J:400:LEU:C	2.51	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:147:VAL:CG2	1:L:496:PRO:HG3	2.14	0.49
1:M:221:LEU:HD12	1:M:249:ILE:HG23	1.95	0.49
1:N:95:LEU:HD13	1:N:504:LEU:HD23	1.95	0.49
1:N:136:VAL:C	1:N:137:PRO:CB	2.79	0.49
1:N:180:GLY:HA2	1:N:380:LYS:HB3	1.93	0.49
2:P:18:LEU:HD13	2:P:51:VAL:HA	1.93	0.49
2:R:18:LEU:HD13	2:R:51:VAL:HA	1.94	0.49
1:C:31:LEU:HD23	1:C:453:GLN:HB3	1.95	0.49
1:C:264:VAL:HG13	1:D:306:GLY:HA3	1.92	0.49
1:E:203:TYR:HH	1:F:286:LYS:CD	2.01	0.49
1:I:214:GLU:HG2	1:I:324:VAL:HG12	1.95	0.49
1:L:383:ALA:CB	1:L:389:MET:HA	2.43	0.49
1:N:179:ASP:OD2	1:N:390:LYS:HG2	2.13	0.49
1:N:221:LEU:HD12	1:N:249:ILE:HG23	1.95	0.49
1:B:451:LEU:O	1:B:451:LEU:HD22	2.12	0.49
1:G:146:GLN:CB	1:G:494:LEU:HG	2.34	0.49
1:H:161:LEU:HD12	1:H:161:LEU:N	2.28	0.49
1:K:399:ALA:O	1:K:400:LEU:C	2.51	0.49
1:L:179:ASP:OD2	1:L:390:LYS:HG2	2.13	0.49
1:M:95:LEU:HD13	1:M:504:LEU:HD23	1.95	0.49
1:A:409:GLU:O	1:A:497:THR:HB	2.13	0.48
1:D:409:GLU:O	1:D:497:THR:HB	2.13	0.48
1:E:409:GLU:HB2	1:E:498:LYS:HB2	1.95	0.48
1:F:365:LEU:O	1:F:369:VAL:HG13	2.13	0.48
1:G:31:LEU:HD23	1:G:453:GLN:HB3	1.95	0.48
1:G:365:LEU:O	1:G:369:VAL:HG13	2.13	0.48
1:G:409:GLU:HB2	1:G:498:LYS:HB2	1.94	0.48
1:J:161:LEU:HD12	1:J:161:LEU:N	2.28	0.48
1:L:137:PRO:C	1:L:410:GLY:HA2	2.34	0.48
1:L:221:LEU:HD12	1:L:249:ILE:HG23	1.95	0.48
1:H:95:LEU:HD13	1:H:504:LEU:HD23	1.95	0.48
1:M:383:ALA:CB	1:M:389:MET:HA	2.43	0.48
1:A:150:ILE:CD1	1:A:493:ILE:HA	2.43	0.48
1:A:338:GLU:CD	1:A:338:GLU:H	2.17	0.48
1:A:365:LEU:O	1:A:369:VAL:HG13	2.13	0.48
1:A:451:LEU:O	1:A:451:LEU:HD22	2.12	0.48
1:D:338:GLU:CD	1:D:338:GLU:H	2.17	0.48
1:F:31:LEU:HD23	1:F:453:GLN:HB3	1.95	0.48
1:G:44:PHE:H	1:G:44:PHE:HD1	1.55	0.48
1:I:179:ASP:OD2	1:I:390:LYS:HG2	2.13	0.48
1:I:290:GLN:HB3	1:I:345:ARG:HH21	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:290:GLN:HB3	1:J:345:ARG:HH21	1.77	0.48
1:K:383:ALA:CB	1:K:389:MET:HA	2.43	0.48
1:N:137:PRO:C	1:N:410:GLY:HA2	2.34	0.48
1:A:146:GLN:HB3	1:A:494:LEU:CG	2.35	0.48
1:A:409:GLU:HB2	1:A:498:LYS:HB2	1.95	0.48
1:B:31:LEU:HD23	1:B:453:GLN:HB3	1.95	0.48
1:D:451:LEU:O	1:D:451:LEU:HD22	2.12	0.48
1:E:365:LEU:O	1:E:369:VAL:HG13	2.13	0.48
1:H:221:LEU:HD12	1:H:249:ILE:HG23	1.95	0.48
1:J:31:LEU:HD23	1:J:453:GLN:HB3	1.95	0.48
1:K:149:THR:CG2	1:K:159:GLY:HA3	2.37	0.48
1:M:402:ALA:O	1:M:406:ALA:N	2.32	0.48
1:N:31:LEU:HD23	1:N:453:GLN:HB3	1.95	0.48
1:N:399:ALA:O	1:N:400:LEU:C	2.51	0.48
1:E:409:GLU:O	1:E:497:THR:HB	2.14	0.48
1:F:338:GLU:H	1:F:338:GLU:CD	2.17	0.48
1:H:399:ALA:O	1:H:400:LEU:C	2.51	0.48
1:I:95:LEU:HD13	1:I:504:LEU:HD23	1.95	0.48
1:K:290:GLN:HB3	1:K:345:ARG:HH21	1.77	0.48
1:L:402:ALA:O	1:L:406:ALA:N	2.32	0.48
2:P:17:ILE:CD1	2:Q:108:CYS:HB3	2.34	0.48
1:A:95:LEU:HD13	1:A:504:LEU:HD23	1.95	0.48
1:E:237:LEU:HD21	1:E:271:VAL:HG21	1.95	0.48
1:J:451:LEU:O	1:J:451:LEU:HD22	2.12	0.48
1:K:221:LEU:HD12	1:K:249:ILE:HG23	1.95	0.48
1:M:179:ASP:OD2	1:M:390:LYS:HG2	2.13	0.48
1:N:44:PHE:H	1:N:44:PHE:HD1	1.55	0.48
1:A:44:PHE:H	1:A:44:PHE:HD1	1.55	0.48
1:B:409:GLU:O	1:B:497:THR:HB	2.13	0.48
1:C:409:GLU:O	1:C:497:THR:HB	2.13	0.48
1:G:95:LEU:HD13	1:G:504:LEU:HD23	1.95	0.48
1:G:146:GLN:HB3	1:G:494:LEU:CG	2.36	0.48
1:G:150:ILE:CD1	1:G:493:ILE:HA	2.43	0.48
1:G:338:GLU:CD	1:G:338:GLU:H	2.17	0.48
1:G:409:GLU:O	1:G:497:THR:HB	2.13	0.48
1:I:221:LEU:HD12	1:I:249:ILE:HG23	1.95	0.48
1:M:31:LEU:HD23	1:M:453:GLN:HB3	1.95	0.48
1:M:135:SER:HG	1:M:137:PRO:CA	2.14	0.48
1:M:161:LEU:HD12	1:M:161:LEU:N	2.28	0.48
1:M:399:ALA:O	1:M:400:LEU:C	2.51	0.48
2:Q:18:LEU:HD13	2:Q:51:VAL:HA	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:ILE:HG22	1:G:263:VAL:HG12	1.96	0.48
1:B:338:GLU:CD	1:B:338:GLU:H	2.17	0.48
1:F:237:LEU:HD21	1:F:271:VAL:HG21	1.95	0.48
1:F:409:GLU:O	1:F:497:THR:HB	2.13	0.48
1:F:409:GLU:HB2	1:F:498:LYS:HB2	1.95	0.48
1:I:31:LEU:HD23	1:I:453:GLN:HB3	1.95	0.48
1:I:161:LEU:HD12	1:I:161:LEU:N	2.28	0.48
1:J:221:LEU:HD12	1:J:249:ILE:HG23	1.95	0.48
1:K:136:VAL:C	1:K:137:PRO:HB2	2.34	0.48
1:M:160:LYS:HG2	1:M:164:GLU:OE2	2.14	0.48
1:N:136:VAL:C	1:N:137:PRO:HB2	2.34	0.48
1:A:263:VAL:HG12	1:B:305:ILE:HG22	1.96	0.48
1:B:146:GLN:HB2	1:B:494:LEU:HD12	1.96	0.48
1:C:146:GLN:HB2	1:C:494:LEU:HD12	1.96	0.48
1:D:237:LEU:HD21	1:D:271:VAL:HG21	1.95	0.48
1:J:383:ALA:CB	1:J:389:MET:HA	2.43	0.48
1:K:451:LEU:O	1:K:451:LEU:HD22	2.12	0.48
1:A:31:LEU:HD23	1:A:453:GLN:HB3	1.95	0.48
1:C:338:GLU:H	1:C:338:GLU:CD	2.17	0.48
1:E:31:LEU:HD23	1:E:453:GLN:HB3	1.95	0.48
1:K:31:LEU:HD23	1:K:453:GLN:HB3	1.95	0.48
1:K:161:LEU:HD12	1:K:161:LEU:N	2.28	0.48
1:L:161:LEU:HD12	1:L:161:LEU:N	2.28	0.48
1:N:383:ALA:CB	1:N:389:MET:HA	2.43	0.48
1:B:237:LEU:HD21	1:B:271:VAL:HG21	1.95	0.47
1:E:338:GLU:H	1:E:338:GLU:CD	2.17	0.47
1:L:160:LYS:HG2	1:L:164:GLU:OE2	2.14	0.47
1:N:161:LEU:HD12	1:N:161:LEU:N	2.28	0.47
1:A:266:THR:HG23	1:A:272:LYS:HA	1.96	0.47
1:B:266:THR:HG23	1:B:272:LYS:HA	1.97	0.47
1:B:365:LEU:O	1:B:369:VAL:HG13	2.14	0.47
1:D:365:LEU:O	1:D:369:VAL:HG13	2.13	0.47
1:F:263:VAL:HG12	1:G:305:ILE:HG22	1.96	0.47
1:I:136:VAL:C	1:I:137:PRO:HB2	2.34	0.47
1:M:136:VAL:C	1:M:137:PRO:CB	2.79	0.47
1:N:160:LYS:HG2	1:N:164:GLU:OE2	2.14	0.47
1:B:409:GLU:HB2	1:B:498:LYS:HB2	1.94	0.47
1:F:266:THR:HG23	1:F:272:LYS:HA	1.96	0.47
1:G:100:ILE:HG13	1:G:511:ALA:HB1	1.97	0.47
1:H:169:VAL:CG1	1:H:173:GLY:HA3	2.42	0.47
1:L:399:ALA:O	1:L:400:LEU:C	2.51	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:175:ILE:N	1:N:175:ILE:CD1	2.77	0.47
1:A:100:ILE:HG13	1:A:511:ALA:HB1	1.97	0.47
1:C:237:LEU:HD21	1:C:271:VAL:HG21	1.95	0.47
1:D:146:GLN:HB2	1:D:494:LEU:HD12	1.96	0.47
1:E:266:THR:HG23	1:E:272:LYS:HA	1.97	0.47
1:H:31:LEU:HD23	1:H:453:GLN:HB3	1.95	0.47
1:K:192:GLY:CA	1:K:376:VAL:CG2	2.83	0.47
2:R:10:ARG:O	2:S:108:CYS:CA	2.62	0.47
1:A:237:LEU:HD21	1:A:271:VAL:HG21	1.95	0.47
1:B:289:LEU:HA	1:B:292:ILE:HD12	1.97	0.47
1:D:409:GLU:HB2	1:D:498:LYS:HB2	1.94	0.47
1:G:266:THR:HG23	1:G:272:LYS:HA	1.96	0.47
1:H:383:ALA:CB	1:H:389:MET:HA	2.43	0.47
1:I:100:ILE:HG13	1:I:511:ALA:HB1	1.97	0.47
1:I:399:ALA:O	1:I:400:LEU:C	2.51	0.47
1:J:160:LYS:HG2	1:J:164:GLU:OE2	2.14	0.47
1:A:218:PRO:HB3	1:A:246:PRO:HB2	1.97	0.47
1:A:289:LEU:HA	1:A:292:ILE:HD12	1.97	0.47
1:C:266:THR:HG23	1:C:272:LYS:HA	1.96	0.47
1:C:289:LEU:HA	1:C:292:ILE:HD12	1.97	0.47
1:D:266:THR:HG23	1:D:272:LYS:HA	1.96	0.47
1:F:100:ILE:HG13	1:F:511:ALA:HB1	1.97	0.47
1:I:383:ALA:CB	1:I:389:MET:HA	2.43	0.47
1:J:100:ILE:HG13	1:J:511:ALA:HB1	1.97	0.47
1:L:136:VAL:C	1:L:137:PRO:HB2	2.34	0.47
1:M:136:VAL:C	1:M:137:PRO:HB2	2.35	0.47
1:M:313:THR:HG22	1:M:314:LEU:H	1.80	0.47
1:N:169:VAL:CG1	1:N:173:GLY:HA3	2.42	0.47
1:B:100:ILE:HG13	1:B:511:ALA:HB1	1.97	0.47
1:B:150:ILE:CD1	1:B:493:ILE:HA	2.43	0.47
1:B:218:PRO:HB3	1:B:246:PRO:HB2	1.97	0.47
1:D:150:ILE:CD1	1:D:493:ILE:HA	2.43	0.47
1:E:174:VAL:CG2	1:E:367:GLU:HA	2.39	0.47
1:F:146:GLN:HB2	1:F:494:LEU:HD12	1.96	0.47
1:F:150:ILE:CD1	1:F:493:ILE:HA	2.43	0.47
1:F:218:PRO:HB3	1:F:246:PRO:HB2	1.97	0.47
1:G:237:LEU:HD21	1:G:271:VAL:HG21	1.95	0.47
1:G:289:LEU:HA	1:G:292:ILE:HD12	1.97	0.47
1:H:100:ILE:HG13	1:H:511:ALA:HB1	1.97	0.47
1:I:147:VAL:CG2	1:I:496:PRO:CB	2.93	0.47
1:I:169:VAL:CG1	1:I:173:GLY:HA3	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:31:LEU:HD23	1:L:453:GLN:HB3	1.95	0.47
1:C:365:LEU:O	1:C:369:VAL:HG13	2.14	0.47
1:D:289:LEU:HA	1:D:292:ILE:HD12	1.97	0.47
1:E:146:GLN:HB2	1:E:494:LEU:HD12	1.96	0.47
1:E:263:VAL:HG12	1:F:305:ILE:HG22	1.96	0.47
1:F:351:GLN:O	1:F:351:GLN:HG2	2.15	0.47
1:G:146:GLN:HB2	1:G:494:LEU:HD12	1.96	0.47
1:H:147:VAL:CG2	1:H:496:PRO:CB	2.93	0.47
1:I:160:LYS:HG2	1:I:164:GLU:OE2	2.14	0.47
1:K:160:LYS:HG2	1:K:164:GLU:OE2	2.14	0.47
1:K:175:ILE:N	1:K:175:ILE:CD1	2.77	0.47
1:L:313:THR:HG22	1:L:314:LEU:H	1.80	0.47
1:M:228:SER:O	1:M:257:GLU:HB3	2.15	0.47
1:H:160:LYS:HG2	1:H:164:GLU:OE2	2.14	0.47
1:G:218:PRO:HB3	1:G:246:PRO:HB2	1.97	0.47
1:I:513:LEU:HD23	1:I:513:LEU:HA	1.72	0.47
1:M:137:PRO:C	1:M:410:GLY:HA2	2.33	0.47
1:N:100:ILE:HG13	1:N:511:ALA:HB1	1.97	0.47
1:N:228:SER:O	1:N:257:GLU:HB3	2.15	0.47
1:N:313:THR:HG22	1:N:314:LEU:H	1.80	0.47
2:P:83:PHE:HA	2:P:88:LEU:HD12	1.97	0.47
2:T:7:LEU:HB3	2:T:8:PRO:HD2	1.97	0.47
1:A:351:GLN:O	1:A:351:GLN:HG2	2.15	0.46
1:H:136:VAL:C	1:H:137:PRO:HB2	2.34	0.46
1:H:157:THR:O	1:H:161:LEU:CD1	2.64	0.46
1:H:175:ILE:N	1:H:175:ILE:CD1	2.77	0.46
1:H:217:SER:HA	1:H:320:ALA:O	2.16	0.46
1:J:147:VAL:CG2	1:J:496:PRO:CB	2.93	0.46
1:K:217:SER:HA	1:K:320:ALA:O	2.16	0.46
1:K:313:THR:HG22	1:K:314:LEU:H	1.79	0.46
1:N:147:VAL:CG2	1:N:496:PRO:CB	2.93	0.46
2:O:10:ARG:O	2:P:108:CYS:CA	2.62	0.46
2:O:83:PHE:HA	2:O:88:LEU:HD12	1.97	0.46
2:U:7:LEU:HB3	2:U:8:PRO:HD2	1.97	0.46
1:C:218:PRO:HB3	1:C:246:PRO:HB2	1.97	0.46
1:E:100:ILE:HG13	1:E:511:ALA:HB1	1.97	0.46
1:E:218:PRO:HB3	1:E:246:PRO:HB2	1.97	0.46
1:F:289:LEU:HA	1:F:292:ILE:HD12	1.97	0.46
1:I:313:THR:HG22	1:I:314:LEU:H	1.79	0.46
1:J:136:VAL:C	1:J:137:PRO:HB2	2.34	0.46
1:J:313:THR:HG22	1:J:314:LEU:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:100:ILE:HG13	1:K:511:ALA:HB1	1.97	0.46
1:M:513:LEU:HD23	1:M:513:LEU:HA	1.72	0.46
2:Q:10:ARG:O	2:R:108:CYS:CA	2.62	0.46
2:S:7:LEU:HB3	2:S:8:PRO:HD2	1.97	0.46
1:C:351:GLN:O	1:C:351:GLN:HG2	2.15	0.46
1:E:289:LEU:HA	1:E:292:ILE:HD12	1.97	0.46
1:E:461:GLU:OE1	1:L:463:SER:HB3	2.13	0.46
1:I:228:SER:O	1:I:257:GLU:HB3	2.15	0.46
1:L:192:GLY:CA	1:L:376:VAL:CG2	2.83	0.46
1:L:228:SER:O	1:L:257:GLU:HB3	2.15	0.46
1:N:157:THR:O	1:N:161:LEU:CD1	2.64	0.46
2:P:7:LEU:HB3	2:P:8:PRO:HD2	1.97	0.46
2:Q:7:LEU:HB3	2:Q:8:PRO:HD2	1.98	0.46
2:R:7:LEU:HB3	2:R:8:PRO:HD2	1.97	0.46
1:D:351:GLN:O	1:D:351:GLN:HG2	2.15	0.46
1:D:464:VAL:HB	1:K:467:ASN:HD21	1.78	0.46
2:Q:83:PHE:HA	2:Q:88:LEU:HD12	1.97	0.46
1:A:464:VAL:HB	1:H:467:ASN:HD21	1.78	0.46
1:D:218:PRO:HB3	1:D:246:PRO:HB2	1.97	0.46
1:D:263:VAL:HG12	1:E:305:ILE:HG22	1.96	0.46
1:I:149:THR:HG22	1:I:156:GLU:O	2.16	0.46
1:J:137:PRO:C	1:J:410:GLY:HA2	2.33	0.46
1:M:149:THR:HG22	1:M:156:GLU:O	2.16	0.46
2:O:7:LEU:HB3	2:O:8:PRO:HD2	1.97	0.46
1:B:351:GLN:HG2	1:B:351:GLN:O	2.15	0.46
1:B:513:LEU:HA	1:B:513:LEU:HD23	1.73	0.46
1:C:100:ILE:HG13	1:C:511:ALA:HB1	1.97	0.46
1:G:351:GLN:HG2	1:G:351:GLN:O	2.15	0.46
1:H:228:SER:O	1:H:257:GLU:HB3	2.15	0.46
1:H:389:MET:HE1	1:H:389:MET:O	2.14	0.46
1:J:149:THR:HG22	1:J:156:GLU:O	2.16	0.46
1:K:228:SER:O	1:K:257:GLU:HB3	2.15	0.46
1:L:100:ILE:HG13	1:L:511:ALA:HB1	1.97	0.46
1:M:169:VAL:CG1	1:M:173:GLY:HA3	2.42	0.46
1:H:149:THR:HG22	1:H:156:GLU:O	2.16	0.46
1:H:513:LEU:HD23	1:H:513:LEU:HA	1.72	0.46
1:J:217:SER:HA	1:J:320:ALA:O	2.16	0.46
1:K:227:ILE:HD12	1:K:309:LEU:HD11	1.98	0.46
1:M:100:ILE:HG13	1:M:511:ALA:HB1	1.97	0.46
1:M:227:ILE:HD12	1:M:309:LEU:HD11	1.98	0.46
1:N:149:THR:HG22	1:N:156:GLU:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:217:SER:HA	1:N:320:ALA:O	2.16	0.46
2:P:10:ARG:O	2:Q:108:CYS:CA	2.62	0.46
2:U:83:PHE:HA	2:U:88:LEU:HD12	1.97	0.46
1:C:263:VAL:HG12	1:D:305:ILE:HG22	1.96	0.46
1:H:137:PRO:C	1:H:410:GLY:HA2	2.34	0.46
1:J:169:VAL:CG1	1:J:173:GLY:HA3	2.42	0.46
1:D:461:GLU:OE1	1:K:463:SER:HB3	2.13	0.46
1:M:157:THR:O	1:M:161:LEU:CD1	2.64	0.46
2:S:10:ARG:O	2:T:108:CYS:CA	2.62	0.46
1:A:146:GLN:HB2	1:A:494:LEU:HD12	1.96	0.46
1:D:136:VAL:CA	1:D:137:PRO:CD	2.83	0.46
1:H:313:THR:HG22	1:H:314:LEU:H	1.80	0.46
1:J:228:SER:O	1:J:257:GLU:HB3	2.15	0.46
1:D:100:ILE:HG13	1:D:511:ALA:HB1	1.97	0.45
1:F:461:GLU:OE1	1:M:463:SER:HB3	2.13	0.45
1:I:217:SER:HA	1:I:320:ALA:O	2.16	0.45
1:J:192:GLY:CA	1:J:376:VAL:CG2	2.83	0.45
1:L:217:SER:HA	1:L:320:ALA:O	2.16	0.45
1:N:227:ILE:HD12	1:N:309:LEU:HD11	1.98	0.45
1:F:366:GLN:O	1:F:369:VAL:HG22	2.16	0.45
1:J:227:ILE:HD12	1:J:309:LEU:HD11	1.98	0.45
2:R:83:PHE:HA	2:R:88:LEU:HD12	1.97	0.45
2:T:83:PHE:HA	2:T:88:LEU:HD12	1.97	0.45
1:G:366:GLN:O	1:G:369:VAL:HG22	2.16	0.45
1:H:227:ILE:HD12	1:H:309:LEU:HD11	1.98	0.45
2:S:83:PHE:HA	2:S:88:LEU:HD12	1.97	0.45
1:C:22:VAL:HG11	1:C:62:LEU:HD11	1.99	0.45
1:E:351:GLN:HG2	1:E:351:GLN:O	2.15	0.45
1:I:227:ILE:HD12	1:I:309:LEU:HD11	1.98	0.45
1:K:147:VAL:CG2	1:K:496:PRO:CB	2.93	0.45
1:L:149:THR:HG22	1:L:156:GLU:O	2.16	0.45
1:L:175:ILE:N	1:L:175:ILE:CD1	2.77	0.45
1:M:175:ILE:N	1:M:175:ILE:CD1	2.77	0.45
1:B:22:VAL:HG11	1:B:62:LEU:HD11	1.99	0.45
1:G:320:ALA:HA	1:G:335:GLY:HA2	1.99	0.45
1:J:178:GLU:O	1:J:380:LYS:HA	2.17	0.45
1:K:22:VAL:HG11	1:K:62:LEU:HD11	1.99	0.45
1:K:137:PRO:C	1:K:410:GLY:HA2	2.34	0.45
1:L:22:VAL:HG11	1:L:62:LEU:HD11	1.99	0.45
2:R:80:PRO:HD2	2:S:70:SER:CB	2.47	0.45
1:A:366:GLN:O	1:A:369:VAL:HG22	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:366:GLN:O	1:E:369:VAL:HG22	2.16	0.45
1:H:187:LEU:HD23	1:H:187:LEU:C	2.37	0.45
1:J:389:MET:HE1	1:J:389:MET:O	2.16	0.45
1:L:157:THR:O	1:L:161:LEU:CD1	2.64	0.45
1:M:217:SER:HA	1:M:320:ALA:O	2.15	0.45
2:O:80:PRO:HD2	2:P:70:SER:CB	2.47	0.45
1:C:197:ARG:CD	1:C:277:LYS:HB2	2.23	0.45
1:C:461:GLU:OE1	1:J:463:SER:HB3	2.13	0.45
1:D:22:VAL:HG11	1:D:62:LEU:HD11	1.99	0.45
1:G:197:ARG:CD	1:G:277:LYS:HB2	2.23	0.45
1:I:187:LEU:HD23	1:I:187:LEU:C	2.37	0.45
1:K:149:THR:HG22	1:K:156:GLU:O	2.16	0.45
1:K:157:THR:O	1:K:161:LEU:CD1	2.64	0.45
1:K:169:VAL:CG1	1:K:173:GLY:HA3	2.42	0.45
1:L:169:VAL:CG1	1:L:173:GLY:HA3	2.42	0.45
1:N:513:LEU:HD23	1:N:513:LEU:HA	1.72	0.45
2:O:70:SER:CB	2:U:80:PRO:HD2	2.47	0.45
2:O:108:CYS:CA	2:U:10:ARG:O	2.62	0.45
1:B:464:VAL:HB	1:I:467:ASN:HD21	1.78	0.45
1:D:366:GLN:O	1:D:369:VAL:HG22	2.16	0.45
1:G:464:VAL:HB	1:N:467:ASN:HD21	1.78	0.45
1:I:178:GLU:O	1:I:380:LYS:HA	2.17	0.45
1:K:178:GLU:O	1:K:380:LYS:HA	2.17	0.45
