



Full wwPDB EM Validation Report (i)

Mar 18, 2024 – 05:37 pm GMT

PDB ID : 8QHD
EMDB ID : EMD-18408
Title : Hantaan virus polymerase in hexameric state
Authors : Durieux Trouilletton, Q.; Arragain, B.; Malet, H.
Deposited on : 2023-09-07
Resolution : 3.60 Å(reported)
Based on initial model : 8C4S

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 (i) 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 \(i\)](#)) were used in the production of this report:

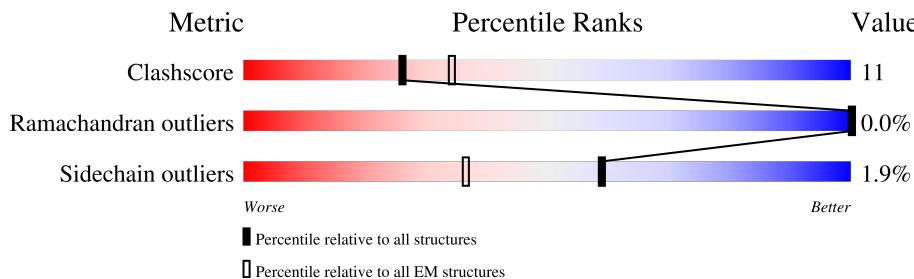
EMDB validation analysis : 0.0.1.dev92
MolProbit : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

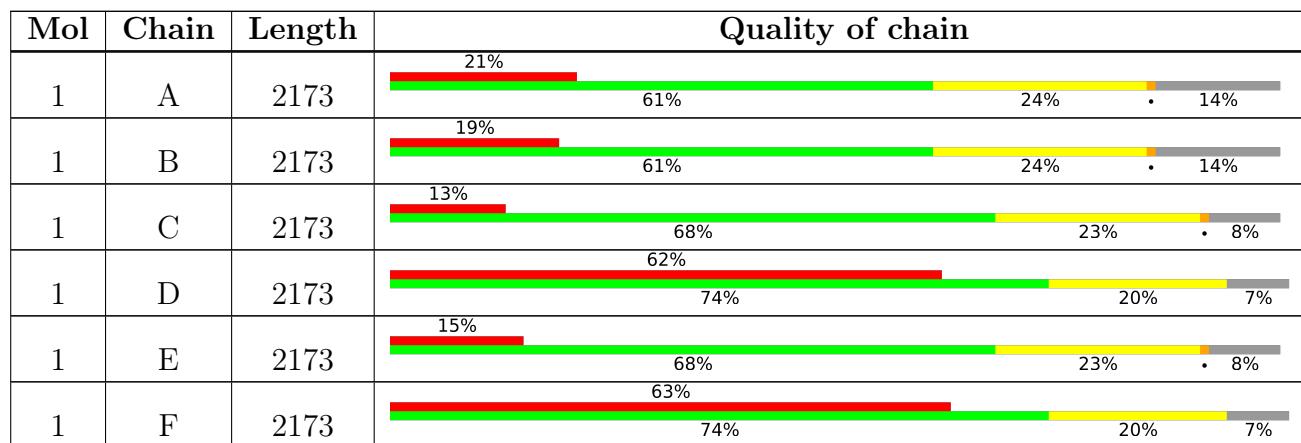
The reported resolution of this entry is 3.60 Å.

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 <=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.



2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 95348 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	D	2030	Total	C	N	O	S	0	0
			16400	10555	2764	2994	87		
1	B	1873	Total	C	N	O	S	0	0
			15128	9747	2547	2756	78		
1	C	1999	Total	C	N	O	S	0	0
			16146	10400	2714	2945	87		
1	F	2030	Total	C	N	O	S	0	0
			16400	10555	2764	2994	87		
1	A	1873	Total	C	N	O	S	0	0
			15128	9747	2547	2756	78		
1	E	1999	Total	C	N	O	S	0	0
			16146	10400	2714	2945	87		

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-21	MET	-	initiating methionine	UNP P23456
D	-20	GLY	-	expression tag	UNP P23456
D	-19	HIS	-	expression tag	UNP P23456
D	-18	HIS	-	expression tag	UNP P23456
D	-17	HIS	-	expression tag	UNP P23456
D	-16	HIS	-	expression tag	UNP P23456
D	-15	HIS	-	expression tag	UNP P23456
D	-14	HIS	-	expression tag	UNP P23456
D	-13	ASP	-	expression tag	UNP P23456
D	-12	TYR	-	expression tag	UNP P23456
D	-11	ASP	-	expression tag	UNP P23456
D	-10	ILE	-	expression tag	UNP P23456
D	-9	PRO	-	expression tag	UNP P23456
D	-8	THR	-	expression tag	UNP P23456
D	-7	THR	-	expression tag	UNP P23456
D	-6	GLU	-	expression tag	UNP P23456
D	-5	ASN	-	expression tag	UNP P23456
D	-4	LEU	-	expression tag	UNP P23456

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-3	TYR	-	expression tag	UNP P23456
D	-2	PHE	-	expression tag	UNP P23456
D	-1	GLN	-	expression tag	UNP P23456
D	0	GLY	-	expression tag	UNP P23456
B	-21	MET	-	initiating methionine	UNP P23456
B	-20	GLY	-	expression tag	UNP P23456
B	-19	HIS	-	expression tag	UNP P23456
B	-18	HIS	-	expression tag	UNP P23456
B	-17	HIS	-	expression tag	UNP P23456
B	-16	HIS	-	expression tag	UNP P23456
B	-15	HIS	-	expression tag	UNP P23456
B	-14	HIS	-	expression tag	UNP P23456
B	-13	ASP	-	expression tag	UNP P23456
B	-12	TYR	-	expression tag	UNP P23456
B	-11	ASP	-	expression tag	UNP P23456
B	-10	ILE	-	expression tag	UNP P23456
B	-9	PRO	-	expression tag	UNP P23456
B	-8	THR	-	expression tag	UNP P23456
B	-7	THR	-	expression tag	UNP P23456
B	-6	GLU	-	expression tag	UNP P23456
B	-5	ASN	-	expression tag	UNP P23456
B	-4	LEU	-	expression tag	UNP P23456
B	-3	TYR	-	expression tag	UNP P23456
B	-2	PHE	-	expression tag	UNP P23456
B	-1	GLN	-	expression tag	UNP P23456
B	0	GLY	-	expression tag	UNP P23456
C	-21	MET	-	initiating methionine	UNP P23456
C	-20	GLY	-	expression tag	UNP P23456
C	-19	HIS	-	expression tag	UNP P23456
C	-18	HIS	-	expression tag	UNP P23456
C	-17	HIS	-	expression tag	UNP P23456
C	-16	HIS	-	expression tag	UNP P23456
C	-15	HIS	-	expression tag	UNP P23456
C	-14	HIS	-	expression tag	UNP P23456
C	-13	ASP	-	expression tag	UNP P23456
C	-12	TYR	-	expression tag	UNP P23456
C	-11	ASP	-	expression tag	UNP P23456
C	-10	ILE	-	expression tag	UNP P23456
C	-9	PRO	-	expression tag	UNP P23456
C	-8	THR	-	expression tag	UNP P23456
C	-7	THR	-	expression tag	UNP P23456
C	-6	GLU	-	expression tag	UNP P23456

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	ASN	-	expression tag	UNP P23456
C	-4	LEU	-	expression tag	UNP P23456
C	-3	TYR	-	expression tag	UNP P23456
C	-2	PHE	-	expression tag	UNP P23456
C	-1	GLN	-	expression tag	UNP P23456
C	0	GLY	-	expression tag	UNP P23456
F	-21	MET	-	initiating methionine	UNP P23456
F	-20	GLY	-	expression tag	UNP P23456
F	-19	HIS	-	expression tag	UNP P23456
F	-18	HIS	-	expression tag	UNP P23456
F	-17	HIS	-	expression tag	UNP P23456
F	-16	HIS	-	expression tag	UNP P23456
F	-15	HIS	-	expression tag	UNP P23456
F	-14	HIS	-	expression tag	UNP P23456
F	-13	ASP	-	expression tag	UNP P23456
F	-12	TYR	-	expression tag	UNP P23456
F	-11	ASP	-	expression tag	UNP P23456
F	-10	ILE	-	expression tag	UNP P23456
F	-9	PRO	-	expression tag	UNP P23456
F	-8	THR	-	expression tag	UNP P23456
F	-7	THR	-	expression tag	UNP P23456
F	-6	GLU	-	expression tag	UNP P23456
F	-5	ASN	-	expression tag	UNP P23456
F	-4	LEU	-	expression tag	UNP P23456
F	-3	TYR	-	expression tag	UNP P23456
F	-2	PHE	-	expression tag	UNP P23456
F	-1	GLN	-	expression tag	UNP P23456
F	0	GLY	-	expression tag	UNP P23456
A	-21	MET	-	initiating methionine	UNP P23456
A	-20	GLY	-	expression tag	UNP P23456
A	-19	HIS	-	expression tag	UNP P23456
A	-18	HIS	-	expression tag	UNP P23456
A	-17	HIS	-	expression tag	UNP P23456
A	-16	HIS	-	expression tag	UNP P23456
A	-15	HIS	-	expression tag	UNP P23456
A	-14	HIS	-	expression tag	UNP P23456
A	-13	ASP	-	expression tag	UNP P23456
A	-12	TYR	-	expression tag	UNP P23456
A	-11	ASP	-	expression tag	UNP P23456
A	-10	ILE	-	expression tag	UNP P23456
A	-9	PRO	-	expression tag	UNP P23456
A	-8	THR	-	expression tag	UNP P23456