1:L:421:ARG:HA	1:L:421:ARG:HD3	1.78	0.45
1:M:313:THR:HG22	1:M:314:LEU:HD12	1.99	0.45
2:T:10:ARG:O	2:U:108:CYS:CA	2.62	0.45
2:T:21:GLU:HA	2:T:22:PRO:HD3	1.88	0.45
1:A:320:ALA:HA	1:A:335:GLY:HA2	1.99	0.45
1:B:263:VAL:HG12	1:C:305:ILE:HG22	1.96	0.45
1:F:320:ALA:HA	1:F:335:GLY:HA2	1.99	0.45
1:I:18:ARG:NH1	1:I:18:ARG:CG	2.70	0.45
1:I:137:PRO:C	1:I:410:GLY:HA2	2.33	0.45
1:J:157:THR:O	1:J:161:LEU:CD1	2.64	0.45
1:L:313:THR:HG22	1:L:314:LEU:HD12	1.99	0.45
1:M:147:VAL:CG2	1:M:496:PRO:CB	2.93	0.45
1:N:187:LEU:HD23	1:N:187:LEU:C	2.37	0.45
1:B:366:GLN:O	1:B:369:VAL:HG22	2.16	0.45
1:B:461:GLU:OE1	1:I:463:SER:HB3	2.13	0.45
1:C:444:LEU:O	1:C:447:MET:HB2	2.17	0.45
1:I:22:VAL:HG11	1:I:62:LEU:HD11	1.99	0.45
1:M:514:MET:HE3	1:M:514:MET:HB2	1.89	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:VAL:HG11	1:A:62:LEU:HD11	1.99	0.44
1:F:444:LEU:O	1:F:447:MET:HB2	2.17	0.44
1:H:18:ARG:NH1	1:H:18:ARG:CG	2.70	0.44
1:I:421:ARG:HD3	1:I:421:ARG:HA	1.78	0.44
1:J:187:LEU:C	1:J:187:LEU:HD23	2.37	0.44
1:L:227:ILE:HD12	1:L:309:LEU:HD11	1.98	0.44
1:C:366:GLN:O	1:C:369:VAL:HG22	2.16	0.44
1:F:136:VAL:CA	1:F:137:PRO:CD	2.83	0.44
1:H:22:VAL:HG11	1:H:62:LEU:HD11	1.99	0.44
1:K:513:LEU:HA	1:K:513:LEU:HD23	1.72	0.44
2:S:80:PRO:HD2	2:T:70:SER:CB	2.47	0.44
1:A:225:LYS:HG2	1:A:303:GLU:HB2	1.99	0.44
1:A:421:ARG:HA	1:A:421:ARG:HD3	1.78	0.44
1:F:174:VAL:CG2	1:F:367:GLU:HA	2.39	0.44
1:H:178:GLU:O	1:H:380:LYS:HA	2.17	0.44
1:K:313:THR:HG22	1:K:314:LEU:HD12	1.99	0.44
1:M:22:VAL:HG11	1:M:62:LEU:HD11	1.99	0.44
1:N:178:GLU:O	1:N:380:LYS:HA	2.17	0.44
1:B:225:LYS:HG2	1:B:303:GLU:HB2	1.99	0.44
1:D:444:LEU:O	1:D:447:MET:HB2	2.17	0.44
1:E:320:ALA:HA	1:E:335:GLY:HA2	1.99	0.44
1:I:44:PHE:H	1:I:44:PHE:HD1	1.55	0.44
1:J:313:THR:HG22	1:J:314:LEU:HD12	1.99	0.44
1:L:135:SER:HG	1:L:137:PRO:CA	2.14	0.44
1:L:187:LEU:HD23	1:L:187:LEU:C	2.37	0.44
1:M:187:LEU:HD23	1:M:187:LEU:C	2.37	0.44
1:N:313:THR:HG22	1:N:314:LEU:HD12	1.99	0.44
2:Q:85:ALA:HA	2:R:48:LEU:HD22	1.99	0.44
2:U:21:GLU:HA	2:U:22:PRO:HD3	1.88	0.44
1:A:461:GLU:OE1	1:H:463:SER:HB3	2.13	0.44
1:B:86:GLY:HA3	1:B:401:HIS:CB	2.48	0.44
1:E:225:LYS:HG2	1:E:303:GLU:HB2	1.99	0.44
1:E:444:LEU:O	1:E:447:MET:HB2	2.17	0.44
1:F:233:MET:HB3	1:F:237:LEU:HD12	1.99	0.44
1:G:173:GLY:HA2	1:G:370:ALA:CB	2.45	0.44
1:K:187:LEU:HD23	1:K:187:LEU:C	2.37	0.44
2:Q:80:PRO:HD2	2:R:70:SER:CB	2.47	0.44
2:T:80:PRO:HD2	2:U:70:SER:CB	2.47	0.44
2:T:85:ALA:HA	2:U:48:LEU:HD22	1.99	0.44
1:A:86:GLY:HA3	1:A:401:HIS:CB	2.48	0.44
1:C:162:ILE:HG12	1:C:400:LEU:HD23	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:225:LYS:HG2	1:D:303:GLU:HB2	1.99	0.44
1:J:22:VAL:HG11	1:J:62:LEU:HD11	1.99	0.44
1:N:444:LEU:O	1:N:447:MET:HB2	2.17	0.44
1:A:162:ILE:HG12	1:A:400:LEU:HD23	2.00	0.44
1:B:162:ILE:HG12	1:B:400:LEU:HD23	2.00	0.44
1:B:234:LEU:HB2	1:B:235:PRO:HD3	2.00	0.44
1:C:320:ALA:HA	1:C:335:GLY:HA2	1.99	0.44
1:E:22:VAL:HG11	1:E:62:LEU:HD11	1.99	0.44
1:F:22:VAL:HG11	1:F:62:LEU:HD11	1.99	0.44
1:F:234:LEU:HB2	1:F:235:PRO:HD3	2.00	0.44
1:G:225:LYS:HG2	1:G:303:GLU:HB2	1.99	0.44
1:G:513:LEU:HA	1:G:513:LEU:HD23	1.73	0.44
1:H:444:LEU:O	1:H:447:MET:HB2	2.17	0.44
1:L:165:ALA:O	1:L:168:LYS:HB2	2.18	0.44
1:M:421:ARG:HA	1:M:421:ARG:HD3	1.78	0.44
1:N:22:VAL:HG11	1:N:62:LEU:HD11	1.99	0.44
1:B:320:ALA:HA	1:B:335:GLY:HA2	1.99	0.44
1:D:162:ILE:HG12	1:D:400:LEU:HD23	2.00	0.44
1:D:320:ALA:HA	1:D:335:GLY:HA2	1.99	0.44
1:H:455:VAL:HG11	1:H:462:PRO:HA	2.00	0.44
1:I:444:LEU:O	1:I:447:MET:HB2	2.17	0.44
1:J:444:LEU:O	1:J:447:MET:HB2	2.17	0.44
1:M:178:GLU:O	1:M:380:LYS:HA	2.17	0.44
2:P:85:ALA:HA	2:Q:48:LEU:HD22	1.99	0.44
2:R:85:ALA:HA	2:S:48:LEU:HD22	1.99	0.44
2:T:83:PHE:HD2	2:T:89:LYS:HD2	1.83	0.44
1:E:233:MET:HB3	1:E:237:LEU:HD12	1.99	0.44
1:G:162:ILE:HG12	1:G:400:LEU:HD23	2.00	0.44
1:G:233:MET:HB3	1:G:237:LEU:HD12	1.99	0.44
1:I:286:LYS:NZ	1:I:304:GLU:OE1	2.51	0.44
1:J:421:ARG:HA	1:J:421:ARG:HD3	1.78	0.44
1:K:158:VAL:C	1:K:160:LYS:N	2.71	0.44
1:K:165:ALA:O	1:K:168:LYS:HB2	2.18	0.44
1:K:421:ARG:HD3	1:K:421:ARG:HA	1.78	0.44
1:K:455:VAL:HG11	1:K:462:PRO:HA	2.00	0.44
1:L:178:GLU:O	1:L:380:LYS:HA	2.17	0.44
1:L:513:LEU:HD23	1:L:513:LEU:HA	1.72	0.44
2:P:80:PRO:HD2	2:Q:70:SER:CB	2.47	0.44
1:B:444:LEU:O	1:B:447:MET:HB2	2.17	0.43
1:C:234:LEU:HB2	1:C:235:PRO:HD3	2.00	0.43
1:C:464:VAL:HB	1:J:467:ASN:HD21	1.78	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:22:VAL:HG11	1:G:62:LEU:HD11	1.99	0.43
1:G:234:LEU:HB2	1:G:235:PRO:HD3	2.00	0.43
1:I:153:ASN:O	1:I:154:SER:HB2	2.18	0.43
1:J:153:ASN:O	1:J:154:SER:HB2	2.18	0.43
1:L:147:VAL:CG2	1:L:496:PRO:CB	2.93	0.43
1:M:444:LEU:O	1:M:447:MET:HB2	2.17	0.43
1:N:455:VAL:HG11	1:N:462:PRO:HA	2.00	0.43
2:U:83:PHE:HD2	2:U:89:LYS:HD2	1.83	0.43
1:A:234:LEU:HB2	1:A:235:PRO:HD3	2.00	0.43
1:C:225:LYS:HG2	1:C:303:GLU:HB2	1.99	0.43
1:D:78:ALA:HB2	1:D:93:THR:OG1	2.19	0.43
1:D:233:MET:HB3	1:D:237:LEU:HD12	1.99	0.43
1:G:514:MET:HE3	1:G:514:MET:HB2	1.87	0.43
1:H:313:THR:HG22	1:H:314:LEU:HD12	1.99	0.43
1:I:313:THR:HG22	1:I:314:LEU:HD12	1.99	0.43
1:J:286:LYS:NZ	1:J:304:GLU:OE1	2.51	0.43
1:J:455:VAL:HG11	1:J:462:PRO:HA	2.00	0.43
1:K:149:THR:HG21	1:K:156:GLU:HA	1.99	0.43
1:K:153:ASN:O	1:K:154:SER:HB2	2.18	0.43
1:M:20:VAL:HG13	1:M:74:VAL:HG11	2.00	0.43
1:M:286:LYS:NZ	1:M:304:GLU:OE1	2.51	0.43
1:N:78:ALA:HB2	1:N:93:THR:OG1	2.18	0.43
2:S:83:PHE:HD2	2:S:89:LYS:HD2	1.83	0.43
2:S:86:LEU:HD23	2:T:68:LEU:CD2	2.49	0.43
1:A:78:ALA:HB2	1:A:93:THR:OG1	2.18	0.43
1:E:234:LEU:HB2	1:E:235:PRO:HD3	2.00	0.43
1:F:455:VAL:HG11	1:F:462:PRO:HA	2.00	0.43
1:G:86:GLY:HA3	1:G:401:HIS:CB	2.48	0.43
1:G:455:VAL:HG11	1:G:462:PRO:HA	2.00	0.43
1:I:157:THR:O	1:I:161:LEU:CD1	2.64	0.43
1:I:165:ALA:O	1:I:168:LYS:HB2	2.18	0.43
1:I:389:MET:O	1:I:389:MET:HE1	2.18	0.43
1:I:514:MET:HE3	1:I:514:MET:HB2	1.92	0.43
1:J:165:ALA:O	1:J:168:LYS:HB2	2.18	0.43
1:N:20:VAL:HG13	1:N:74:VAL:HG11	2.00	0.43
2:O:85:ALA:HA	2:P:48:LEU:HD22	1.99	0.43
2:O:86:LEU:HD23	2:P:68:LEU:CD2	2.49	0.43
2:P:83:PHE:HD2	2:P:89:LYS:HD2	1.83	0.43
1:A:444:LEU:O	1:A:447:MET:HB2	2.17	0.43
1:B:78:ALA:HB2	1:B:93:THR:OG1	2.18	0.43
1:B:193:MET:HG3	1:B:371:LYS:HB3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:247:LEU:HB3	1:D:273:VAL:HG12	2.01	0.43
1:G:147:VAL:HG22	1:G:403:THR:HG22	1.99	0.43
1:H:165:ALA:O	1:H:168:LYS:HB2	2.18	0.43
1:J:18:ARG:NH1	1:J:18:ARG:CG	2.70	0.43
1:L:153:ASN:O	1:L:154:SER:HB2	2.18	0.43
1:L:389:MET:HE1	1:L:393:LYS:HB2	2.01	0.43
1:L:444:LEU:O	1:L:447:MET:HB2	2.17	0.43
1:M:149:THR:H	1:M:159:GLY:HA3	1.84	0.43
1:N:158:VAL:C	1:N:160:LYS:N	2.71	0.43
1:N:286:LYS:NZ	1:N:304:GLU:OE1	2.51	0.43
2:Q:83:PHE:HD2	2:Q:89:LYS:HD2	1.83	0.43
2:R:12:VAL:HG23	2:S:106:ILE:O	2.19	0.43
2:S:85:ALA:HA	2:T:48:LEU:HD22	1.99	0.43
1:C:20:VAL:HG13	1:C:74:VAL:HG11	2.00	0.43
1:C:193:MET:HG3	1:C:371:LYS:HB3	2.00	0.43
1:E:162:ILE:HG12	1:E:400:LEU:HD23	2.00	0.43
1:F:173:GLY:HA2	1:F:370:ALA:CB	2.45	0.43
1:F:225:LYS:HG2	1:F:303:GLU:HB2	1.99	0.43
1:K:44:PHE:H	1:K:44:PHE:HD1	1.55	0.43
1:K:197:ARG:HG2	1:K:277:LYS:O	2.19	0.43
1:L:20:VAL:HG13	1:L:74:VAL:HG11	2.00	0.43
1:L:455:VAL:HG11	1:L:462:PRO:HA	2.00	0.43
1:M:165:ALA:O	1:M:168:LYS:HB2	2.18	0.43
1:N:149:THR:H	1:N:159:GLY:HA3	1.84	0.43
1:N:165:ALA:O	1:N:168:LYS:HB2	2.18	0.43
2:Q:12:VAL:HG23	2:R:106:ILE:O	2.19	0.43
1:A:147:VAL:HG22	1:A:403:THR:HG22	1.99	0.43
1:C:247:LEU:HB3	1:C:273:VAL:HG12	2.01	0.43
1:D:234:LEU:HB2	1:D:235:PRO:HD3	2.00	0.43
1:F:162:ILE:HG12	1:F:400:LEU:HD23	2.00	0.43
1:H:153:ASN:O	1:H:154:SER:HB2	2.18	0.43
1:H:286:LYS:NZ	1:H:304:GLU:OE1	2.51	0.43
1:I:455:VAL:HG11	1:I:462:PRO:HA	2.00	0.43
1:M:153:ASN:O	1:M:154:SER:HB2	2.18	0.43
1:B:20:VAL:HG13	1:B:74:VAL:HG11	2.00	0.43
1:C:233:MET:HB3	1:C:237:LEU:HD12	1.99	0.43
1:E:197:ARG:CD	1:E:277:LYS:HB2	2.23	0.43
1:F:193:MET:HG3	1:F:371:LYS:HB3	2.01	0.43
1:G:444:LEU:O	1:G:447:MET:HB2	2.17	0.43
1:I:78:ALA:HB2	1:I:93:THR:OG1	2.19	0.43
2:T:86:LEU:HD23	2:U:68:LEU:CD2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:173:GLY:HA2	1:A:370:ALA:CB	2.45	0.43
1:D:147:VAL:HG22	1:D:403:THR:HG22	1.99	0.43
1:D:455:VAL:HG11	1:D:462:PRO:HA	2.00	0.43
1:E:455:VAL:HG11	1:E:462:PRO:HA	2.00	0.43
1:E:514:MET:HE3	1:E:514:MET:HB2	1.92	0.43
1:F:513:LEU:HD23	1:F:513:LEU:HA	1.73	0.43
1:G:78:ALA:HB2	1:G:93:THR:OG1	2.18	0.43
1:G:193:MET:HG3	1:G:371:LYS:HB3	2.00	0.43
1:J:262:LEU:HD22	1:J:273:VAL:HG21	2.01	0.43
1:K:78:ALA:HB2	1:K:93:THR:OG1	2.19	0.43
1:K:149:THR:H	1:K:159:GLY:HA3	1.83	0.43
1:K:286:LYS:NZ	1:K:304:GLU:OE1	2.51	0.43
1:L:389:MET:CE	1:L:389:MET:C	2.87	0.43
2:S:12:VAL:HG23	2:T:106:ILE:O	2.19	0.43
1:A:233:MET:HB3	1:A:237:LEU:HD12	1.99	0.43
1:A:455:VAL:HG11	1:A:462:PRO:HA	2.00	0.43
1:B:147:VAL:HG22	1:B:403:THR:HG22	1.99	0.43
1:B:233:MET:HB3	1:B:237:LEU:HD12	1.99	0.43
1:C:78:ALA:HB2	1:C:93:THR:OG1	2.19	0.43
1:C:147:VAL:HG22	1:C:403:THR:HG22	1.99	0.43
1:C:455:VAL:HG11	1:C:462:PRO:HA	2.00	0.43
1:C:513:LEU:HA	1:C:513:LEU:HD23	1.73	0.43
1:D:222:LEU:HD12	1:D:293:ALA:HB2	2.01	0.43
1:F:464:VAL:HB	1:M:467:ASN:HD21	1.78	0.43
1:H:149:THR:H	1:H:159:GLY:HA3	1.84	0.43
1:J:78:ALA:HB2	1:J:93:THR:OG1	2.19	0.43
1:J:149:THR:H	1:J:159:GLY:HA3	1.84	0.43
1:J:197:ARG:HG2	1:J:277:LYS:O	2.19	0.43
1:K:20:VAL:HG13	1:K:74:VAL:HG11	2.00	0.43
1:K:389:MET:CE	1:K:389:MET:C	2.87	0.43
1:K:444:LEU:O	1:K:447:MET:HB2	2.17	0.43
1:M:389:MET:CE	1:M:389:MET:C	2.87	0.43
1:N:153:ASN:O	1:N:154:SER:HB2	2.18	0.43
1:N:197:ARG:HG2	1:N:277:LYS:O	2.19	0.43
1:N:389:MET:CE	1:N:389:MET:C	2.87	0.43
1:B:247:LEU:HB3	1:B:273:VAL:HG12	2.01	0.43
1:E:147:VAL:HG22	1:E:403:THR:HG22	1.99	0.43
1:E:247:LEU:HB3	1:E:273:VAL:HG12	2.01	0.43
1:F:147:VAL:HG22	1:F:403:THR:HG22	1.99	0.43
1:H:20:VAL:HG13	1:H:74:VAL:HG11	2.00	0.43
1:J:158:VAL:C	1:J:160:LYS:N	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:262:LEU:HD22	1:K:273:VAL:HG21	2.01	0.43
1:L:286:LYS:NZ	1:L:304:GLU:OE1	2.51	0.43
1:M:44:PHE:H	1:M:44:PHE:HD1	1.55	0.43
1:M:78:ALA:HB2	1:M:93:THR:OG1	2.19	0.43
1:M:455:VAL:HG11	1:M:462:PRO:HA	2.00	0.43
2:O:106:ILE:O	2:U:12:VAL:HG23	2.19	0.43
2:P:86:LEU:HD23	2:Q:68:LEU:CD2	2.49	0.43
1:F:86:GLY:HA3	1:F:401:HIS:CB	2.48	0.42
1:J:389:MET:CE	1:J:389:MET:C	2.87	0.42
1:K:198:GLY:O	1:K:276:VAL:HG12	2.19	0.42
2:O:48:LEU:HD22	2:U:85:ALA:HA	1.99	0.42
2:R:83:PHE:HD2	2:R:89:LYS:HD2	1.83	0.42
2:S:21:GLU:HA	2:S:22:PRO:HD3	1.88	0.42
1:D:20:VAL:HG13	1:D:74:VAL:HG11	2.00	0.42
1:D:193:MET:HG3	1:D:371:LYS:HB3	2.01	0.42
1:E:78:ALA:HB2	1:E:93:THR:OG1	2.18	0.42
1:E:193:MET:HG3	1:E:371:LYS:HB3	2.01	0.42
1:E:222:LEU:HD12	1:E:293:ALA:HB2	2.01	0.42
1:E:236:VAL:O	1:E:240:VAL:HG23	2.20	0.42
1:E:513:LEU:HA	1:E:513:LEU:HD23	1.73	0.42
1:G:174:VAL:CG2	1:G:367:GLU:HA	2.40	0.42
1:G:477:GLY:CA	1:G:488:MET:SD	3.07	0.42
1:L:262:LEU:HD22	1:L:273:VAL:HG21	2.01	0.42
1:M:147:VAL:CG2	1:M:496:PRO:CG	2.75	0.42
1:N:262:LEU:HD22	1:N:273:VAL:HG21	2.01	0.42
2:O:68:LEU:CD2	2:U:86:LEU:HD23	2.49	0.42
2:O:83:PHE:HD2	2:O:89:LYS:HD2	1.83	0.42
1:C:259:LEU:O	1:C:263:VAL:HG23	2.19	0.42
1:C:405:ALA:HB1	1:C:498:LYS:HD3	2.01	0.42
1:C:463:SER:CB	1:J:464:VAL:HG21	2.27	0.42
1:D:259:LEU:O	1:D:263:VAL:HG23	2.20	0.42
1:E:259:LEU:O	1:E:263:VAL:HG23	2.20	0.42
1:F:20:VAL:HG13	1:F:74:VAL:HG11	2.00	0.42
1:F:78:ALA:HB2	1:F:93:THR:OG1	2.18	0.42
1:G:146:GLN:HB2	1:G:494:LEU:HD11	1.95	0.42
1:H:78:ALA:HB2	1:H:93:THR:OG1	2.18	0.42
1:H:389:MET:CE	1:H:389:MET:C	2.87	0.42
1:I:197:ARG:HG2	1:I:277:LYS:O	2.19	0.42
1:I:198:GLY:O	1:I:276:VAL:HG12	2.19	0.42
1:I:389:MET:CE	1:I:389:MET:C	2.87	0.42
1:K:118:ARG:HH22	1:L:34:LYS:HE2	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:389:MET:HE1	1:K:393:LYS:HB2	2.02	0.42
1:L:149:THR:H	1:L:159:GLY:HA3	1.84	0.42
1:M:197:ARG:HG2	1:M:277:LYS:O	2.19	0.42
2:Q:86:LEU:HD23	2:R:68:LEU:CD2	2.49	0.42
1:A:193:MET:HG3	1:A:371:LYS:HB3	2.01	0.42
1:A:247:LEU:HB3	1:A:273:VAL:HG12	2.01	0.42
1:A:464:VAL:HG23	1:H:464:VAL:HA	2.01	0.42
1:B:455:VAL:HG11	1:B:462:PRO:HA	2.00	0.42
1:C:222:LEU:HD12	1:C:293:ALA:HB2	2.01	0.42
1:D:86:GLY:HA3	1:D:401:HIS:CB	2.48	0.42
1:D:405:ALA:HB1	1:D:498:LYS:HD3	2.02	0.42
1:E:421:ARG:HD3	1:E:421:ARG:HA	1.78	0.42
1:G:238:GLU:OE2	1:G:238:GLU:HA	2.20	0.42
1:I:103:GLY:HA3	1:I:515:ILE:HG21	2.02	0.42
1:I:176:THR:HG21	1:I:333:ILE:CD1	2.48	0.42
1:J:262:LEU:O	1:J:266:THR:HG23	2.19	0.42
1:L:78:ALA:HB2	1:L:93:THR:OG1	2.19	0.42
1:L:136:VAL:C	1:L:137:PRO:CB	2.79	0.42
2:R:86:LEU:HD23	2:S:68:LEU:CD2	2.49	0.42
1:A:370:ALA:HB1	1:A:375:GLY:O	2.20	0.42
1:B:222:LEU:HD12	1:B:293:ALA:HB2	2.01	0.42
1:B:464:VAL:HG23	1:I:464:VAL:HA	2.01	0.42
1:E:86:GLY:HA3	1:E:401:HIS:CB	2.48	0.42
1:G:20:VAL:HG13	1:G:74:VAL:HG11	2.01	0.42
1:H:149:THR:N	1:H:159:GLY:HA3	2.35	0.42
1:H:197:ARG:HG2	1:H:277:LYS:O	2.19	0.42
1:J:20:VAL:HG13	1:J:74:VAL:HG11	2.00	0.42
1:J:198:GLY:O	1:J:276:VAL:HG12	2.19	0.42
1:K:103:GLY:HA3	1:K:515:ILE:HG21	2.02	0.42
1:M:158:VAL:C	1:M:160:LYS:N	2.71	0.42
1:N:136:VAL:C	1:N:137:PRO:CD	2.87	0.42
1:B:370:ALA:HB1	1:B:375:GLY:O	2.20	0.42
1:C:238:GLU:HA	1:C:238:GLU:OE2	2.20	0.42
1:D:238:GLU:HA	1:D:238:GLU:OE2	2.20	0.42
1:F:146:GLN:HB2	1:F:494:LEU:HD11	1.95	0.42
1:F:259:LEU:O	1:F:263:VAL:HG23	2.20	0.42
1:J:103:GLY:HA3	1:J:515:ILE:HG21	2.02	0.42
1:L:103:GLY:HA3	1:L:515:ILE:HG21	2.02	0.42
1:L:149:THR:N	1:L:159:GLY:HA3	2.35	0.42
1:M:149:THR:N	1:M:159:GLY:HA3	2.35	0.42
1:M:198:GLY:O	1:M:276:VAL:HG12	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:198:GLY:O	1:N:276:VAL:HG12	2.19	0.42
1:N:477:GLY:CA	1:N:488:MET:SD	3.07	0.42
2:P:12:VAL:HG23	2:Q:106:ILE:O	2.19	0.42
1:B:27:VAL:HG12	1:B:90:THR:HG23	2.02	0.42
1:C:174:VAL:CG2	1:C:367:GLU:HA	2.40	0.42