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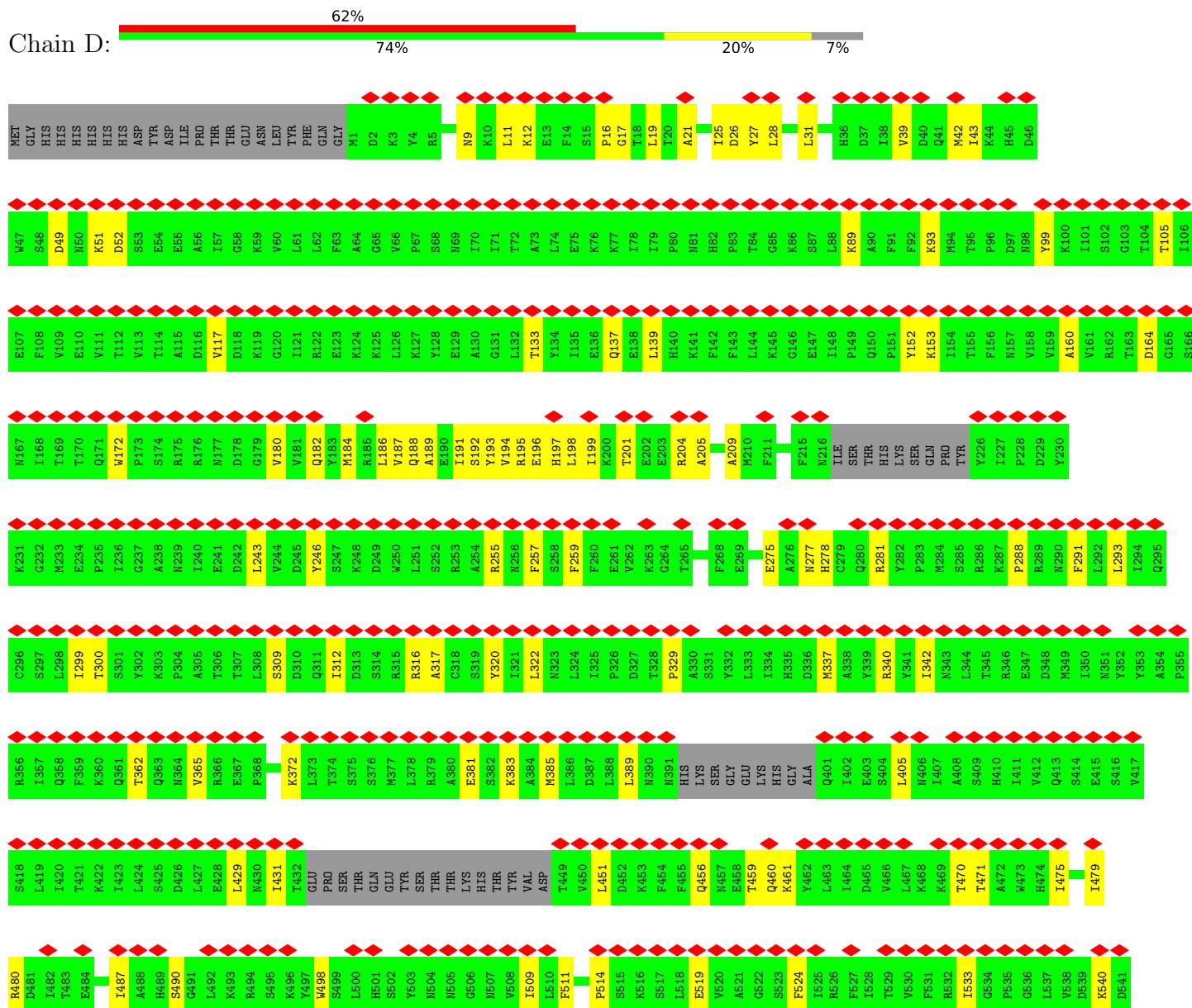
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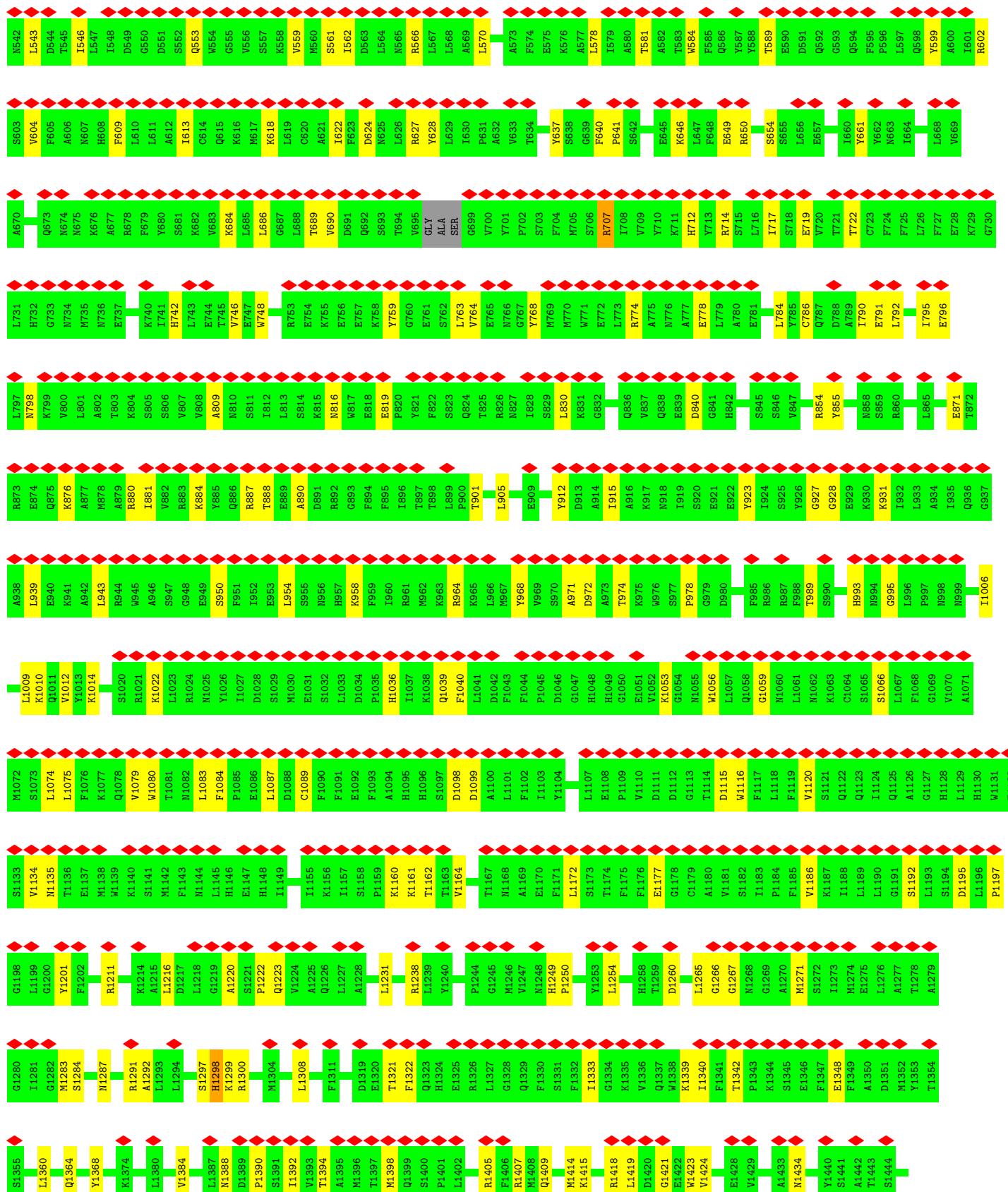
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	THR	-	expression tag	UNP P23456
A	-6	GLU	-	expression tag	UNP P23456
A	-5	ASN	-	expression tag	UNP P23456
A	-4	LEU	-	expression tag	UNP P23456
A	-3	TYR	-	expression tag	UNP P23456
A	-2	PHE	-	expression tag	UNP P23456
A	-1	GLN	-	expression tag	UNP P23456
A	0	GLY	-	expression tag	UNP P23456
E	-21	MET	-	initiating methionine	UNP P23456
E	-20	GLY	-	expression tag	UNP P23456
E	-19	HIS	-	expression tag	UNP P23456
E	-18	HIS	-	expression tag	UNP P23456
E	-17	HIS	-	expression tag	UNP P23456
E	-16	HIS	-	expression tag	UNP P23456
E	-15	HIS	-	expression tag	UNP P23456
E	-14	HIS	-	expression tag	UNP P23456
E	-13	ASP	-	expression tag	UNP P23456
E	-12	TYR	-	expression tag	UNP P23456
E	-11	ASP	-	expression tag	UNP P23456
E	-10	ILE	-	expression tag	UNP P23456
E	-9	PRO	-	expression tag	UNP P23456
E	-8	THR	-	expression tag	UNP P23456
E	-7	THR	-	expression tag	UNP P23456
E	-6	GLU	-	expression tag	UNP P23456
E	-5	ASN	-	expression tag	UNP P23456
E	-4	LEU	-	expression tag	UNP P23456
E	-3	TYR	-	expression tag	UNP P23456
E	-2	PHE	-	expression tag	UNP P23456
E	-1	GLN	-	expression tag	UNP P23456
E	0	GLY	-	expression tag	UNP P23456

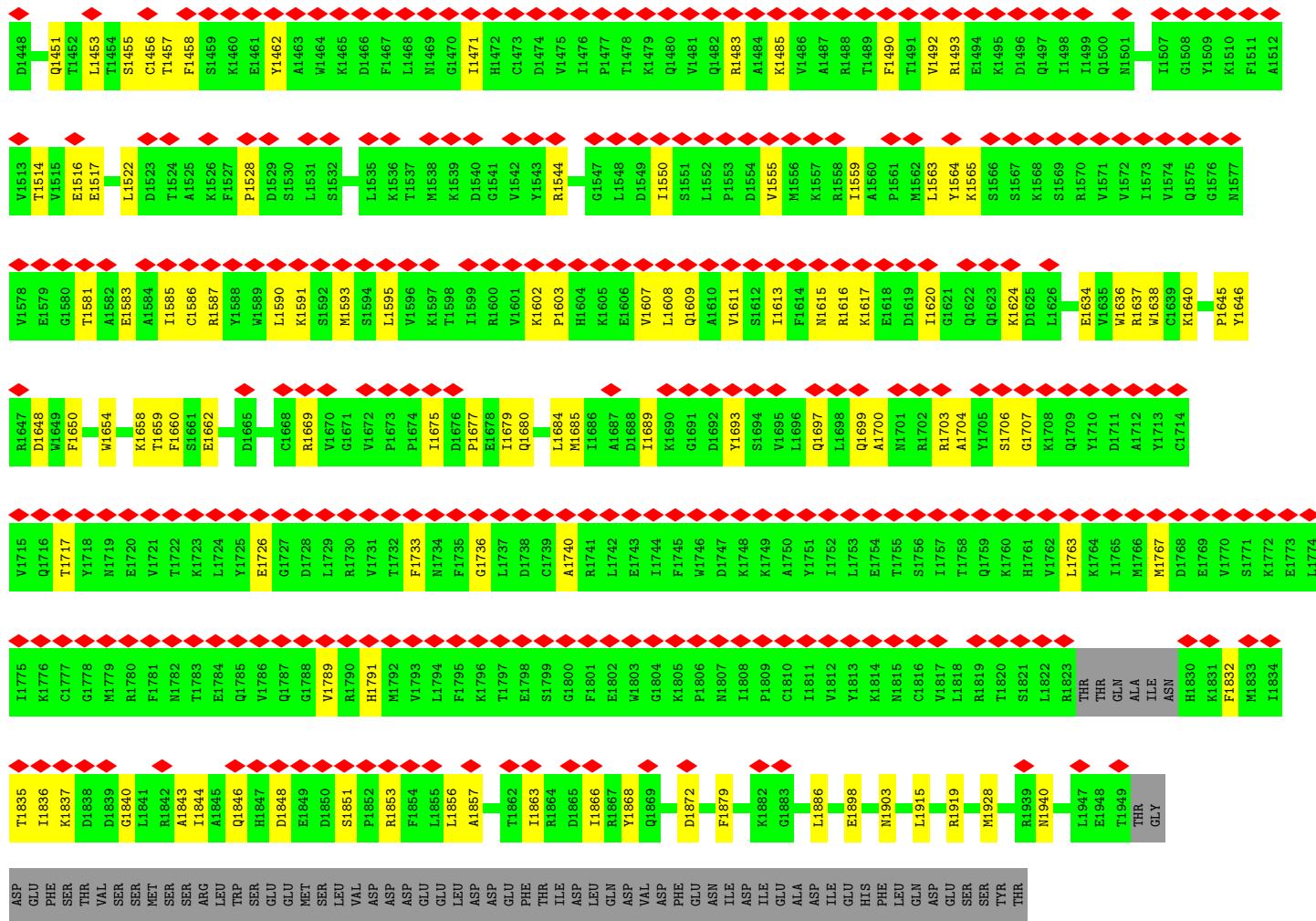
3 Residue-property plots

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: RNA-directed RNA polymerase L