1:F:238:GLU:HA	1:F:238:GLU:OE2	2.20	0.42
1:F:405:ALA:HB1	1:F:498:LYS:HD3	2.01	0.42
1:F:477:GLY:CA	1:F:488:MET:SD	3.07	0.42
1:G:236:VAL:O	1:G:240:VAL:HG23	2.19	0.42
1:G:259:LEU:O	1:G:263:VAL:HG23	2.20	0.42
1:H:103:GLY:HA3	1:H:515:ILE:HG21	2.02	0.42
1:H:118:ARG:HH22	1:I:34:LYS:HE2	1.85	0.42
1:H:262:LEU:HD22	1:H:273:VAL:HG21	2.01	0.42
1:I:262:LEU:HD22	1:I:273:VAL:HG21	2.01	0.42
1:J:477:GLY:CA	1:J:488:MET:SD	3.07	0.42
1:K:262:LEU:O	1:K:266:THR:HG23	2.19	0.42
1:L:149:THR:HG21	1:L:156:GLU:HA	1.99	0.42
1:L:197:ARG:HG2	1:L:277:LYS:O	2.19	0.42
1:M:336:VAL:O	1:M:336:VAL:HG12	2.20	0.42
1:A:174:VAL:CG2	1:A:367:GLU:HA	2.39	0.42
1:B:174:VAL:CG2	1:B:367:GLU:HA	2.40	0.42
1:B:245:LYS:HA	1:B:246:PRO:HD3	1.94	0.42
1:C:146:GLN:HE21	1:C:146:GLN:HB2	1.66	0.42
1:G:302:SER:HB3	1:G:305:ILE:HG12	2.02	0.42
1:G:405:ALA:HB1	1:G:498:LYS:HD3	2.01	0.42
1:I:20:VAL:HG13	1:I:74:VAL:HG11	2.00	0.42
1:I:262:LEU:O	1:I:266:THR:HG23	2.19	0.42
1:J:385:THR:HG23	1:J:388:GLU:CB	2.50	0.42
1:M:103:GLY:HA3	1:M:515:ILE:HG21	2.02	0.42
2:Q:90:GLN:H	2:Q:90:GLN:HG3	1.72	0.42
1:A:27:VAL:HG12	1:A:90:THR:HG23	2.02	0.42
1:A:238:GLU:HA	1:A:238:GLU:OE2	2.20	0.42
1:A:302:SER:HB3	1:A:305:ILE:HG12	2.02	0.42
1:B:405:ALA:HB1	1:B:498:LYS:HD3	2.01	0.42
1:C:103:GLY:HA3	1:C:515:ILE:HG21	2.02	0.42
1:C:477:GLY:CA	1:C:488:MET:SD	3.07	0.42
1:D:27:VAL:HG12	1:D:90:THR:HG23	2.02	0.42
1:F:222:LEU:HD12	1:F:293:ALA:HB2	2.01	0.42
1:F:236:VAL:O	1:F:240:VAL:HG23	2.19	0.42
1:G:247:LEU:HB3	1:G:273:VAL:HG12	2.01	0.42
1:G:461:GLU:OE1	1:N:463:SER:HB3	2.13	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:149:THR:H	1:I:159:GLY:HA3	1.84	0.42
1:J:27:VAL:HG12	1:J:90:THR:HG23	2.02	0.42
1:K:27:VAL:HG12	1:K:90:THR:HG23	2.02	0.42
1:M:118:ARG:HH22	1:N:34:LYS:HE2	1.85	0.42
1:M:262:LEU:HD22	1:M:273:VAL:HG21	2.01	0.42
1:N:389:MET:HE1	1:N:393:LYS:HB2	2.02	0.42
2:O:12:VAL:HG23	2:P:106:ILE:O	2.19	0.42
1:A:20:VAL:HG13	1:A:74:VAL:HG11	2.00	0.42
1:A:236:VAL:O	1:A:240:VAL:HG23	2.19	0.42
1:C:86:GLY:HA3	1:C:401:HIS:CB	2.48	0.42
1:C:463:SER:HG	1:J:464:VAL:HG23	1.75	0.42
1:F:247:LEU:HB3	1:F:273:VAL:HG12	2.01	0.42
1:G:464:VAL:HG23	1:N:464:VAL:HA	2.01	0.42
1:H:336:VAL:O	1:H:336:VAL:HG12	2.20	0.42
1:J:137:PRO:O	1:J:410:GLY:CA	2.68	0.42
1:K:477:GLY:CA	1:K:488:MET:SD	3.07	0.42
1:L:198:GLY:O	1:L:276:VAL:HG12	2.19	0.42
1:N:336:VAL:HG12	1:N:336:VAL:O	2.20	0.42
2:T:12:VAL:HG23	2:U:106:ILE:O	2.19	0.42
1:A:405:ALA:HA	1:A:498:LYS:HD3	2.02	0.41
1:B:103:GLY:HA3	1:B:515:ILE:HG21	2.02	0.41
1:C:302:SER:HB3	1:C:305:ILE:HG12	2.02	0.41
1:C:370:ALA:HB1	1:C:375:GLY:O	2.20	0.41
1:C:464:VAL:HG23	1:J:464:VAL:HA	2.01	0.41
1:D:463:SER:CB	1:K:464:VAL:HG21	2.27	0.41
1:E:146:GLN:HE21	1:E:146:GLN:HB2	1.66	0.41
1:E:370:ALA:HB1	1:E:375:GLY:O	2.20	0.41
1:E:464:VAL:HG23	1:L:464:VAL:HA	2.01	0.41
1:F:103:GLY:HA3	1:F:515:ILE:HG21	2.02	0.41
1:G:370:ALA:HB1	1:G:375:GLY:O	2.20	0.41
1:M:389:MET:HE1	1:M:389:MET:C	2.41	0.41
1:N:389:MET:HE1	1:N:389:MET:O	2.20	0.41
1:A:222:LEU:HD12	1:A:293:ALA:HB2	2.01	0.41
1:A:405:ALA:HB1	1:A:498:LYS:HD3	2.01	0.41
1:B:405:ALA:HA	1:B:498:LYS:HD3	2.02	0.41
1:C:27:VAL:HG12	1:C:90:THR:HG23	2.02	0.41
1:G:405:ALA:HA	1:G:498:LYS:HD3	2.02	0.41
1:H:198:GLY:O	1:H:276:VAL:HG12	2.19	0.41
1:I:27:VAL:HG12	1:I:90:THR:HG23	2.02	0.41
1:I:385:THR:HG23	1:I:388:GLU:CB	2.49	0.41
1:J:149:THR:N	1:J:159:GLY:HA3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:336:VAL:O	1:L:336:VAL:HG12	2.20	0.41
1:M:266:THR:HG22	1:M:273:VAL:H	1.85	0.41
1:M:385:THR:HG23	1:M:388:GLU:N	2.35	0.41
1:N:103:GLY:HA3	1:N:515:ILE:HG21	2.02	0.41
1:N:137:PRO:O	1:N:410:GLY:CA	2.68	0.41
1:N:149:THR:N	1:N:159:GLY:HA3	2.35	0.41
1:B:477:GLY:CA	1:B:488:MET:SD	3.07	0.41
1:C:225:LYS:H	1:C:225:LYS:HG3	1.66	0.41
1:D:236:VAL:O	1:D:240:VAL:HG23	2.19	0.41
1:D:421:ARG:HA	1:D:421:ARG:HD3	1.78	0.41
1:D:464:VAL:HG23	1:K:464:VAL:HA	2.01	0.41
1:D:477:GLY:CA	1:D:488:MET:SD	3.07	0.41
1:E:20:VAL:HG13	1:E:74:VAL:HG11	2.01	0.41
1:E:27:VAL:HG12	1:E:90:THR:HG23	2.02	0.41
1:E:146:GLN:HB2	1:E:494:LEU:HD11	1.95	0.41
1:E:225:LYS:H	1:E:225:LYS:HG3	1.66	0.41
1:E:477:GLY:CA	1:E:488:MET:SD	3.07	0.41
1:G:421:ARG:HD3	1:G:421:ARG:HA	1.78	0.41
1:H:262:LEU:O	1:H:266:THR:HG23	2.19	0.41
1:K:389:MET:HE1	1:K:389:MET:O	2.20	0.41
1:L:27:VAL:HG12	1:L:90:THR:HG23	2.02	0.41
1:L:262:LEU:O	1:L:266:THR:HG23	2.19	0.41
1:N:266:THR:HG22	1:N:273:VAL:H	1.85	0.41
2:R:81:HIS:CG	2:R:94:ILE:HG21	2.56	0.41
1:B:302:SER:HB3	1:B:305:ILE:HG12	2.02	0.41
1:B:463:SER:CB	1:I:464:VAL:HG21	2.27	0.41
1:C:405:ALA:HA	1:C:498:LYS:HD3	2.02	0.41
1:D:38:VAL:HG22	1:E:519:CYS:HB3	2.03	0.41
1:D:103:GLY:HA3	1:D:515:ILE:HG21	2.02	0.41
1:F:302:SER:HB3	1:F:305:ILE:HG12	2.02	0.41
1:H:385:THR:HG23	1:H:388:GLU:CB	2.49	0.41
1:H:401:HIS:O	1:H:402:ALA:C	2.59	0.41
1:I:147:VAL:CG2	1:I:496:PRO:CG	2.75	0.41
1:I:149:THR:N	1:I:159:GLY:HA3	2.35	0.41
1:I:158:VAL:C	1:I:160:LYS:N	2.71	0.41
1:I:336:VAL:O	1:I:336:VAL:HG12	2.20	0.41
1:I:477:GLY:CA	1:I:488:MET:SD	3.07	0.41
1:J:118:ARG:HH22	1:K:34:LYS:HE2	1.85	0.41
1:K:336:VAL:HG12	1:K:336:VAL:O	2.20	0.41
1:L:266:THR:HG22	1:L:273:VAL:H	1.85	0.41
1:N:262:LEU:O	1:N:266:THR:HG23	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:90:GLN:H	2:P:90:GLN:HG3	1.73	0.41
1:A:21:ASN:HD22	1:A:21:ASN:HA	1.67	0.41
1:B:38:VAL:HG22	1:C:519:CYS:HB3	2.03	0.41
1:B:512:GLY:O	1:B:515:ILE:HG13	2.21	0.41
1:C:38:VAL:HG22	1:D:519:CYS:HB3	2.03	0.41
1:D:302:SER:HB3	1:D:305:ILE:HG12	2.02	0.41
1:F:405:ALA:HA	1:F:498:LYS:HD3	2.02	0.41
1:F:464:VAL:HG23	1:M:464:VAL:HA	2.01	0.41
1:G:103:GLY:HA3	1:G:515:ILE:HG21	2.02	0.41
1:H:34:LYS:HE2	1:N:118:ARG:HH22	1.85	0.41
1:I:150:ILE:HG21	1:I:494:LEU:O	2.21	0.41
1:L:118:ARG:HH22	1:M:34:LYS:HE2	1.85	0.41
1:M:262:LEU:O	1:M:266:THR:HG23	2.19	0.41
1:N:401:HIS:O	1:N:402:ALA:C	2.59	0.41
1:A:103:GLY:HA3	1:A:515:ILE:HG21	2.02	0.41
1:B:236:VAL:O	1:B:240:VAL:HG23	2.20	0.41
1:B:259:LEU:O	1:B:263:VAL:HG23	2.20	0.41
1:C:236:VAL:O	1:C:240:VAL:HG23	2.19	0.41
1:D:405:ALA:HA	1:D:498:LYS:HD3	2.02	0.41
1:E:405:ALA:HB1	1:E:498:LYS:HD3	2.02	0.41
1:E:461:GLU:HA	1:E:462:PRO:HD3	1.93	0.41
1:E:512:GLY:O	1:E:515:ILE:HG13	2.21	0.41
1:H:166:MET:HE2	1:H:171:LYS:CA	2.40	0.41
1:J:136:VAL:C	1:J:137:PRO:CD	2.87	0.41
1:J:336:VAL:O	1:J:336:VAL:HG12	2.20	0.41
1:K:149:THR:N	1:K:159:GLY:HA3	2.35	0.41
1:A:146:GLN:HB2	1:A:494:LEU:HD11	1.95	0.41
1:B:238:GLU:OE2	1:B:238:GLU:HA	2.20	0.41
1:E:238:GLU:HA	1:E:238:GLU:OE2	2.20	0.41
1:F:197:ARG:CD	1:F:277:LYS:HB2	2.23	0.41
1:G:27:VAL:HG12	1:G:90:THR:HG23	2.02	0.41
1:G:222:LEU:HD12	1:G:293:ALA:HB2	2.01	0.41
1:H:27:VAL:HG12	1:H:90:THR:HG23	2.02	0.41
1:H:266:THR:HG22	1:H:273:VAL:H	1.85	0.41
1:I:118:ARG:HH22	1:J:34:LYS:HE2	1.85	0.41
1:I:137:PRO:O	1:I:410:GLY:CA	2.68	0.41
1:I:247:LEU:HB3	1:I:273:VAL:HG12	2.02	0.41
1:J:247:LEU:HB3	1:J:273:VAL:HG12	2.03	0.41
1:K:514:MET:HE3	1:K:514:MET:HB2	1.95	0.41
1:L:385:THR:HG23	1:L:388:GLU:CB	2.50	0.41
1:L:401:HIS:O	1:L:402:ALA:C	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:477:GLY:CA	1:L:488:MET:SD	3.07	0.41
1:B:173:GLY:HA2	1:B:370:ALA:CB	2.45	0.41
1:C:173:GLY:HA2	1:C:370:ALA:CB	2.45	0.41
1:E:38:VAL:HG22	1:F:519:CYS:HB3	2.03	0.41
1:E:302:SER:HB3	1:E:305:ILE:HG12	2.02	0.41
1:F:370:ALA:HB1	1:F:375:GLY:O	2.20	0.41
1:G:224:ASP:CB	1:G:302:SER:HA	2.51	0.41
1:J:513:LEU:HD23	1:J:513:LEU:HA	1.72	0.41
1:K:137:PRO:O	1:K:410:GLY:CA	2.68	0.41
1:M:149:THR:HG21	1:M:156:GLU:HA	1.99	0.41
1:M:512:GLY:O	1:M:515:ILE:HG13	2.20	0.41
2:O:81:HIS:CG	2:O:94:ILE:HG21	2.56	0.41
2:P:81:HIS:CG	2:P:94:ILE:HG21	2.56	0.41
2:S:81:HIS:CG	2:S:94:ILE:HG21	2.56	0.41
2:T:81:HIS:CG	2:T:94:ILE:HG21	2.56	0.41
2:U:81:HIS:CG	2:U:94:ILE:HG21	2.56	0.41
1:A:38:VAL:HG22	1:B:519:CYS:HB3	2.03	0.41
1:A:259:LEU:O	1:A:263:VAL:HG23	2.20	0.41
1:A:351:GLN:O	1:A:354:GLU:HB2	2.21	0.41
1:C:224:ASP:CB	1:C:302:SER:HA	2.51	0.41
1:C:512:GLY:O	1:C:515:ILE:HG13	2.21	0.41
1:D:174:VAL:CG2	1:D:367:GLU:HA	2.40	0.41
1:D:370:ALA:HB1	1:D:375:GLY:O	2.20	0.41
1:E:103:GLY:HA3	1:E:515:ILE:HG21	2.02	0.41
1:E:405:ALA:HA	1:E:498:LYS:HD3	2.02	0.41
1:F:27:VAL:HG12	1:F:90:THR:HG23	2.02	0.41
1:I:389:MET:HE1	1:I:393:LYS:HB2	2.03	0.41
1:I:401:HIS:O	1:I:402:ALA:C	2.59	0.41
1:J:150:ILE:HG21	1:J:494:LEU:O	2.21	0.41
1:J:285:ARG:HA	1:J:288:MET:HB2	2.03	0.41
1:J:385:THR:HG23	1:J:388:GLU:N	2.35	0.41
1:J:401:HIS:O	1:J:402:ALA:C	2.59	0.41
1:J:512:GLY:O	1:J:515:ILE:HG13	2.21	0.41
1:K:176:THR:HG21	1:K:333:ILE:CD1	2.48	0.41
1:K:285:ARG:HA	1:K:288:MET:HB2	2.03	0.41
1:K:512:GLY:O	1:K:515:ILE:HG13	2.21	0.41
1:L:137:PRO:O	1:L:410:GLY:CA	2.68	0.41
1:L:142:LYS:O	1:L:146:GLN:HB2	2.21	0.41
1:L:512:GLY:O	1:L:515:ILE:HG13	2.21	0.41
1:M:27:VAL:HG12	1:M:90:THR:HG23	2.02	0.41
1:M:137:PRO:O	1:M:410:GLY:CA	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:187:LEU:HD23	1:M:188:ASP:N	2.36	0.41
1:M:247:LEU:HB3	1:M:273:VAL:HG12	2.02	0.41
1:M:385:THR:HG23	1:M:388:GLU:CB	2.49	0.41
1:M:401:HIS:O	1:M:402:ALA:C	2.59	0.41
1:M:502:SER:O	1:M:503:ALA:C	2.60	0.41
1:N:285:ARG:HA	1:N:288:MET:HB2	2.03	0.41
1:N:385:THR:HG23	1:N:388:GLU:CB	2.49	0.41
1:N:385:THR:HG23	1:N:388:GLU:N	2.35	0.41
1:N:512:GLY:O	1:N:515:ILE:HG13	2.20	0.41
2:Q:81:HIS:CG	2:Q:94:ILE:HG21	2.56	0.41
1:A:512:GLY:O	1:A:515:ILE:HG13	2.21	0.41
1:B:421:ARG:HD3	1:B:421:ARG:HA	1.78	0.41
1:E:463:SER:CB	1:L:464:VAL:HG21	2.27	0.41
1:F:512:GLY:O	1:F:515:ILE:HG13	2.21	0.41
1:H:137:PRO:O	1:H:410:GLY:CA	2.68	0.41
1:H:158:VAL:C	1:H:160:LYS:N	2.71	0.41
1:H:172:GLU:OE1	1:H:172:GLU:N	2.54	0.41
1:J:142:LYS:O	1:J:146:GLN:HB2	2.21	0.41
1:K:3:ALA:CB	1:L:63:GLU:CB	2.94	0.41
1:K:187:LEU:HD23	1:K:188:ASP:N	2.36	0.41
1:L:389:MET:HE1	1:L:389:MET:O	2.21	0.41
1:N:187:LEU:HD23	1:N:188:ASP:N	2.36	0.41
1:D:351:GLN:O	1:D:354:GLU:HB2	2.21	0.40
1:E:351:GLN:O	1:E:354:GLU:HB2	2.21	0.40
1:I:3:ALA:CB	1:J:63:GLU:CB	2.94	0.40
1:I:385:THR:HG23	1:I:388:GLU:N	2.35	0.40
1:K:172:GLU:OE1	1:K:172:GLU:N	2.54	0.40
1:K:247:LEU:HB3	1:K:273:VAL:HG12	2.02	0.40
1:L:187:LEU:HD23	1:L:188:ASP:N	2.36	0.40
1:M:142:LYS:O	1:M:146:GLN:HB2	2.21	0.40
1:N:27:VAL:HG12	1:N:90:THR:HG23	2.02	0.40
1:A:165:ALA:O	1:A:169:VAL:HG22	2.21	0.40
1:B:146:GLN:HB2	1:B:494:LEU:HD11	1.95	0.40
1:C:351:GLN:O	1:C:354:GLU:HB2	2.21	0.40
1:K:385:THR:HG23	1:K:388:GLU:N	2.35	0.40
1:K:401:HIS:O	1:K:402:ALA:C	2.59	0.40
1:C:165:ALA:O	1:C:169:VAL:HG22	2.21	0.40
1:D:146:GLN:HB2	1:D:494:LEU:HD11	1.95	0.40
1:E:165:ALA:O	1:E:169:VAL:HG22	2.21	0.40
1:G:165:ALA:O	1:G:169:VAL:HG22	2.21	0.40
1:G:351:GLN:O	1:G:354:GLU:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:512:GLY:O	1:G:515:ILE:HG13	2.21	0.40
1:H:193:MET:HG2	1:H:194:GLN:N	2.36	0.40
1:H:285:ARG:HA	1:H:288:MET:HB2	2.03	0.40
1:H:385:THR:HG23	1:H:388:GLU:N	2.35	0.40
1:I:142:LYS:O	1:I:146:GLN:HB2	2.21	0.40
1:I:266:THR:HG22	1:I:273:VAL:H	1.85	0.40
1:K:266:THR:HG22	1:K:273:VAL:H	1.85	0.40
1:M:158:VAL:O	1:M:159:GLY:C	2.60	0.40
1:M:477:GLY:CA	1:M:488:MET:SD	3.07	0.40
1:N:158:VAL:O	1:N:159:GLY:C	2.60	0.40
1:N:176:THR:HG21	1:N:333:ILE:CD1	2.48	0.40
1:N:247:LEU:HB3	1:N:273:VAL:HG12	2.02	0.40
2:R:21:GLU:HA	2:R:22:PRO:HD3	1.88	0.40
2:R:90:GLN:H	2:R:90:GLN:HG3	1.73	0.40
1:F:38:VAL:HG22	1:G:519:CYS:HB3	2.03	0.40
1:G:246:PRO:HB3	1:G:272:LYS:HB3	2.04	0.40
1:H:150:ILE:HG21	1:H:494:LEU:O	2.21	0.40
1:H:247:LEU:HB3	1:H:273:VAL:HG12	2.03	0.40
1:I:172:GLU:OE1	1:I:172:GLU:N	2.54	0.40
1:I:193:MET:HG2	1:I:194:GLN:N	2.36	0.40
1:I:512:GLY:O	1:I:515:ILE:HG13	2.21	0.40
1:J:178:GLU:HG2	1:J:322:ARG:CZ	2.52	0.40
1:L:247:LEU:HB3	1:L:273:VAL:HG12	2.03	0.40
1:M:165:ALA:O	1:M:168:LYS:N	2.38	0.40
1:N:142:LYS:O	1:N:146:GLN:HB2	2.21	0.40
1:N:193:MET:HG2	1:N:194:GLN:N	2.36	0.40
1:A:147:VAL:HG11	1:A:411:VAL:HG12	2.04	0.40
1:A:477:GLY:CA	1:A:488:MET:SD	3.07	0.40
1:A:519:CYS:HB3	1:G:38:VAL:HG22	2.03	0.40
1:B:165:ALA:O	1:B:169:VAL:HG22	2.21	0.40
1:C:146:GLN:HB2	1:C:494:LEU:HD11	1.95	0.40
1:E:224:ASP:CB	1:E:302:SER:HA	2.51	0.40
1:F:21:ASN:HD22	1:F:21:ASN:HA	1.67	0.40
1:F:147:VAL:HG11	1:F:411:VAL:HG12	2.04	0.40
1:F:246:PRO:HB3	1:F:272:LYS:HB3	2.04	0.40
1:G:147:VAL:HG11	1:G:411:VAL:HG12	2.04	0.40
1:I:502:SER:O	1:I:503:ALA:C	2.60	0.40
1:K:158:VAL:O	1:K:159:GLY:C	2.60	0.40
1:K:385:THR:HG23	1:K:388:GLU:CB	2.49	0.40
1:M:172:GLU:OE1	1:M:172:GLU:N	2.54	0.40
1:M:285:ARG:HA	1:M:288:MET:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:149:THR:HG21	1:N:156:GLU:HA	1.99	0.40
1:N:166:MET:HE2	1:N:171:LYS:CA	2.40	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	520/547 (95%)	483 (93%)	31 (6%)	6 (1%)	13	50
1	B	520/547 (95%)	483 (93%)	31 (6%)	6 (1%)	13	50
1	C	520/547 (95%)	483 (93%)	31 (6%)	6 (1%)	13	50
1	D	520/547 (95%)	483 (93%)	31 (6%)	6 (1%)	13	50
1	E	520/547 (95%)	483 (93%)	31 (6%)	6 (1%)	13	50
1	F	520/547 (95%)	483 (93%)	31 (6%)	6 (1%)	13	50
1	G	520/547 (95%)	483 (93%)	31 (6%)	6 (1%)	13	50
1	H	505/547 (92%)	447 (88%)	45 (9%)	13 (3%)	5	31
1	I	505/547 (92%)	447 (88%)	45 (9%)	13 (3%)	5	31
1	J	505/547 (92%)	447 (88%)	45 (9%)	13 (3%)	5	31
1	K	505/547 (92%)	447 (88%)	45 (9%)	13 (3%)	5	31
1	L	505/547 (92%)	447 (88%)	45 (9%)	13 (3%)	5	31
1	M	505/547 (92%)	447 (88%)	45 (9%)	13 (3%)	5	31
1	N	505/547 (92%)	447 (88%)	45 (9%)	13 (3%)	5	31
2	O	79/111 (71%)	76 (96%)	3 (4%)	0	100	100
2	P	79/111 (71%)	76 (96%)	3 (4%)	0	100	100
2	Q	79/111 (71%)	76 (96%)	3 (4%)	0	100	100
2	R	79/111 (71%)	76 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	S	79/111 (71%)	76 (96%)	3 (4%)	0	100	100
2	T	79/111 (71%)	76 (96%)	3 (4%)	0	100	100
2	U	79/111 (71%)	76 (96%)	3 (4%)	0	100	100
All	All	7728/8435 (92%)	7042 (91%)	553 (7%)	133 (2%)	13	42