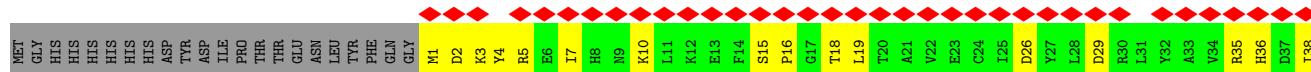


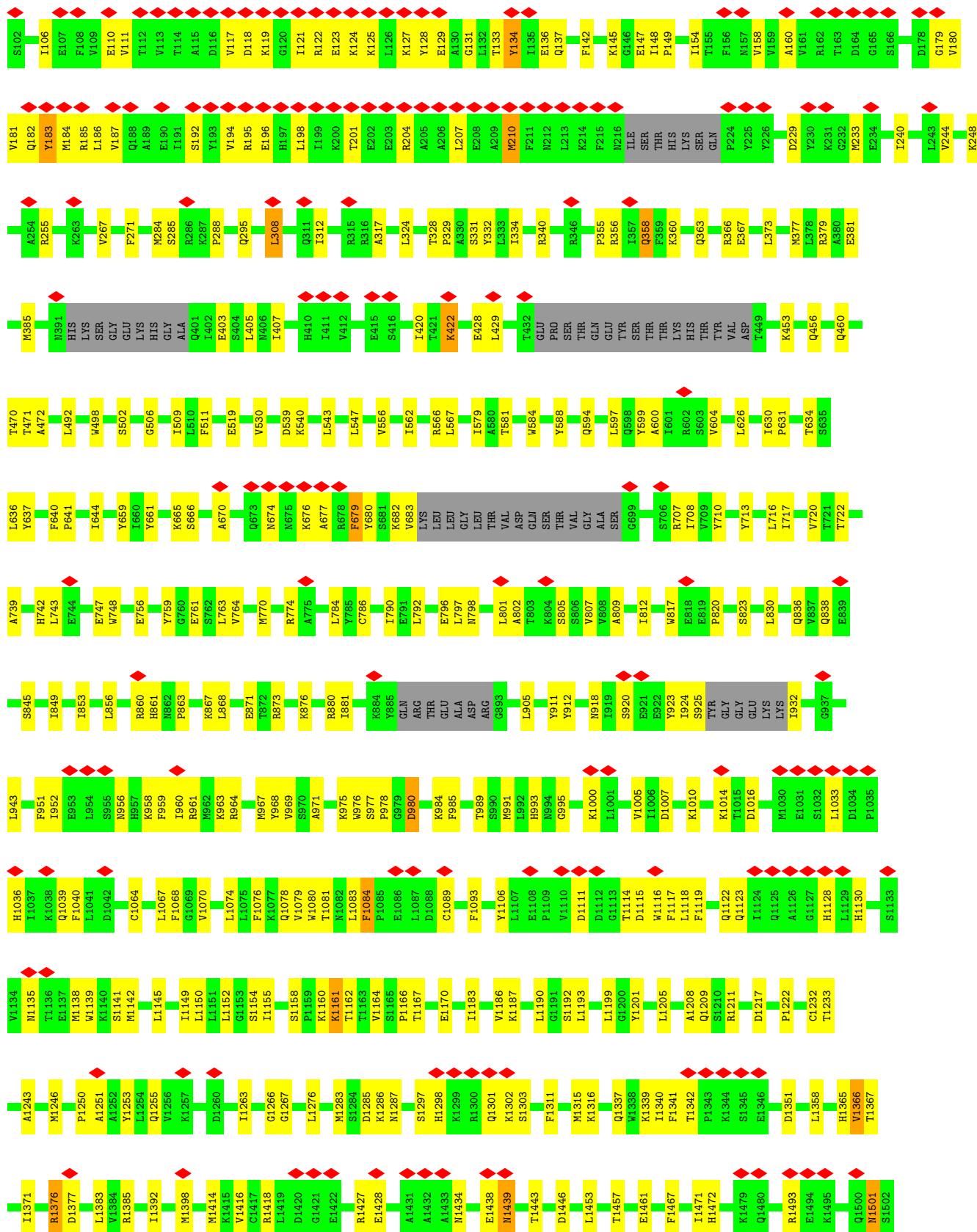


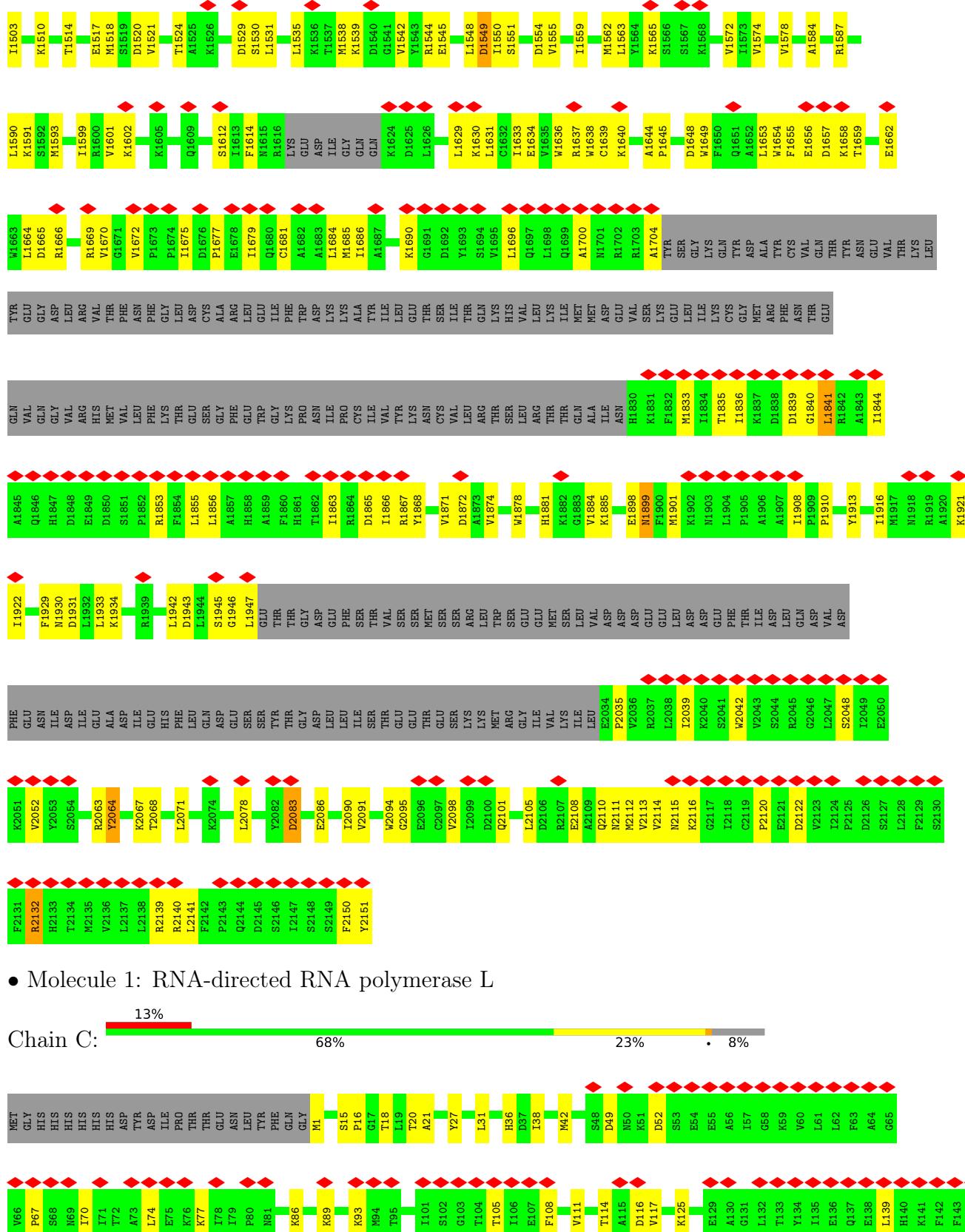


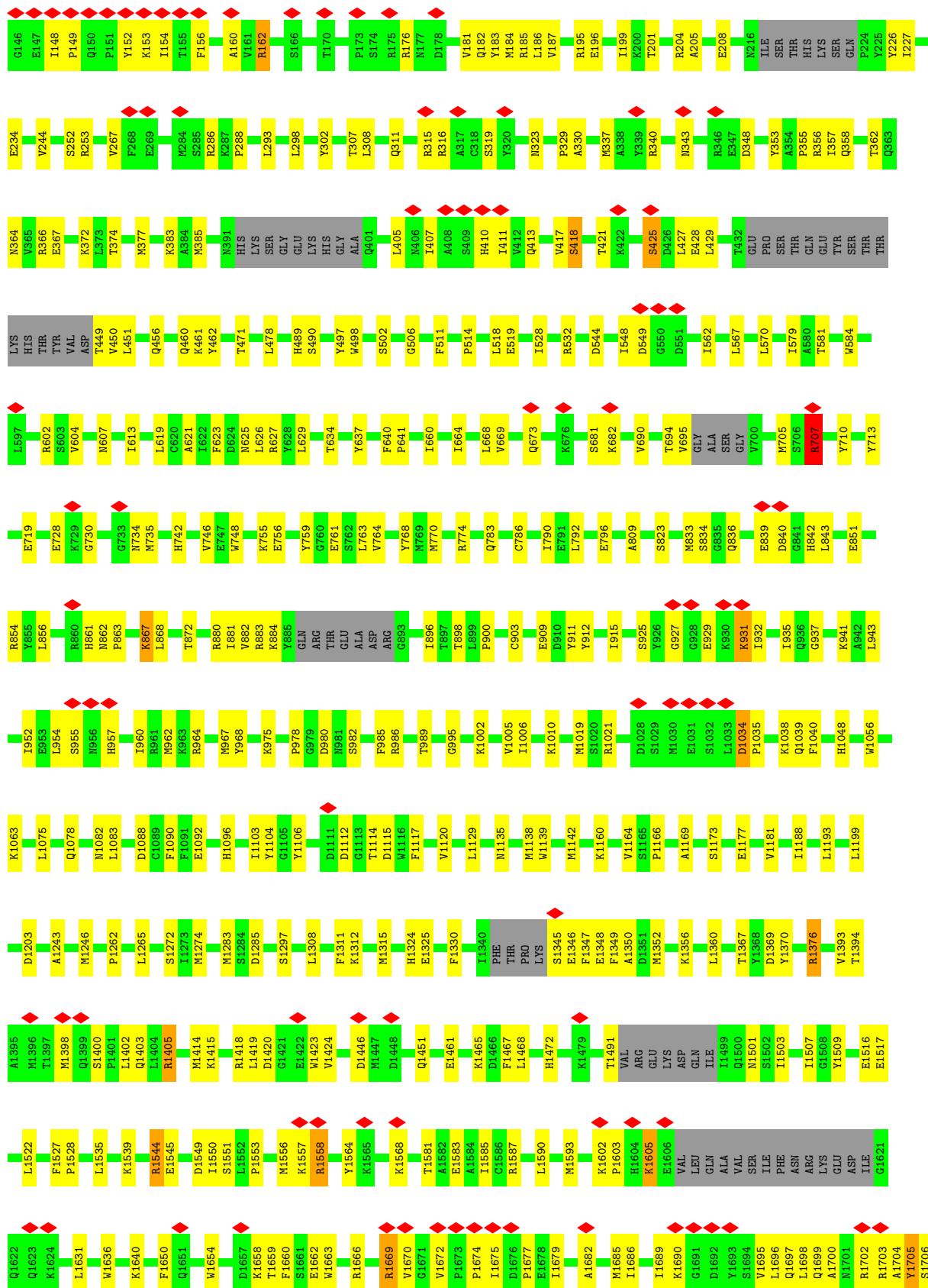
- Molecule 1: RNA-directed RNA polymerase L