All (133) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	44	PHE
1	A	137	PRO
1	A	337	GLY
1	B	44	PHE
1	B	137	PRO
1	B	337	GLY
1	C	44	PHE
1	C	137	PRO
1	C	337	GLY
1	D	44	PHE
1	D	137	PRO
1	D	337	GLY
1	E	44	PHE
1	E	137	PRO
1	E	337	GLY
1	F	44	PHE
1	F	137	PRO
1	F	337	GLY
1	G	44	PHE
1	G	137	PRO
1	G	337	GLY
1	H	44	PHE
1	H	146	GLN
1	H	401	HIS
1	I	44	PHE
1	I	146	GLN
1	I	401	HIS
1	J	44	PHE
1	J	146	GLN
1	J	401	HIS
1	K	44	PHE
1	K	146	GLN
1	K	401	HIS

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Mol	Chain	Res	Type
1	L	44	PHE
1	L	146	GLN
1	L	401	HIS
1	M	44	PHE
1	M	146	GLN
1	M	401	HIS
1	N	44	PHE
1	N	146	GLN
1	N	401	HIS
1	A	374	GLY
1	B	374	GLY
1	C	374	GLY
1	D	374	GLY
1	E	374	GLY
1	F	374	GLY
1	G	374	GLY
1	H	270	ILE
1	H	389	MET
1	I	270	ILE
1	I	389	MET
1	J	270	ILE
1	J	389	MET
1	K	270	ILE
1	K	389	MET
1	L	270	ILE
1	L	389	MET
1	M	270	ILE
1	M	389	MET
1	N	270	ILE
1	N	389	MET
1	A	205	ILE
1	B	205	ILE
1	C	205	ILE
1	D	205	ILE
1	E	205	ILE
1	F	205	ILE
1	G	205	ILE
1	H	155	ASP
1	I	155	ASP
1	J	155	ASP
1	K	155	ASP
1	L	155	ASP

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Mol	Chain	Res	Type
1	M	155	ASP
1	N	155	ASP
1	L	398	ASP
1	H	153	ASN
1	H	398	ASP
1	I	153	ASN
1	I	398	ASP
1	J	153	ASN
1	J	398	ASP
1	K	153	ASN
1	K	160	LYS
1	K	398	ASP
1	L	153	ASN
1	L	160	LYS
1	M	153	ASN
1	M	398	ASP
1	N	153	ASN
1	N	398	ASP
1	H	160	LYS
1	H	165	ALA
1	I	160	LYS
1	I	165	ALA
1	J	160	LYS
1	J	165	ALA
1	K	165	ALA
1	L	165	ALA
1	M	160	LYS
1	M	165	ALA
1	N	160	LYS
1	N	165	ALA
1	A	305	ILE
1	B	305	ILE
1	C	305	ILE
1	D	305	ILE
1	E	305	ILE
1	F	305	ILE
1	G	305	ILE
1	H	256	GLY
1	H	374	GLY
1	I	256	GLY
1	I	374	GLY
1	I	387	VAL

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Mol	Chain	Res	Type
1	J	256	GLY
1	J	374	GLY
1	K	256	GLY
1	K	374	GLY
1	L	256	GLY
1	L	374	GLY
1	M	256	GLY
1	M	374	GLY
1	N	256	GLY
1	N	374	GLY
1	H	387	VAL
1	J	387	VAL
1	K	387	VAL
1	L	387	VAL
1	M	387	VAL
1	N	387	VAL

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	404/414 (98%)	352 (87%)	52 (13%)	4 18
1	B	404/414 (98%)	352 (87%)	52 (13%)	4 18
1	C	404/414 (98%)	352 (87%)	52 (13%)	4 18
1	D	404/414 (98%)	352 (87%)	52 (13%)	4 18
1	E	404/414 (98%)	352 (87%)	52 (13%)	4 18
1	F	404/414 (98%)	352 (87%)	52 (13%)	4 18
1	G	404/414 (98%)	352 (87%)	52 (13%)	4 18
1	H	396/414 (96%)	347 (88%)	49 (12%)	4 19
1	I	396/414 (96%)	347 (88%)	49 (12%)	4 19
1	J	396/414 (96%)	347 (88%)	49 (12%)	4 19
1	K	396/414 (96%)	347 (88%)	49 (12%)	4 19

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L	396/414 (96%)	347 (88%)	49 (12%)	4	19
1	M	396/414 (96%)	347 (88%)	49 (12%)	4	19
1	N	396/414 (96%)	347 (88%)	49 (12%)	4	19
2	O	73/96 (76%)	71 (97%)	2 (3%)	44	65
2	P	73/96 (76%)	71 (97%)	2 (3%)	44	65
2	Q	73/96 (76%)	71 (97%)	2 (3%)	44	65
2	R	73/96 (76%)	71 (97%)	2 (3%)	44	65
2	S	73/96 (76%)	71 (97%)	2 (3%)	44	65
2	T	73/96 (76%)	71 (97%)	2 (3%)	44	65
2	U	73/96 (76%)	71 (97%)	2 (3%)	44	65
All	All	6111/6468 (94%)	5390 (88%)	721 (12%)	8	20