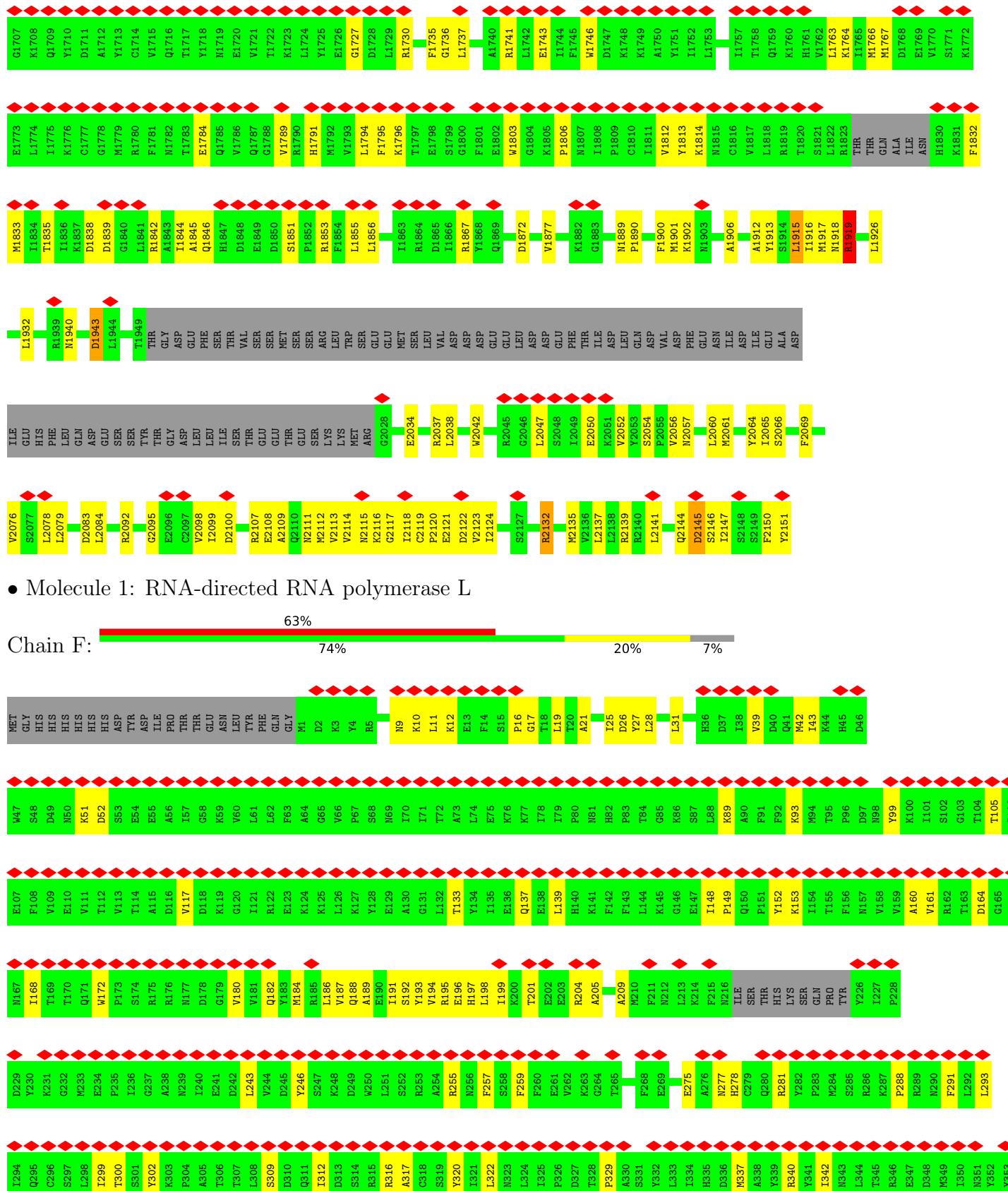
19%

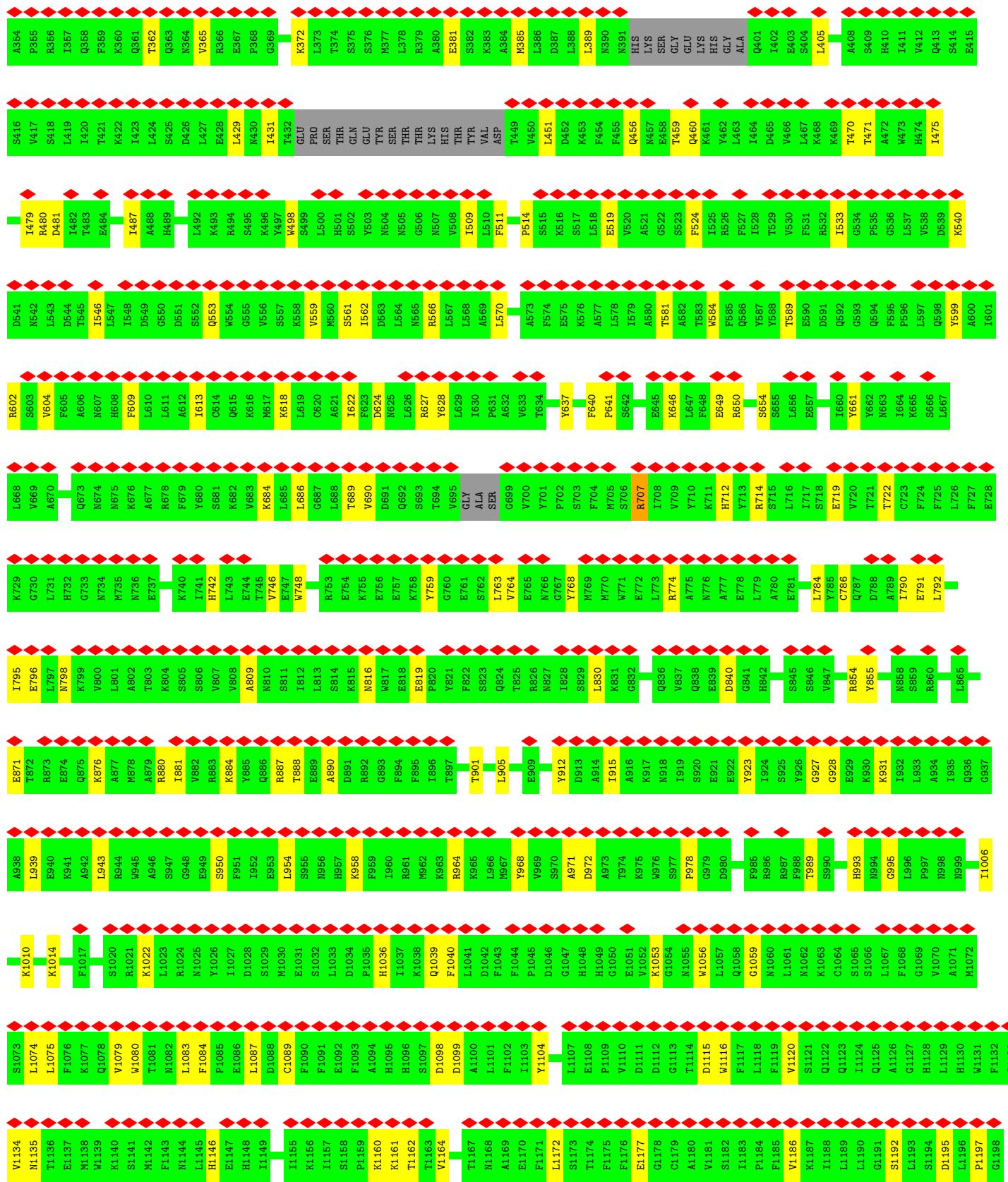


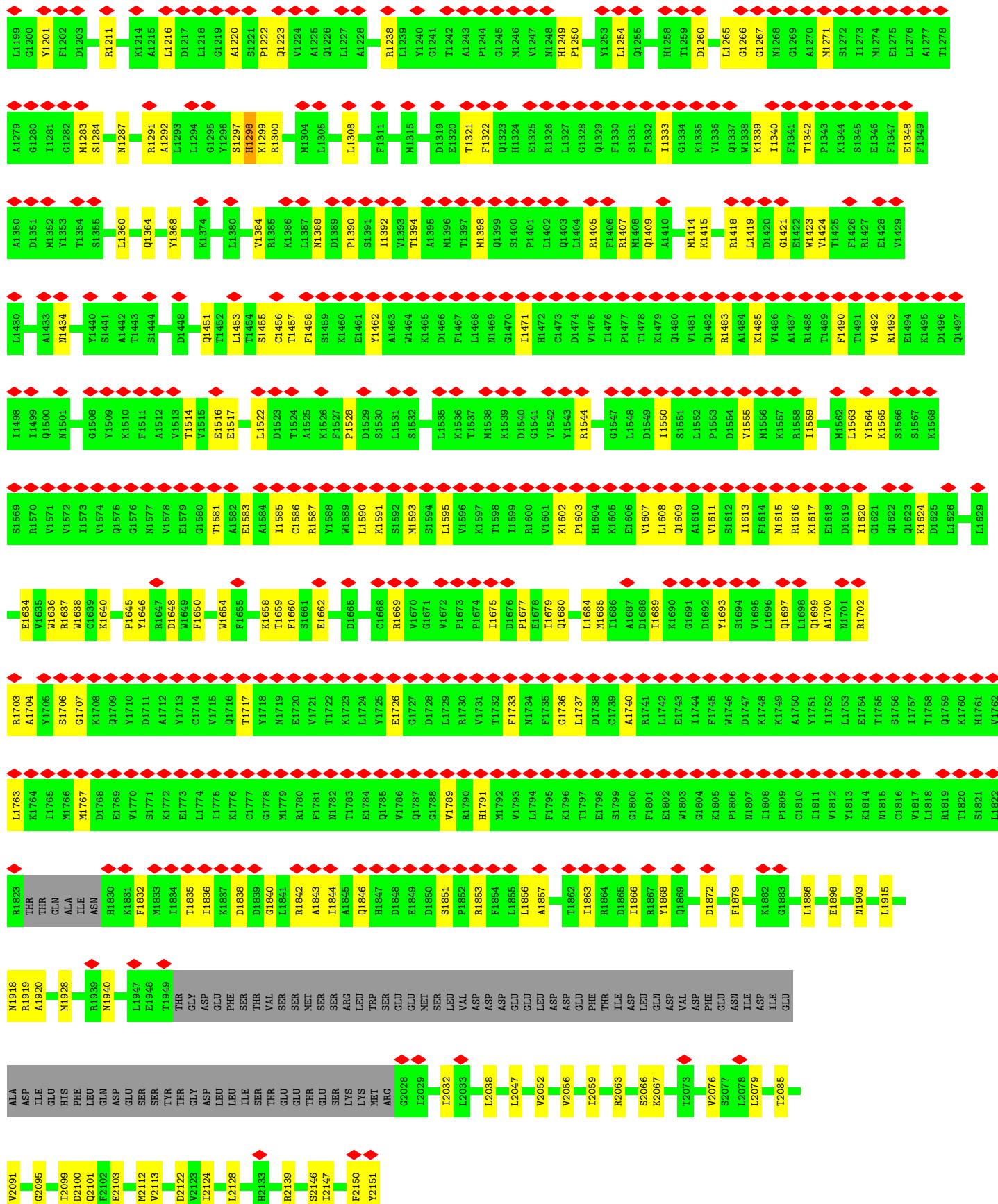




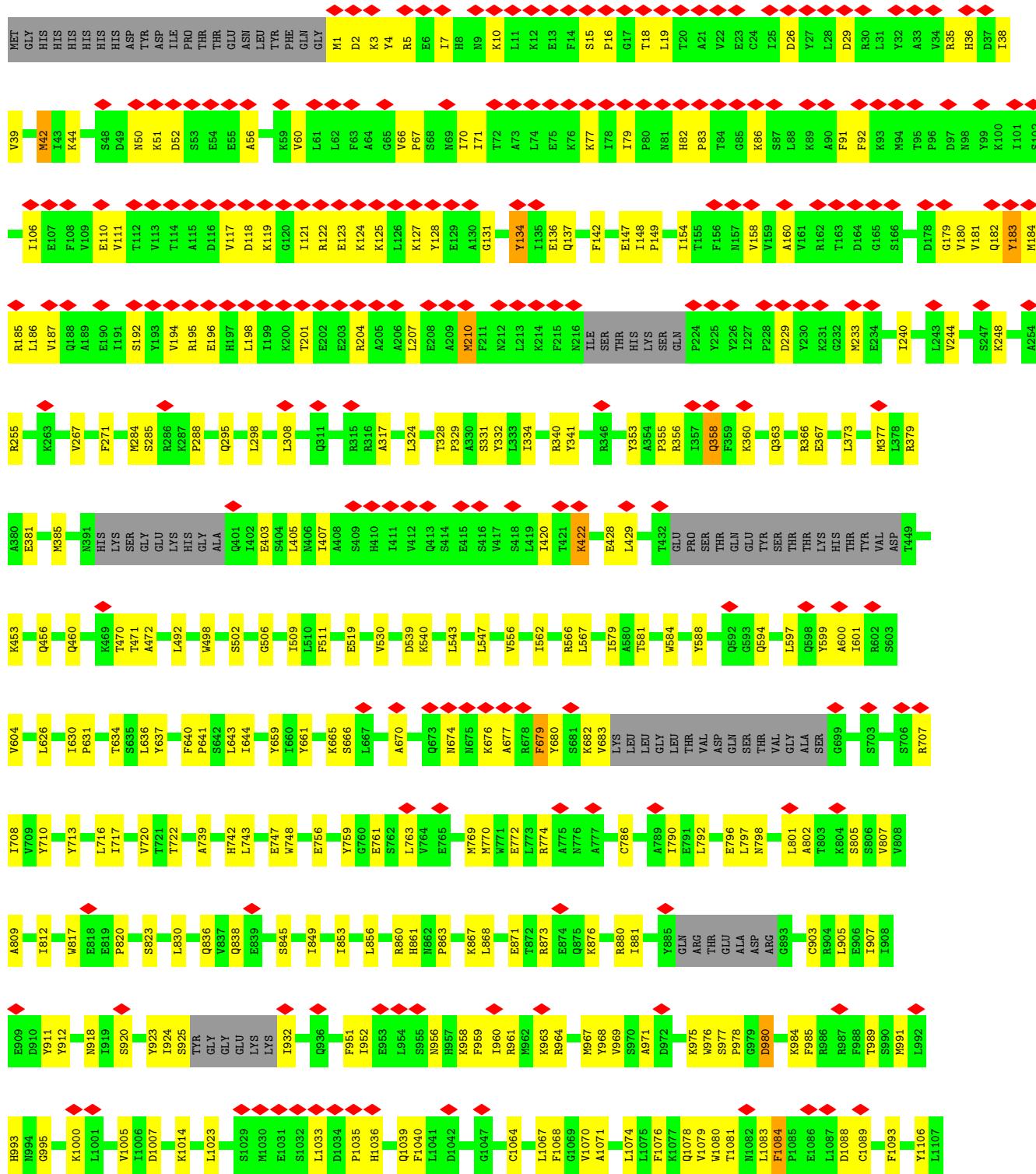