All (721) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	VAL
1	A	18	ARG
1	A	23	LEU
1	A	28	LYS
1	A	43	SER
1	A	44	PHE
1	A	48	THR
1	A	62	LEU
1	A	74	VAL
1	A	97	GLN
1	A	111	MET
1	A	129	GLU
1	A	132	LYS
1	A	138	CYS
1	A	147	VAL
1	A	153	ASN
1	A	168	LYS
1	A	176	THR
1	A	177	VAL
1	A	178	GLU
1	A	183	LEU
1	A	184	GLN
1	A	197	ARG

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Mol	Chain	Res	Type
1	A	225	LYS
1	A	229	ASN
1	A	237	LEU
1	A	268	ARG
1	A	281	PHE
1	A	284	ARG
1	A	288	MET
1	A	322	ARG
1	A	345	ARG
1	A	350	ARG
1	A	351	GLN
1	A	366	GLN
1	A	391	GLU
1	A	398	ASP
1	A	400	LEU
1	A	417	VAL
1	A	419	LEU
1	A	420	ILE
1	A	421	ARG
1	A	422	VAL
1	A	430	ARG
1	A	445	ARG
1	A	451	LEU
1	A	452	ARG
1	A	461	GLU
1	A	494	LEU
1	A	504	LEU
1	A	510	VAL
1	A	514	MET
1	B	6	VAL
1	B	18	ARG
1	B	23	LEU
1	B	28	LYS
1	B	43	SER
1	B	44	PHE
1	B	48	THR
1	B	62	LEU
1	B	74	VAL
1	B	97	GLN
1	B	111	MET
1	B	129	GLU
1	B	132	LYS

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Mol	Chain	Res	Type
1	B	138	CYS
1	B	147	VAL
1	B	153	ASN
1	B	168	LYS
1	B	176	THR
1	B	177	VAL
1	B	178	GLU
1	B	183	LEU
1	B	184	GLN
1	B	197	ARG
1	B	225	LYS
1	B	229	ASN
1	B	237	LEU
1	B	268	ARG
1	B	281	PHE
1	B	284	ARG
1	B	288	MET
1	B	322	ARG
1	B	345	ARG
1	B	350	ARG
1	B	351	GLN
1	B	366	GLN
1	B	391	GLU
1	B	398	ASP
1	B	400	LEU
1	B	417	VAL
1	B	419	LEU
1	B	420	ILE
1	B	421	ARG
1	B	422	VAL
1	B	430	ARG
1	B	445	ARG
1	B	451	LEU
1	B	452	ARG
1	B	461	GLU
1	B	494	LEU
1	B	504	LEU
1	B	510	VAL
1	B	514	MET
1	C	6	VAL
1	C	18	ARG
1	C	23	LEU

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Mol	Chain	Res	Type
1	C	28	LYS
1	C	43	SER
1	C	44	PHE
1	C	48	THR
1	C	62	LEU
1	C	74	VAL
1	C	97	GLN
1	C	111	MET
1	C	129	GLU
1	C	132	LYS
1	C	138	CYS
1	C	147	VAL
1	C	153	ASN
1	C	168	LYS
1	C	176	THR
1	C	177	VAL
1	C	178	GLU
1	C	183	LEU
1	C	184	GLN
1	C	197	ARG
1	C	225	LYS
1	C	229	ASN
1	C	237	LEU
1	C	268	ARG
1	C	281	PHE
1	C	284	ARG
1	C	288	MET
1	C	322	ARG
1	C	345	ARG
1	C	350	ARG
1	C	351	GLN
1	C	366	GLN
1	C	391	GLU
1	C	398	ASP
1	C	400	LEU
1	C	417	VAL
1	C	419	LEU
1	C	420	ILE
1	C	421	ARG
1	C	422	VAL
1	C	430	ARG
1	C	445	ARG

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Mol	Chain	Res	Type
1	C	451	LEU
1	C	452	ARG
1	C	461	GLU
1	C	494	LEU
1	C	504	LEU
1	C	510	VAL
1	C	514	MET
1	D	6	VAL
1	D	18	ARG
1	D	23	LEU
1	D	28	LYS
1	D	43	SER
1	D	44	PHE
1	D	48	THR
1	D	62	LEU
1	D	74	VAL
1	D	97	GLN
1	D	111	MET
1	D	129	GLU
1	D	132	LYS
1	D	138	CYS
1	D	147	VAL
1	D	153	ASN
1	D	168	LYS
1	D	176	THR
1	D	177	VAL
1	D	178	GLU
1	D	183	LEU
1	D	184	GLN
1	D	197	ARG
1	D	225	LYS
1	D	229	ASN
1	D	237	LEU
1	D	268	ARG
1	D	281	PHE
1	D	284	ARG
1	D	288	MET
1	D	322	ARG
1	D	345	ARG
1	D	350	ARG
1	D	351	GLN
1	D	366	GLN

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Mol	Chain	Res	Type
1	D	391	GLU
1	D	398	ASP
1	D	400	LEU
1	D	417	VAL
1	D	419	LEU
1	D	420	ILE
1	D	421	ARG
1	D	422	VAL
1	D	430	ARG
1	D	445	ARG
1	D	451	LEU
1	D	452	ARG
1	D	461	GLU
1	D	494	LEU
1	D	504	LEU
1	D	510	VAL
1	D	514	MET
1	E	6	VAL
1	E	18	ARG
1	E	23	LEU
1	E	28	LYS
1	E	43	SER
1	E	44	PHE
1	E	48	THR
1	E	62	LEU
1	E	74	VAL
1	E	97	GLN
1	E	111	MET
1	E	129	GLU
1	E	132	LYS
1	E	138	CYS
1	E	147	VAL
1	E	153	ASN
1	E	168	LYS
1	E	176	THR
1	E	177	VAL
1	E	178	GLU
1	E	183	LEU
1	E	184	GLN
1	E	197	ARG
1	E	225	LYS
1	E	229	ASN

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Mol	Chain	Res	Type
1	E	237	LEU
1	E	268	ARG
1	E	281	PHE
1	E	284	ARG
1	E	288	MET
1	E	322	ARG
1	E	345	ARG
1	E	350	ARG
1	E	351	GLN
1	E	366	GLN
1	E	391	GLU
1	E	398	ASP
1	E	400	LEU
1	E	417	VAL
1	E	419	LEU
1	E	420	ILE
1	E	421	ARG
1	E	422	VAL
1	E	430	ARG
1	E	445	ARG
1	E	451	LEU
1	E	452	ARG
1	E	461	GLU
1	E	494	LEU
1	E	504	LEU
1	E	510	VAL
1	E	514	MET
1	F	6	VAL
1	F	18	ARG
1	F	23	LEU
1	F	28	LYS
1	F	43	SER
1	F	44	PHE
1	F	48	THR
1	F	62	LEU
1	F	74	VAL
1	F	97	GLN
1	F	111	MET
1	F	129	GLU
1	F	132	LYS
1	F	138	CYS
1	F	147	VAL

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Mol	Chain	Res	Type
1	F	153	ASN
1	F	168	LYS
1	F	176	THR
1	F	177	VAL
1	F	178	GLU
1	F	183	LEU
1	F	184	GLN
1	F	197	ARG
1	F	225	LYS
1	F	229	ASN
1	F	237	LEU
1	F	268	ARG
1	F	281	PHE
1	F	284	ARG
1	F	288	MET
1	F	322	ARG
1	F	345	ARG
1	F	350	ARG
1	F	351	GLN
1	F	366	GLN
1	F	391	GLU
1	F	398	ASP
1	F	400	LEU
1	F	417	VAL
1	F	419	LEU
1	F	420	ILE
1	F	421	ARG
1	F	422	VAL
1	F	430	ARG
1	F	445	ARG
1	F	451	LEU
1	F	452	ARG
1	F	461	GLU
1	F	494	LEU
1	F	504	LEU
1	F	510	VAL
1	F	514	MET
1	G	6	VAL
1	G	18	ARG
1	G	23	LEU
1	G	28	LYS
1	G	43	SER

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Mol	Chain	Res	Type
1	G	44	PHE
1	G	48	THR
1	G	62	LEU
1	G	74	VAL
1	G	97	GLN
1	G	111	MET
1	G	129	GLU
1	G	132	LYS
1	G	138	CYS
1	G	147	VAL
1	G	153	ASN
1	G	168	LYS
1	G	176	THR
1	G	177	VAL
1	G	178	GLU
1	G	183	LEU
1	G	184	GLN
1	G	197	ARG
1	G	225	LYS
1	G	229	ASN
1	G	237	LEU
1	G	268	ARG
1	G	281	PHE
1	G	284	ARG
1	G	288	MET
1	G	322	ARG
1	G	345	ARG
1	G	350	ARG
1	G	351	GLN
1	G	366	GLN
1	G	391	GLU
1	G	398	ASP
1	G	400	LEU
1	G	417	VAL
1	G	419	LEU
1	G	420	ILE
1	G	421	ARG
1	G	422	VAL
1	G	430	ARG
1	G	445	ARG
1	G	451	LEU
1	G	452	ARG

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Mol	Chain	Res	Type
1	G	461	GLU
1	G	494	LEU
1	G	504	LEU
1	G	510	VAL
1	G	514	MET
1	H	6	VAL
1	H	18	ARG
1	H	23	LEU
1	H	28	LYS
1	H	43	SER
1	H	44	PHE
1	H	48	THR
1	H	62	LEU
1	H	74	VAL
1	H	97	GLN
1	H	111	MET
1	H	129	GLU
1	H	132	LYS
1	H	153	ASN
1	H	172	GLU
1	H	197	ARG
1	H	210	THR
1	H	221	LEU
1	H	230	ILE
1	H	232	GLU
1	H	233	MET
1	H	247	LEU
1	H	248	LEU
1	H	255	GLU
1	H	267	MET
1	H	268	ARG
1	H	272	LYS
1	H	284	ARG
1	H	288	MET
1	H	328	ASP
1	H	329	THR
1	H	331	THR
1	H	343	GLN
1	H	364	LYS
1	H	389	MET
1	H	417	VAL
1	H	419	LEU

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Mol	Chain	Res	Type
1	H	420	ILE
1	H	421	ARG
1	H	422	VAL
1	H	430	ARG
1	H	445	ARG
1	H	451	LEU
1	H	452	ARG
1	H	461	GLU
1	H	494	LEU
1	H	504	LEU
1	H	510	VAL
1	H	514	MET
1	I	6	VAL
1	I	18	ARG
1	I	23	LEU
1	I	28	LYS
1	I	43	SER
1	I	44	PHE
1	I	48	THR
1	I	62	LEU
1	I	74	VAL
1	I	97	GLN
1	I	111	MET
1	I	129	GLU
1	I	132	LYS
1	I	153	ASN
1	I	172	GLU
1	I	197	ARG
1	I	210	THR
1	I	221	LEU
1	I	230	ILE
1	I	232	GLU
1	I	233	MET
1	I	247	LEU
1	I	248	LEU
1	I	255	GLU
1	I	267	MET
1	I	268	ARG
1	I	272	LYS
1	I	284	ARG
1	I	288	MET
1	I	328	ASP

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Mol	Chain	Res	Type
1	I	329	THR
1	I	331	THR
1	I	343	GLN
1	I	364	LYS
1	I	389	MET
1	I	417	VAL
1	I	419	LEU
1	I	420	ILE
1	I	421	ARG
1	I	422	VAL
1	I	430	ARG
1	I	445	ARG
1	I	451	LEU
1	I	452	ARG
1	I	461	GLU
1	I	494	LEU
1	I	504	LEU
1	I	510	VAL
1	I	514	MET
1	J	6	VAL
1	J	18	ARG
1	J	23	LEU
1	J	28	LYS
1	J	43	SER
1	J	44	PHE
1	J	48	THR
1	J	62	LEU
1	J	74	VAL
1	J	97	GLN
1	J	111	MET
1	J	129	GLU
1	J	132	LYS
1	J	153	ASN
1	J	172	GLU
1	J	197	ARG
1	J	210	THR
1	J	221	LEU
1	J	230	ILE
1	J	232	GLU
1	J	233	MET
1	J	247	LEU
1	J	248	LEU

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Mol	Chain	Res	Type
1	J	255	GLU
1	J	267	MET
1	J	268	ARG
1	J	272	LYS
1	J	284	ARG
1	J	288	MET
1	J	328	ASP
1	J	329	THR
1	J	331	THR
1	J	343	GLN
1	J	364	LYS
1	J	389	MET
1	J	417	VAL
1	J	419	LEU
1	J	420	ILE
1	J	421	ARG
1	J	422	VAL
1	J	430	ARG
1	J	445	ARG
1	J	451	LEU
1	J	452	ARG
1	J	461	GLU
1	J	494	LEU
1	J	504	LEU
1	J	510	VAL
1	J	514	MET
1	K	6	VAL
1	K	18	ARG
1	K	23	LEU
1	K	28	LYS
1	K	43	SER
1	K	44	PHE
1	K	48	THR
1	K	62	LEU
1	K	74	VAL
1	K	97	GLN
1	K	111	MET
1	K	129	GLU
1	K	132	LYS
1	K	153	ASN
1	K	172	GLU
1	K	197	ARG

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Mol	Chain	Res	Type
1	K	210	THR
1	K	221	LEU
1	K	230	ILE
1	K	232	GLU
1	K	233	MET
1	K	247	LEU
1	K	248	LEU
1	K	255	GLU
1	K	267	MET
1	K	268	ARG
1	K	272	LYS
1	K	284	ARG
1	K	288	MET
1	K	328	ASP
1	K	329	THR
1	K	331	THR
1	K	343	GLN
1	K	364	LYS
1	K	389	MET
1	K	417	VAL
1	K	419	LEU
1	K	420	ILE
1	K	421	ARG
1	K	422	VAL
1	K	430	ARG
1	K	445	ARG
1	K	451	LEU
1	K	452	ARG
1	K	461	GLU
1	K	494	LEU
1	K	504	LEU
1	K	510	VAL
1	K	514	MET
1	L	6	VAL
1	L	18	ARG
1	L	23	LEU
1	L	28	LYS
1	L	43	SER
1	L	44	PHE
1	L	48	THR
1	L	62	LEU
1	L	74	VAL

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Mol	Chain	Res	Type
1	L	97	GLN
1	L	111	MET
1	L	129	GLU
1	L	132	LYS
1	L	153	ASN
1	L	172	GLU
1	L	197	ARG
1	L	210	THR
1	L	221	LEU
1	L	230	ILE
1	L	232	GLU
1	L	233	MET
1	L	247	LEU
1	L	248	LEU
1	L	255	GLU
1	L	267	MET
1	L	268	ARG
1	L	272	LYS
1	L	284	ARG
1	L	288	MET
1	L	328	ASP
1	L	329	THR
1	L	331	THR
1	L	343	GLN
1	L	364	LYS
1	L	389	MET
1	L	417	VAL
1	L	419	LEU
1	L	420	ILE
1	L	421	ARG
1	L	422	VAL
1	L	430	ARG
1	L	445	ARG
1	L	451	LEU
1	L	452	ARG
1	L	461	GLU
1	L	494	LEU
1	L	504	LEU
1	L	510	VAL
1	L	514	MET
1	M	6	VAL
1	M	18	ARG

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Mol	Chain	Res	Type
1	M	23	LEU
1	M	28	LYS
1	M	43	SER
1	M	44	PHE
1	M	48	THR
1	M	62	LEU
1	M	74	VAL
1	M	97	GLN
1	M	111	MET
1	M	129	GLU
1	M	132	LYS
1	M	153	ASN
1	M	172	GLU
1	M	197	ARG
1	M	210	THR
1	M	221	LEU
1	M	230	ILE
1	M	232	GLU
1	M	233	MET
1	M	247	LEU
1	M	248	LEU
1	M	255	GLU
1	M	267	MET
1	M	268	ARG
1	M	272	LYS
1	M	284	ARG
1	M	288	MET
1	M	328	ASP
1	M	329	THR
1	M	331	THR
1	M	343	GLN
1	M	364	LYS
1	M	389	MET
1	M	417	VAL
1	M	419	LEU
1	M	420	ILE
1	M	421	ARG
1	M	422	VAL
1	M	430	ARG
1	M	445	ARG
1	M	451	LEU
1	M	452	ARG

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Mol	Chain	Res	Type
1	M	461	GLU
1	M	494	LEU
1	M	504	LEU
1	M	510	VAL
1	M	514	MET
1	N	6	VAL
1	N	18	ARG
1	N	23	LEU
1	N	28	LYS
1	N	43	SER
1	N	44	PHE
1	N	48	THR
1	N	62	LEU
1	N	74	VAL
1	N	97	GLN
1	N	111	MET
1	N	129	GLU
1	N	132	LYS
1	N	153	ASN
1	N	172	GLU
1	N	197	ARG
1	N	210	THR
1	N	221	LEU
1	N	230	ILE
1	N	232	GLU
1	N	233	MET
1	N	247	LEU
1	N	248	LEU
1	N	255	GLU
1	N	267	MET
1	N	268	ARG
1	N	272	LYS
1	N	284	ARG
1	N	288	MET
1	N	328	ASP
1	N	329	THR
1	N	331	THR
1	N	343	GLN
1	N	364	LYS
1	N	389	MET
1	N	417	VAL
1	N	419	LEU

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Mol	Chain	Res	Type
1	N	420	ILE
1	N	421	ARG
1	N	422	VAL
1	N	430	ARG
1	N	445	ARG
1	N	451	LEU
1	N	452	ARG
1	N	461	GLU
1	N	494	LEU
1	N	504	LEU
1	N	510	VAL
1	N	514	MET
2	O	18	LEU
2	O	90	GLN
2	P	18	LEU
2	P	90	GLN
2	Q	18	LEU
2	Q	90	GLN
2	R	18	LEU
2	R	90	GLN
2	S	18	LEU
2	S	90	GLN
2	T	18	LEU
2	T	90	GLN
2	U	18	LEU
2	U	90	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (152) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	ASN
1	A	97	GLN
1	A	146	GLN
1	A	153	ASN
1	A	348	GLN
1	A	366	GLN
1	A	457	ASN
1	A	475	ASN
1	B	21	ASN
1	B	97	GLN
1	B	146	GLN
1	B	153	ASN

Continued on next page...

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Mol	Chain	Res	Type
1	B	348	GLN
1	B	351	GLN
1	B	457	ASN
1	B	475	ASN
1	C	21	ASN
1	C	97	GLN
1	C	146	GLN
1	C	153	ASN
1	C	348	GLN
1	C	351	GLN
1	C	457	ASN
1	C	475	ASN
1	D	21	ASN
1	D	97	GLN
1	D	146	GLN
1	D	153	ASN
1	D	348	GLN
1	D	351	GLN
1	D	457	ASN
1	D	475	ASN
1	E	21	ASN
1	E	97	GLN
1	E	146	GLN
1	E	153	ASN
1	E	348	GLN
1	E	351	GLN
1	E	366	GLN
1	E	457	ASN
1	E	475	ASN
1	F	21	ASN
1	F	97	GLN
1	F	146	GLN
1	F	153	ASN
1	F	348	GLN
1	F	351	GLN
1	F	366	GLN
1	F	457	ASN
1	F	475	ASN
1	G	21	ASN
1	G	97	GLN
1	G	146	GLN
1	G	153	ASN

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Mol	Chain	Res	Type
1	G	348	GLN
1	G	366	GLN
1	G	457	ASN
1	G	475	ASN
1	H	21	ASN
1	H	97	GLN
1	H	146	GLN
1	H	153	ASN
1	H	319	GLN
1	H	453	GLN
1	H	457	ASN
1	H	467	ASN
1	H	475	ASN
1	I	21	ASN
1	I	97	GLN
1	I	146	GLN
1	I	153	ASN
1	I	319	GLN
1	I	457	ASN
1	I	467	ASN
1	I	475	ASN
1	J	21	ASN
1	J	97	GLN
1	J	146	GLN
1	J	153	ASN
1	J	319	GLN
1	J	457	ASN
1	J	467	ASN
1	J	475	ASN
1	K	21	ASN
1	K	97	GLN
1	K	146	GLN
1	K	153	ASN
1	K	319	GLN
1	K	457	ASN
1	K	467	ASN
1	K	475	ASN
1	L	21	ASN
1	L	97	GLN
1	L	146	GLN
1	L	153	ASN
1	L	319	GLN

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Mol	Chain	Res	Type
1	L	457	ASN
1	L	467	ASN
1	L	475	ASN
1	M	21	ASN
1	M	97	GLN
1	M	146	GLN
1	M	153	ASN
1	M	319	GLN
1	M	453	GLN
1	M	457	ASN
1	M	467	ASN
1	M	475	ASN
1	N	21	ASN
1	N	97	GLN
1	N	146	GLN
1	N	153	ASN
1	N	319	GLN
1	N	453	GLN
1	N	457	ASN
1	N	467	ASN
1	N	475	ASN
2	O	5	GLN
2	O	6	GLN
2	O	52	HIS
2	O	81	HIS
2	O	102	HIS
2	P	5	GLN
2	P	6	GLN
2	P	52	HIS
2	P	81	HIS
2	P	102	HIS
2	Q	5	GLN
2	Q	6	GLN
2	Q	52	HIS
2	Q	81	HIS
2	Q	102	HIS
2	R	5	GLN
2	R	6	GLN
2	R	52	HIS
2	R	81	HIS
2	R	102	HIS
2	S	5	GLN

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Mol	Chain	Res	Type
2	S	6	GLN
2	S	52	HIS
2	S	81	HIS
2	S	102	HIS
2	T	5	GLN
2	T	6	GLN
2	T	52	HIS
2	T	81	HIS
2	T	102	HIS
2	U	5	GLN
2	U	6	GLN
2	U	52	HIS
2	U	81	HIS
2	U	102	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	H	3
1	I	3
1	J	3
1	K	3
1	L	3
1	M	3
1	N	3
1	A	3
1	B	3
1	C	3
1	D	3
1	E	3
1	F	3
1	G	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	409:GLU	C	410:GLY	N	4.21
1	I	409:GLU	C	410:GLY	N	4.21
1	J	409:GLU	C	410:GLY	N	4.21
1	K	409:GLU	C	410:GLY	N	4.21
1	L	409:GLU	C	410:GLY	N	4.21
1	M	409:GLU	C	410:GLY	N	4.21
1	N	409:GLU	C	410:GLY	N	4.21
1	H	191:GLU	C	192:GLY	N	3.08
1	I	191:GLU	C	192:GLY	N	3.08
1	J	191:GLU	C	192:GLY	N	3.08
1	K	191:GLU	C	192:GLY	N	3.08
1	L	191:GLU	C	192:GLY	N	3.08
1	M	191:GLU	C	192:GLY	N	3.08
1	N	191:GLU	C	192:GLY	N	3.08
1	A	409:GLU	C	410:GLY	N	2.83
1	B	409:GLU	C	410:GLY	N	2.83
1	C	409:GLU	C	410:GLY	N	2.83
1	D	409:GLU	C	410:GLY	N	2.83
1	E	409:GLU	C	410:GLY	N	2.83
1	F	409:GLU	C	410:GLY	N	2.83
1	G	409:GLU	C	410:GLY	N	2.83
1	H	136:VAL	C	137:PRO	N	2.40
1	I	136:VAL	C	137:PRO	N	2.40
1	J	136:VAL	C	137:PRO	N	2.40
1	K	136:VAL	C	137:PRO	N	2.40
1	L	136:VAL	C	137:PRO	N	2.40

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	M	136:VAL	C	137:PRO	N	2.40
1	N	136:VAL	C	137:PRO	N	2.40
1	G	136:VAL	C	137:PRO	N	1.85
1	A	136:VAL	C	137:PRO	N	1.84
1	B	136:VAL	C	137:PRO	N	1.84
1	C	136:VAL	C	137:PRO	N	1.84
1	D	136:VAL	C	137:PRO	N	1.84
1	E	136:VAL	C	137:PRO	N	1.84
1	F	136:VAL	C	137:PRO	N	1.84
1	A	191:GLU	C	192:GLY	N	0.56
1	B	191:GLU	C	192:GLY	N	0.56
1	C	191:GLU	C	192:GLY	N	0.56
1	D	191:GLU	C	192:GLY	N	0.56
1	E	191:GLU	C	192:GLY	N	0.56
1	F	191:GLU	C	192:GLY	N	0.56
1	G	191:GLU	C	192:GLY	N	0.56

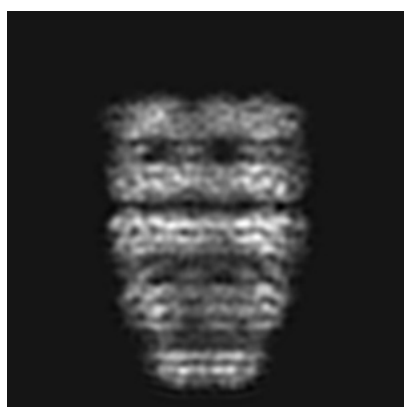
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1202. These allow visual inspection of the internal detail of the map and identification of artifacts.

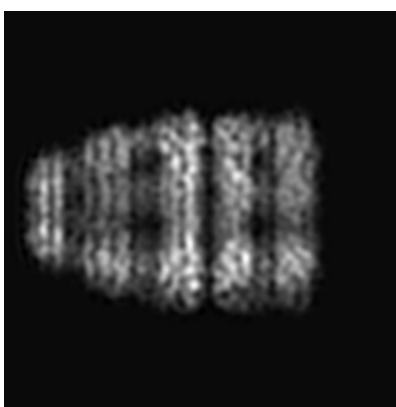
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

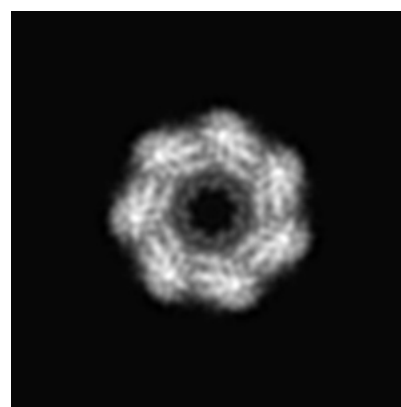
6.1.1 Primary map



X



Y



Z

The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 96



Y Index: 96



Z Index: 96

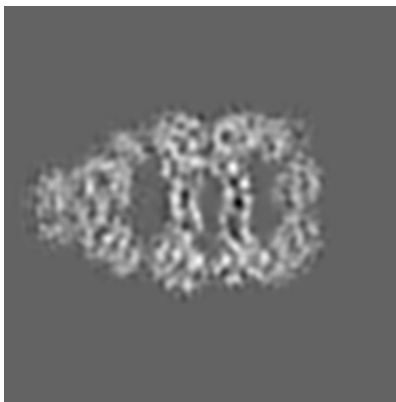
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 75



Y Index: 120



Z Index: 90

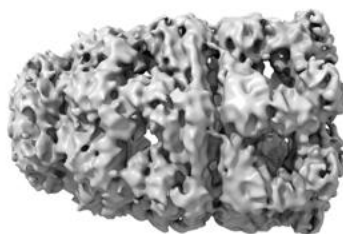
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

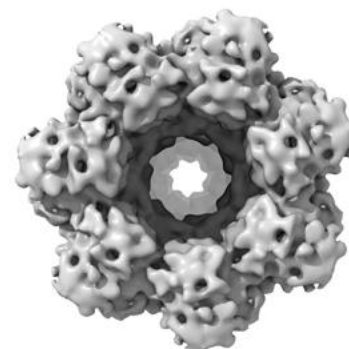
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.452. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

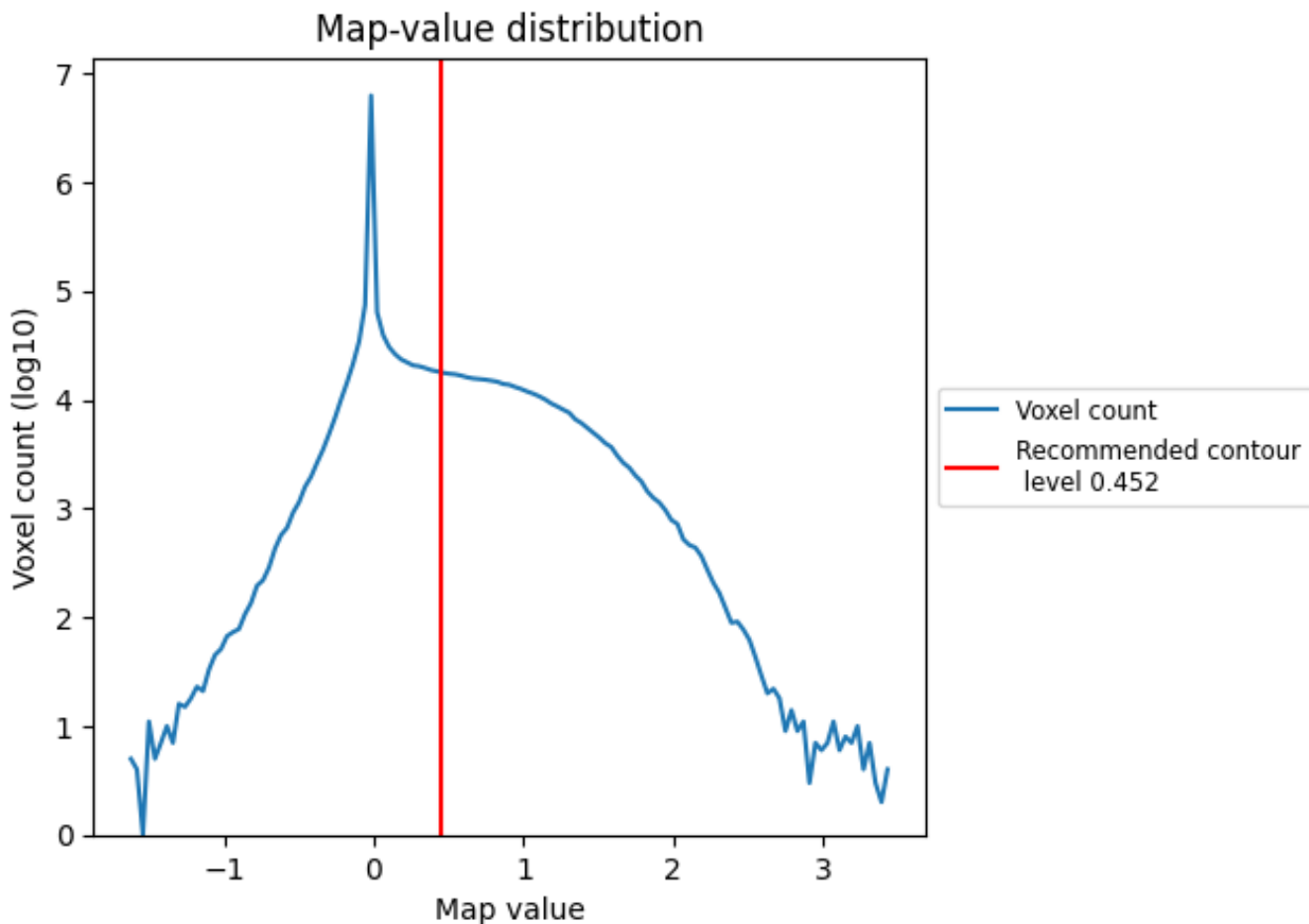
6.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