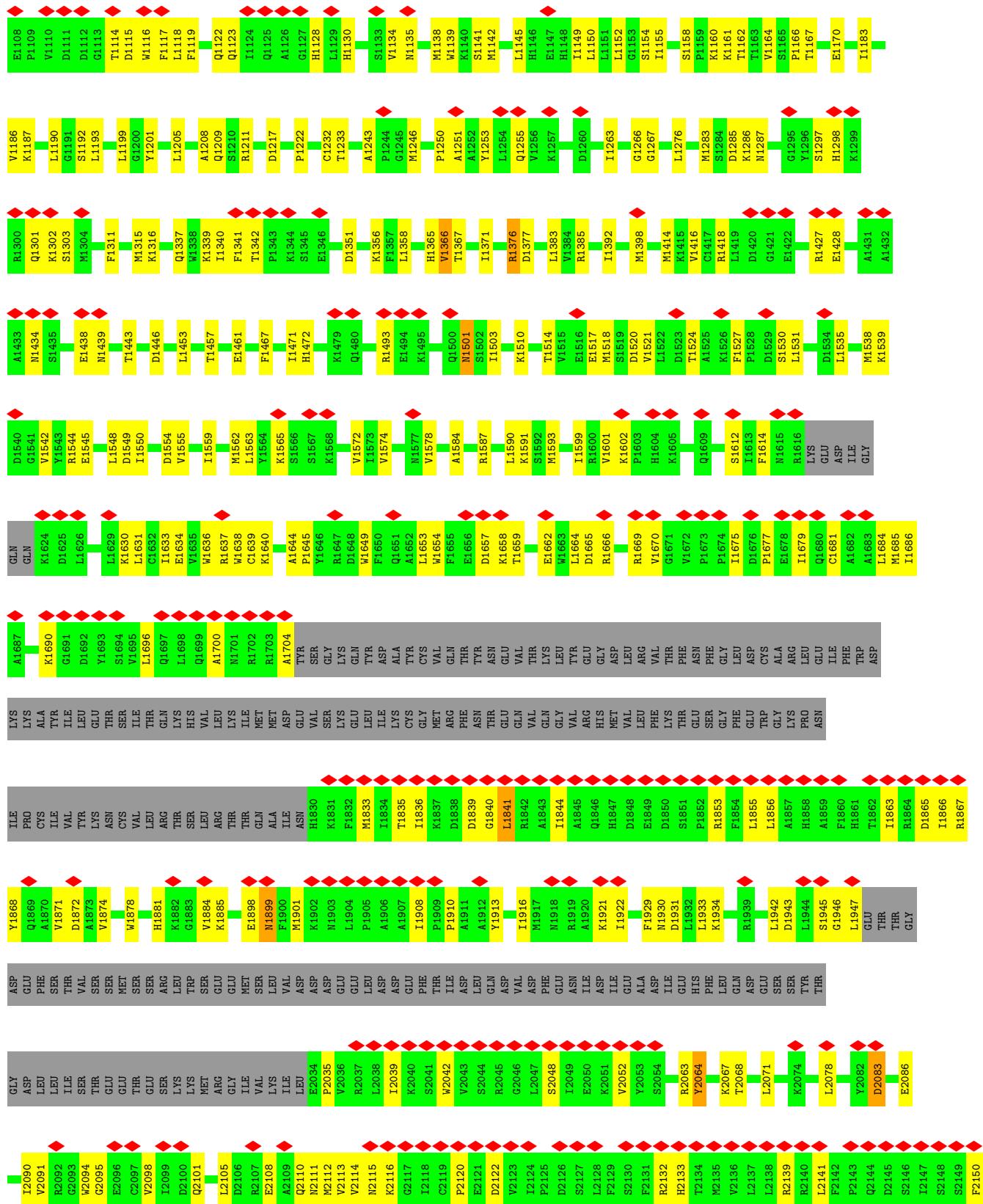




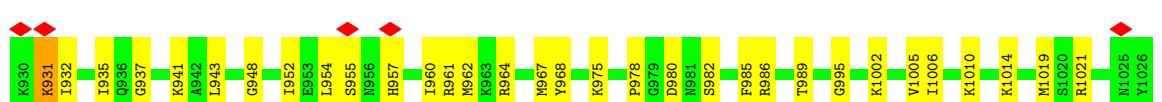
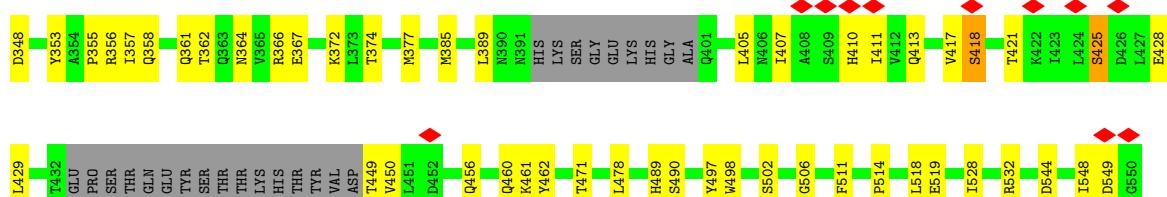
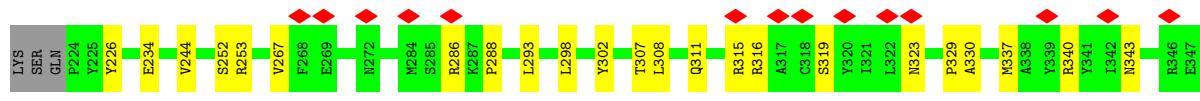


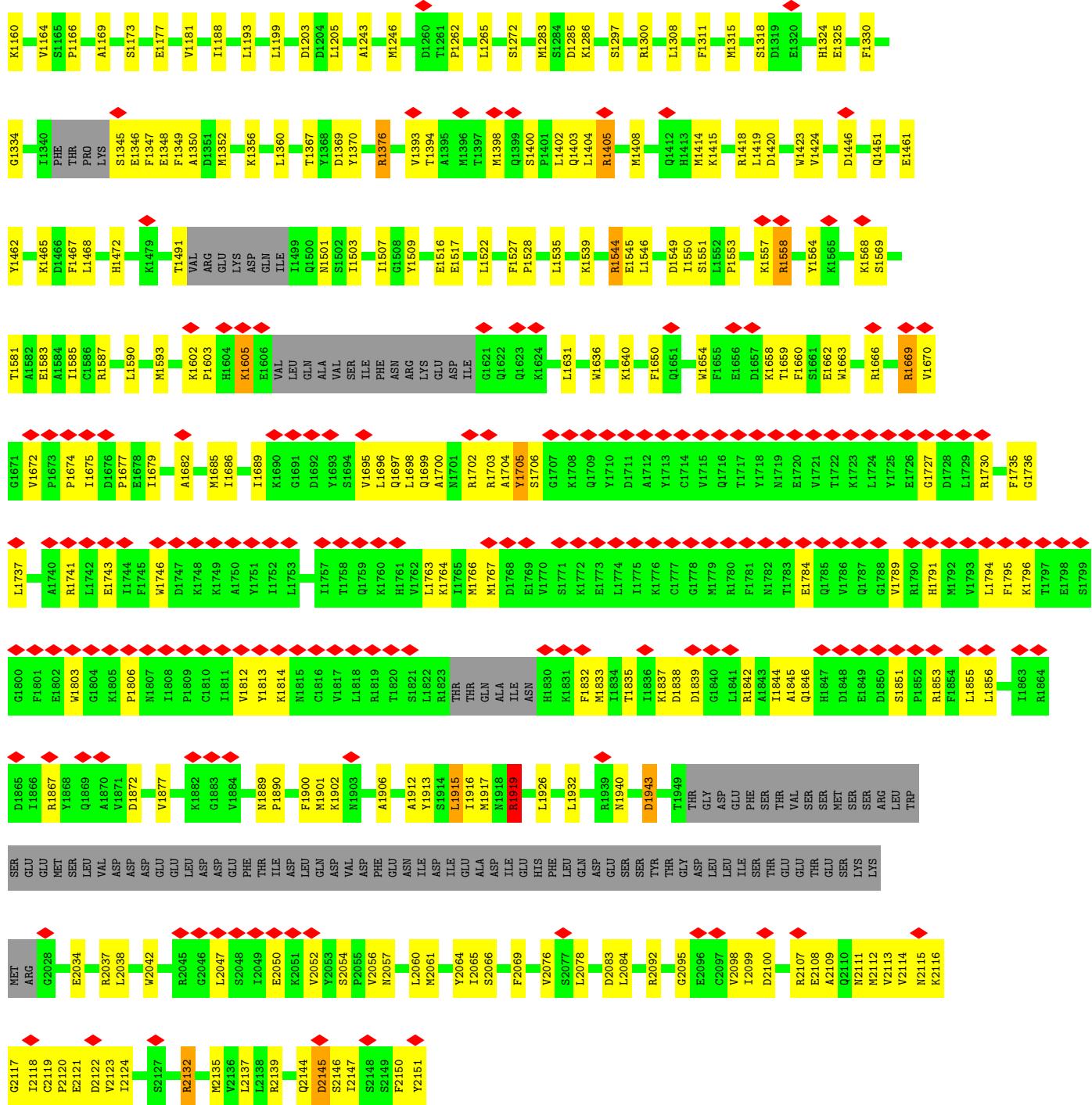
- Molecule 1: RNA-directed RNA polymerase L





- Molecule 1: RNA-directed RNA polymerase L





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	28695	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.980	Depositor
Minimum map value	-1.238	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.305	Depositor
Map size (Å)	587.3, 587.3, 587.3	wwPDB
Map dimensions	700, 700, 700	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.839, 0.839, 0.839	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	0.29	0/15469	0.49	0/20911
1	B	0.29	0/15469	0.49	0/20911
1	C	0.31	0/16505	0.49	0/22303
1	D	0.27	0/16764	0.47	0/22656
1	E	0.31	0/16505	0.49	0/22303
1	F	0.27	0/16764	0.47	0/22656
All	All	0.29	0/97476	0.48	0/131740

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	2
1	C	0	4
1	E	0	4
All	All	0	11

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	2139	ARG	Sidechain
1	B	2132	ARG	Sidechain
1	B	2139	ARG	Sidechain
1	C	162	ARG	Sidechain
1	C	185	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	C	1919	ARG	Sidechain
1	C	707	ARG	Sidechain
1	E	162	ARG	Sidechain
1	E	185	ARG	Sidechain
1	E	1919	ARG	Sidechain
1	E	707	ARG	Sidechain

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	15128	0	15210	413	0
1	B	15128	0	15210	418	0
1	C	16146	0	16240	441	0
1	D	16400	0	16506	381	0
1	E	16146	0	16240	445	0
1	F	16400	0	16506	382	0
All	All	95348	0	95912	2136	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 11.