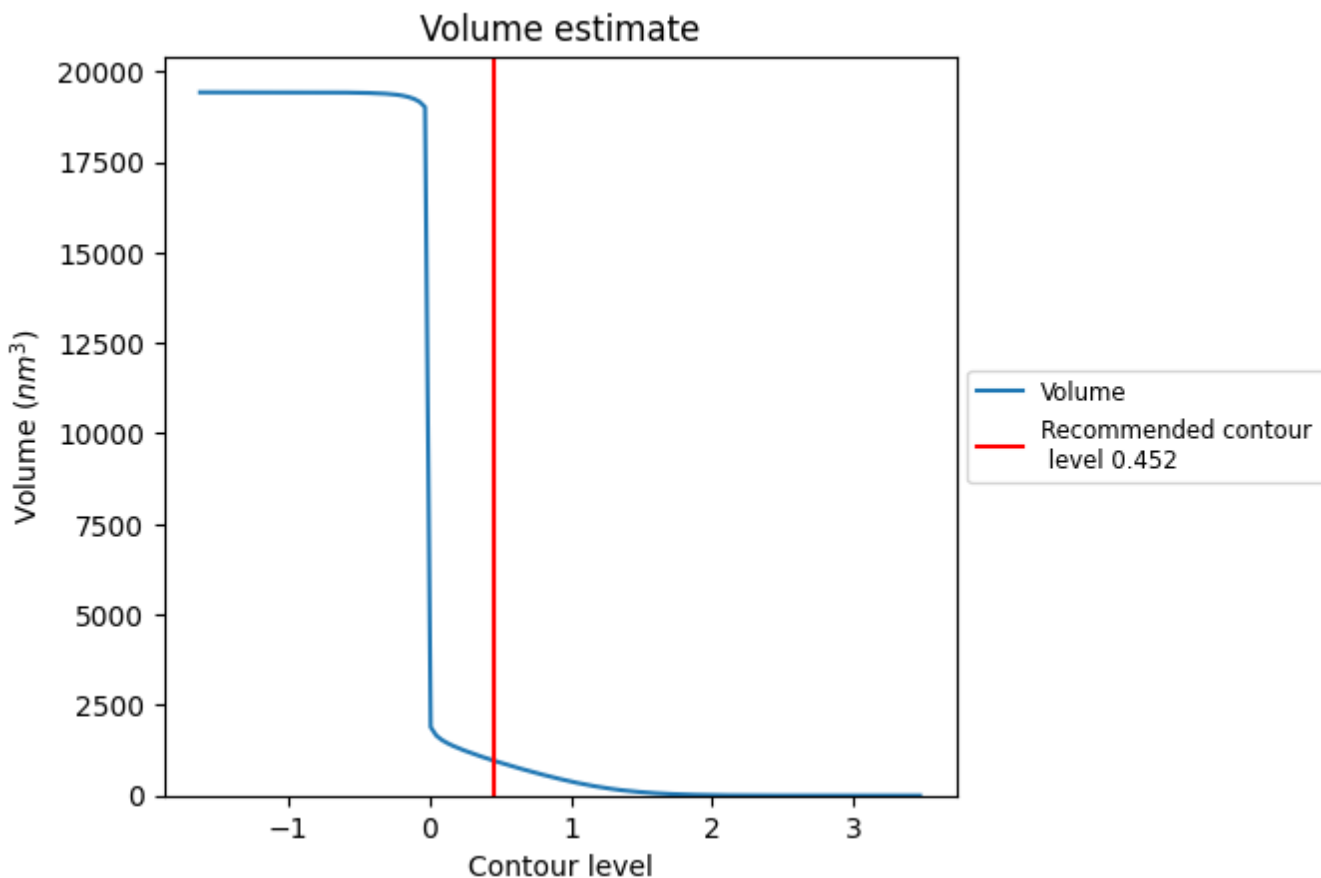
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

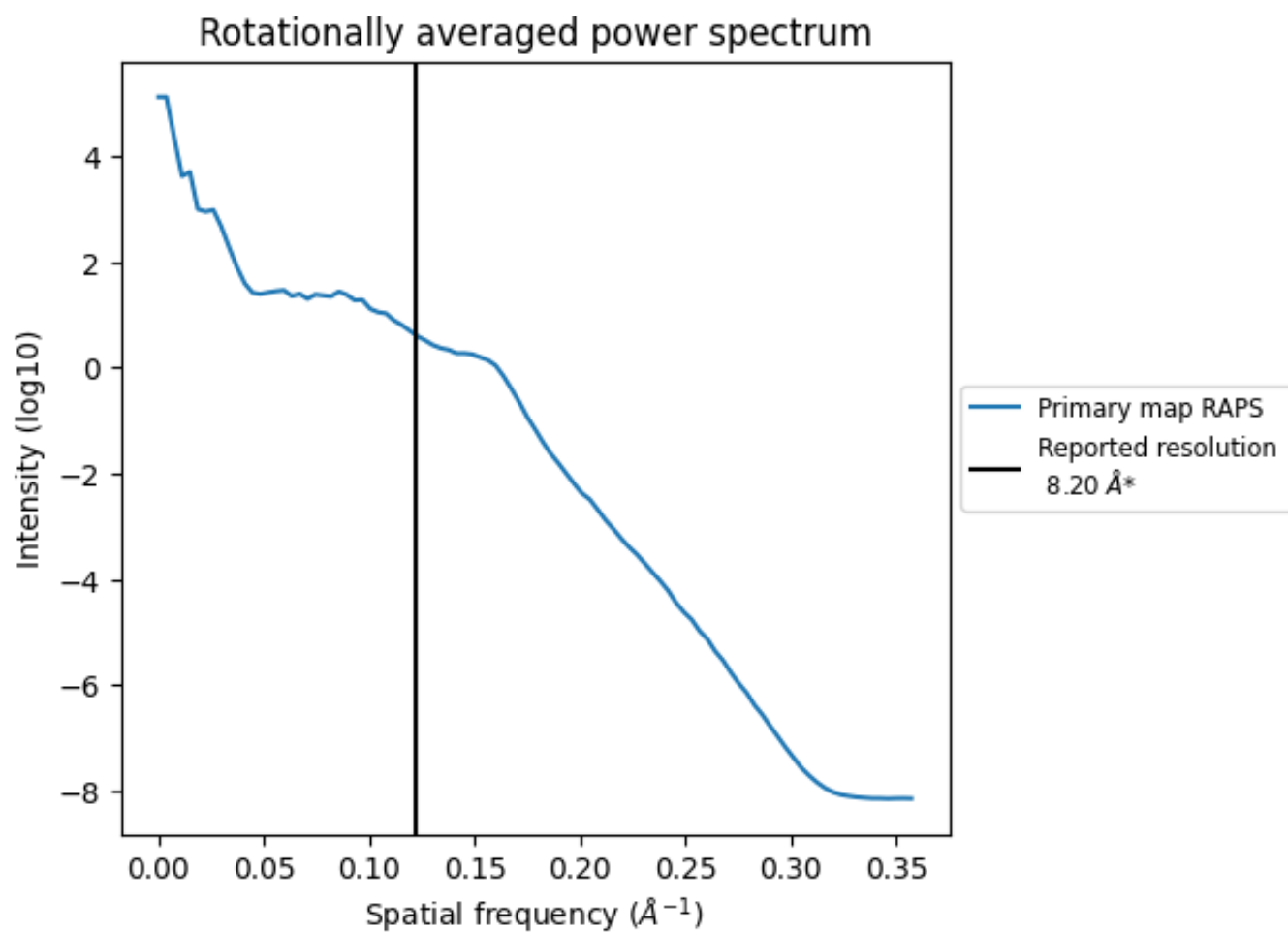
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 969 nm³; this corresponds to an approximate mass of 875 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.122 Å⁻¹

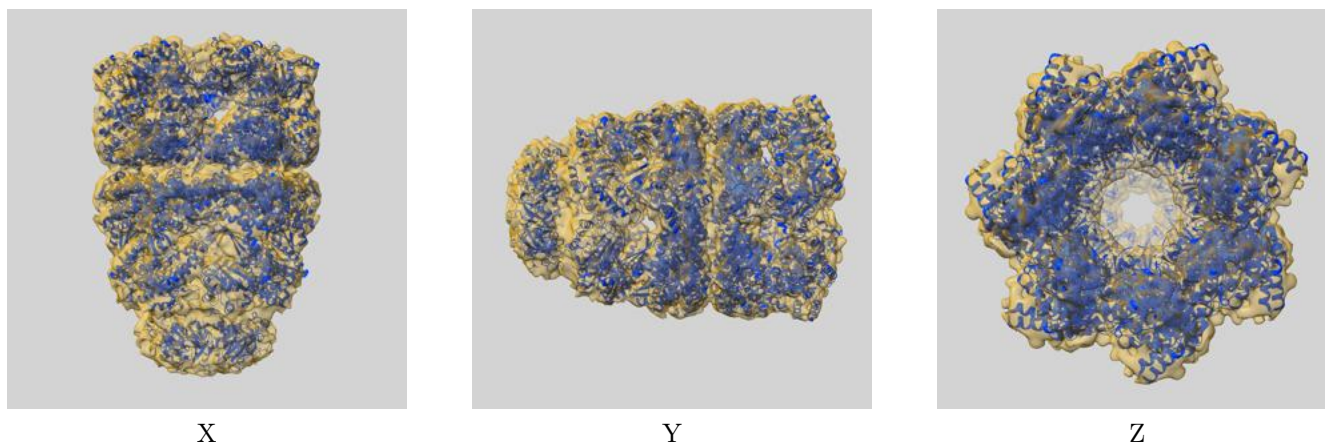
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

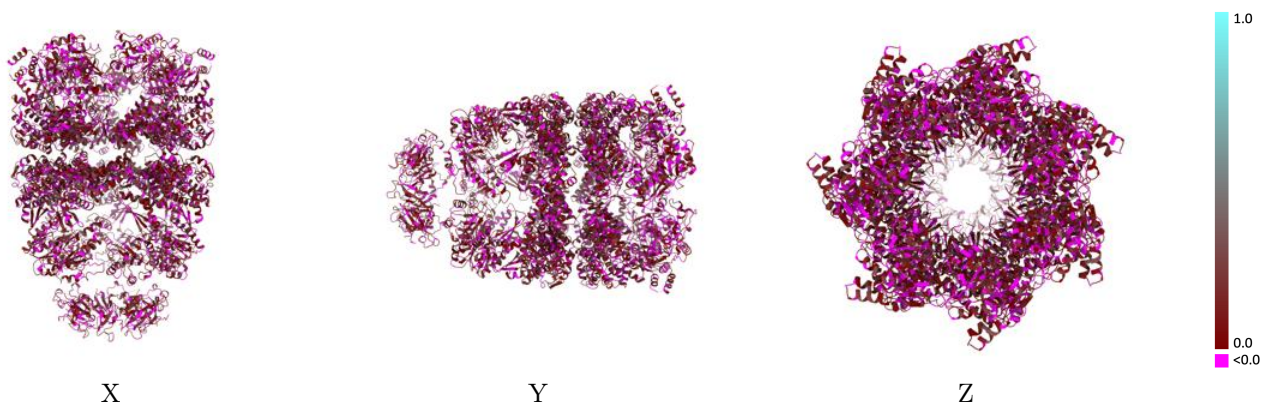
This section contains information regarding the fit between EMDB map EMD-1202 and PDB model 2CGT. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



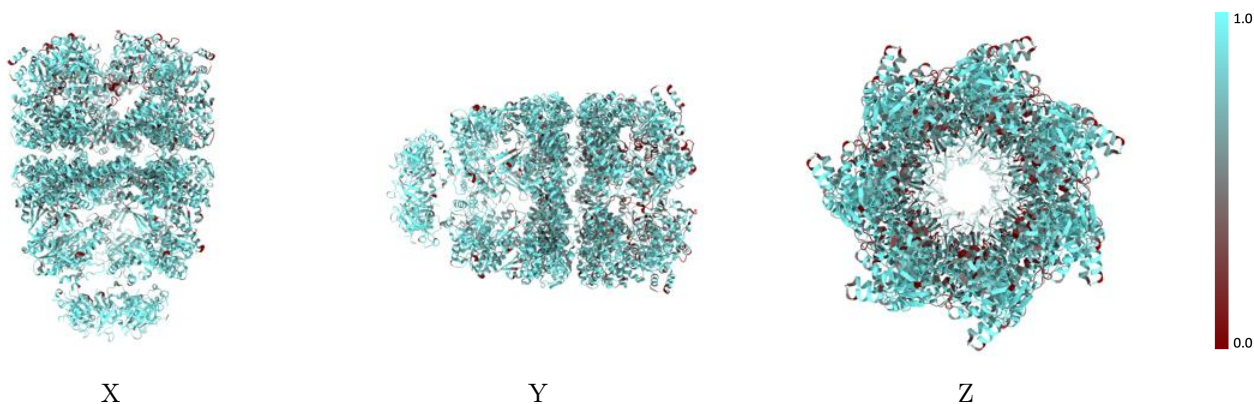
The images above show the 3D surface view of the map at the recommended contour level 0.452 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



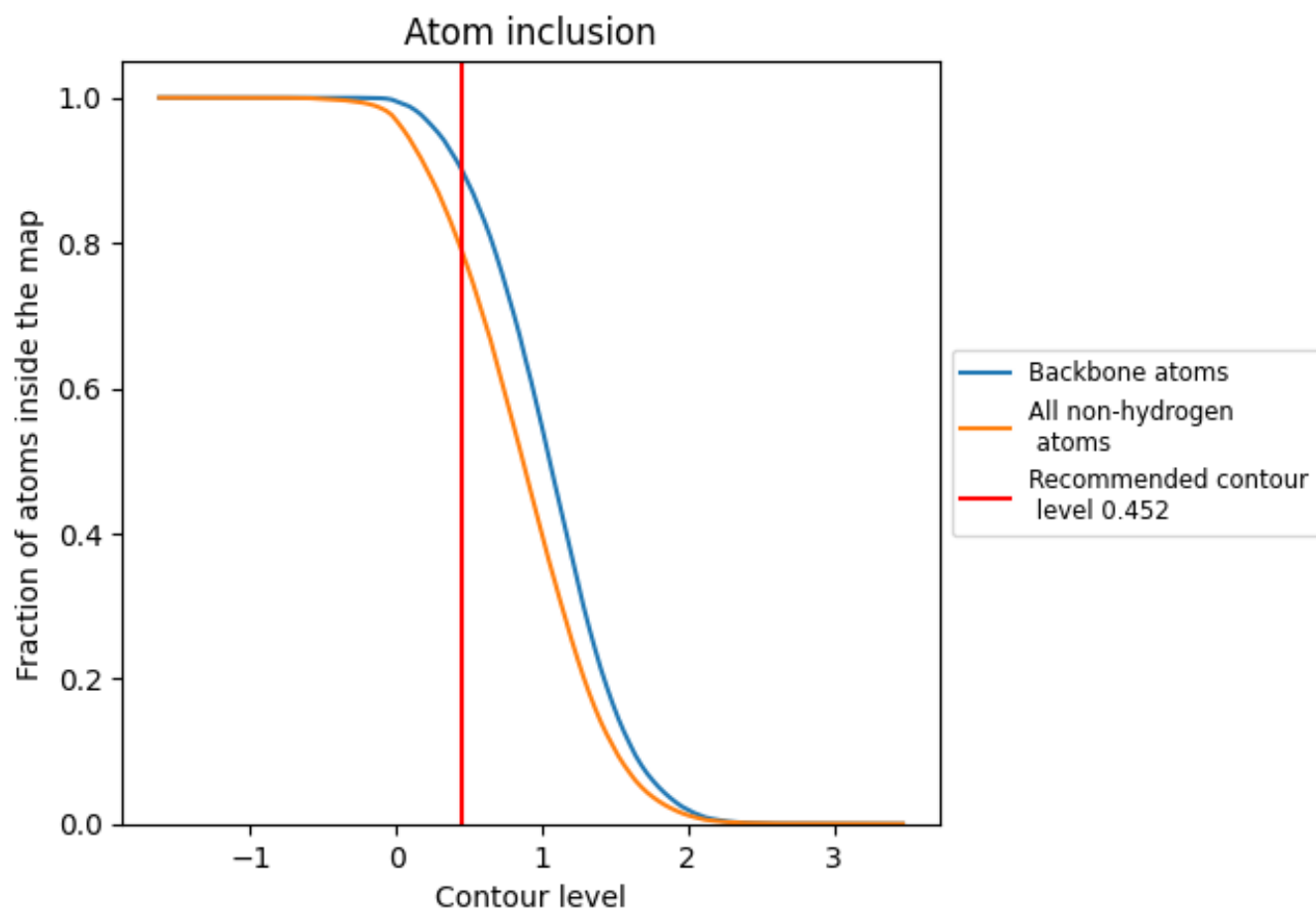
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.452).













































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 79% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.452) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7875	 0.0960
A	 0.8160	 0.1100
B	 0.8076	 0.1070
C	 0.8097	 0.1040
D	 0.8189	 0.1110
E	 0.8202	 0.1110
F	 0.8136	 0.1030
G	 0.8118	 0.1030
H	 0.7493	 0.0850
I	 0.7353	 0.0800
J	 0.7300	 0.0810
K	 0.7431	 0.0860
L	 0.7477	 0.0870
M	 0.7460	 0.0850
N	 0.7514	 0.0850
O	 0.8849	 0.1010
P	 0.8896	 0.1120
Q	 0.8864	 0.1040
R	 0.8896	 0.0910
S	 0.8896	 0.0890
T	 0.8927	 0.0860
U	 0.8896	 0.0860