All (2136) 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:D:196:GLU:HG3	1:C:2056:VAL:CG2	1.66	1.24
1:F:196:GLU:HG3	1:E:2056:VAL:CG2	1.66	1.23
1:D:196:GLU:HG3	1:C:2056:VAL:HG21	1.22	1.20
1:C:417:VAL:HG11	1:A:707:ARG:HB3	1.27	1.16
1:B:707:ARG:HH12	1:E:410:HIS:CE1	1.63	1.16
1:C:410:HIS:CE1	1:A:707:ARG:HH12	1.63	1.15
1:B:1302:LYS:HE3	1:A:1434:ASN:ND2	1.63	1.13
1:F:196:GLU:HG3	1:E:2056:VAL:HG21	1.22	1.13
1:B:1434:ASN:ND2	1:A:1302:LYS:HE3	1.63	1.12
1:F:2150:PHE:HB2	1:E:2113:VAL:HG21	1.19	1.10
1:D:2150:PHE:HB2	1:C:2113:VAL:HG21	1.19	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:2146:SER:HB2	1:E:2117:GLY:HA2	1.35	1.08
1:B:707:ARG:HB3	1:E:417:VAL:HG11	1.27	1.08
1:D:2146:SER:HB2	1:C:2117:GLY:HA2	1.35	1.08
1:F:205:ALA:HB2	1:E:2052:VAL:HG21	1.36	1.07
1:D:189:ALA:CB	1:C:2115:ASN:HB2	1.85	1.07
1:F:189:ALA:CB	1:E:2115:ASN:HB2	1.85	1.06
1:D:1360:LEU:HD23	1:C:2047:LEU:HD13	1.39	1.04
1:F:1514:THR:HG22	1:E:2050:GLU:CG	1.86	1.04
1:D:1514:THR:HG22	1:C:2050:GLU:HG3	1.40	1.03
1:D:1514:THR:HG22	1:C:2050:GLU:CG	1.86	1.03
1:D:205:ALA:HB2	1:C:2052:VAL:HG21	1.36	1.03
1:F:1360:LEU:HD23	1:E:2047:LEU:HD13	1.39	1.02
1:D:201:THR:HB	1:C:2124:ILE:HD13	1.43	1.01
1:F:1514:THR:HG22	1:E:2050:GLU:HG3	1.40	0.99
1:F:201:THR:HB	1:E:2124:ILE:HD13	1.43	0.99
1:D:201:THR:HB	1:C:2124:ILE:CD1	1.92	0.98
1:F:201:THR:HB	1:E:2124:ILE:CD1	1.92	0.98
1:D:2150:PHE:HE2	1:C:2118:ILE:O	1.46	0.97
1:F:2150:PHE:HE2	1:E:2118:ILE:O	1.46	0.96
1:D:2146:SER:HB2	1:C:2117:GLY:CA	1.96	0.96
1:B:597:LEU:CD1	1:E:421:THR:HG22	1.96	0.96
1:F:2146:SER:HB2	1:E:2117:GLY:CA	1.96	0.95
1:C:421:THR:HG21	1:A:599:TYR:CE1	2.02	0.94
1:B:599:TYR:CE1	1:E:421:THR:HG21	2.02	0.94
1:C:421:THR:HG22	1:A:597:LEU:CD1	1.96	0.94
1:D:2150:PHE:CB	1:C:2113:VAL:HG21	1.99	0.93
1:F:2124:ILE:HD12	1:E:204:ARG:NH2	1.84	0.92
1:F:2150:PHE:CB	1:E:2113:VAL:HG21	1.99	0.92
1:D:2124:ILE:HD12	1:C:204:ARG:NH2	1.84	0.91
1:F:164:ASP:HB3	1:E:2107:ARG:HD2	1.52	0.91
1:C:316:ARG:HE	1:E:323:ASN:HD21	1.18	0.89
1:D:164:ASP:HB3	1:C:2107:ARG:HD2	1.52	0.88
1:B:1434:ASN:ND2	1:A:1302:LYS:CE	2.37	0.88
1:C:411:ILE:HD12	1:A:674:ASN:CB	2.03	0.88
1:B:674:ASN:HB2	1:E:411:ILE:HD12	1.57	0.87
1:F:193:TYR:HB2	1:E:2116:LYS:HD3	1.56	0.87
1:F:133:THR:HG22	1:F:137:GLN:HE22	1.40	0.87
1:C:411:ILE:HD12	1:A:674:ASN:HB2	1.57	0.87
1:C:759:TYR:HB3	1:C:763:LEU:HD23	1.57	0.87
1:C:323:ASN:HD21	1:E:316:ARG:HE	1.18	0.86
1:B:674:ASN:CB	1:E:411:ILE:HD12	2.03	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2150:PHE:HB2	1:C:2113:VAL:CG2	2.05	0.86
1:B:1302:LYS:CE	1:A:1434:ASN:ND2	2.37	0.86
1:E:759:TYR:HB3	1:E:763:LEU:HD23	1.57	0.86
1:D:193:TYR:HB2	1:C:2116:LYS:HD3	1.56	0.86
1:B:1434:ASN:HD21	1:A:1302:LYS:HE3	1.41	0.85
1:C:411:ILE:HG21	1:A:674:ASN:HD22	1.42	0.85
1:D:133:THR:HG22	1:D:137:GLN:HE22	1.40	0.84
1:B:2151:TYR:HE1	1:A:2113:VAL:HG11	1.42	0.84
1:D:2047:LEU:HD12	1:C:1360:LEU:CD2	2.07	0.84
1:F:2150:PHE:HB2	1:E:2113:VAL:CG2	2.05	0.84
1:B:1503:ILE:HD13	1:B:1563:LEU:HB3	1.60	0.84
1:A:1503:ILE:HD13	1:A:1563:LEU:HB3	1.60	0.83
1:B:674:ASN:HD22	1:E:411:ILE:HG21	1.42	0.83
1:C:411:ILE:HG21	1:A:674:ASN:ND2	1.92	0.83
1:B:674:ASN:ND2	1:E:411:ILE:HG21	1.92	0.83
1:B:707:ARG:HB3	1:E:417:VAL:CG1	2.09	0.83
1:F:2047:LEU:HD12	1:E:1360:LEU:CD2	2.07	0.83
1:B:2113:VAL:HG11	1:A:2151:TYR:HE1	1.42	0.82
1:F:2150:PHE:CE2	1:E:2118:ILE:O	2.32	0.82
1:B:1434:ASN:HD21	1:A:1302:LYS:CE	1.92	0.82
1:C:417:VAL:CG1	1:A:707:ARG:HB3	2.09	0.82
1:C:1763:LEU:HA	1:C:1766:MET:HG2	1.61	0.82
1:B:1302:LYS:HE3	1:A:1434:ASN:HD21	1.41	0.82
1:B:1302:LYS:CE	1:A:1434:ASN:HD21	1.92	0.82
1:E:1763:LEU:HA	1:E:1766:MET:HG2	1.61	0.81
1:D:2147:ILE:HD12	1:C:2114:VAL:HG13	1.61	0.81
1:F:2147:ILE:HD12	1:E:2114:VAL:HG13	1.61	0.81
1:D:2150:PHE:CE2	1:C:2118:ILE:O	2.32	0.81
1:B:707:ARG:NH1	1:E:410:HIS:NE2	2.30	0.80
1:B:1574:VAL:HG11	1:B:1578:VAL:HB	1.64	0.80
1:F:192:SER:OG	1:E:2112:MET:HB3	1.82	0.80
1:A:1574:VAL:HG11	1:A:1578:VAL:HB	1.64	0.79
1:C:410:HIS:NE2	1:A:707:ARG:NH1	2.30	0.79
1:D:192:SER:OG	1:C:2112:MET:HB3	1.82	0.79
1:B:707:ARG:NH1	1:E:410:HIS:CE1	2.48	0.79
1:B:2064:TYR:HB2	1:A:2150:PHE:CE1	2.18	0.79
1:C:323:ASN:ND2	1:E:316:ARG:HE	1.82	0.78
1:C:410:HIS:CE1	1:A:707:ARG:NH1	2.48	0.78
1:F:1700:ALA:HA	1:F:1704:ALA:HB3	1.66	0.77
1:B:2150:PHE:CE1	1:A:2064:TYR:HB2	2.18	0.77
1:C:316:ARG:HE	1:E:323:ASN:ND2	1.82	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:182:GLN:O	1:F:186:LEU:HD13	1.85	0.77
1:D:193:TYR:CB	1:C:2116:LYS:HD3	2.14	0.77
1:D:189:ALA:HB2	1:C:2115:ASN:HB2	1.67	0.77
1:F:193:TYR:CB	1:E:2116:LYS:HD3	2.14	0.77
1:D:2052:VAL:HG21	1:C:205:ALA:HB2	1.67	0.77
1:D:589:THR:HG21	1:D:1595:LEU:HB3	1.67	0.76
1:D:1700:ALA:HA	1:D:1704:ALA:HB3	1.66	0.76
1:C:954:LEU:HD12	1:C:955:SER:H	1.51	0.76
1:F:2052:VAL:HG21	1:E:205:ALA:HB2	1.67	0.76
1:D:182:GLN:O	1:D:186:LEU:HD13	1.85	0.76
1:F:589:THR:HG21	1:F:1595:LEU:HB3	1.67	0.75
1:B:599:TYR:HE1	1:E:421:THR:HG21	1.51	0.75
1:E:954:LEU:HD12	1:E:955:SER:H	1.51	0.75
1:C:421:THR:HG21	1:A:599:TYR:HE1	1.51	0.75
1:D:2124:ILE:HD12	1:C:204:ARG:HH22	1.52	0.74
1:A:1199:LEU:HA	1:A:1340:ILE:HD11	1.69	0.74
1:D:927:GLY:HA2	1:D:931:LYS:HB3	1.69	0.74
1:F:188:GLN:NE2	1:E:2108:GLU:HG3	2.03	0.74
1:F:201:THR:CB	1:E:2124:ILE:HD13	2.18	0.74
1:D:1636:TRP:HH2	1:D:1684:LEU:HD22	1.53	0.74
1:A:127:LYS:HG3	1:A:128:TYR:HD1	1.53	0.74
1:D:188:GLN:NE2	1:C:2108:GLU:HG3	2.03	0.73
1:C:411:ILE:CD1	1:A:674:ASN:CB	2.66	0.73
1:C:2095:GLY:HA2	1:C:2098:VAL:HG22	1.70	0.73
1:B:2113:VAL:HG11	1:A:2151:TYR:CE1	2.23	0.73
1:B:1199:LEU:HA	1:B:1340:ILE:HD11	1.69	0.73
1:F:1675:ILE:HG22	1:F:1677:PRO:HD2	1.70	0.73
1:D:1675:ILE:HG22	1:D:1677:PRO:HD2	1.70	0.73
1:F:927:GLY:HA2	1:F:931:LYS:HB3	1.69	0.73
1:F:2146:SER:CB	1:E:2118:ILE:H	2.02	0.73
1:E:2095:GLY:HA2	1:E:2098:VAL:HG22	1.70	0.73
1:D:16:PRO:HB2	1:C:2122:ASP:CG	2.09	0.73
1:B:2151:TYR:CE1	1:A:2113:VAL:HG11	2.23	0.73
1:F:16:PRO:HB2	1:E:2122:ASP:CG	2.09	0.73
1:E:1557:LYS:HG3	1:E:1558:ARG:HG2	1.71	0.73
1:D:759:TYR:HB3	1:D:763:LEU:HD23	1.69	0.72
1:F:189:ALA:HB2	1:E:2115:ASN:HB2	1.67	0.72
1:F:759:TYR:HB3	1:F:763:LEU:HD23	1.69	0.72
1:D:2146:SER:CB	1:C:2118:ILE:H	2.02	0.72
1:B:127:LYS:HG3	1:B:128:TYR:HD1	1.53	0.72
1:B:674:ASN:CB	1:E:411:ILE:CD1	2.66	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:201:THR:CB	1:C:2124:ILE:HD13	2.18	0.72
1:F:1636:TRP:HH2	1:F:1684:LEU:HD22	1.53	0.72
1:F:2124:ILE:HD12	1:E:204:ARG:HH22	1.52	0.72
1:C:1120:VAL:HG11	1:C:1135:ASN:HB3	1.72	0.72
1:C:1654:TRP:HB3	1:C:1872:ASP:HB3	1.72	0.72
1:D:1360:LEU:CD2	1:C:2047:LEU:HD13	2.18	0.71
1:C:1557:LYS:HG3	1:C:1558:ARG:HG2	1.71	0.71
1:E:1654:TRP:HB3	1:E:1872:ASP:HB3	1.72	0.71
1:F:2147:ILE:CD1	1:E:2114:VAL:HG22	2.20	0.71
1:D:189:ALA:CB	1:C:2115:ASN:CB	2.68	0.71
1:D:2147:ILE:CD1	1:C:2114:VAL:HG22	2.20	0.71
1:F:1360:LEU:HD23	1:E:2047:LEU:CD1	2.19	0.71
1:D:1360:LEU:HD23	1:C:2047:LEU:CD1	2.19	0.71
1:F:28:LEU:HD22	1:F:191:ILE:HG23	1.72	0.71
1:F:1492:VAL:HG13	1:F:1493:ARG:HG3	1.72	0.71
1:D:1492:VAL:HG13	1:D:1493:ARG:HG3	1.72	0.71
1:D:28:LEU:HD22	1:D:191:ILE:HG23	1.72	0.71
1:D:1364:GLN:OE1	1:C:2047:LEU:HA	1.91	0.71
1:B:759:TYR:HB3	1:B:763:LEU:HD23	1.73	0.70
1:C:2139:ARG:HH21	1:C:2144:GLN:HB3	1.56	0.70
1:C:316:ARG:NE	1:E:323:ASN:HD21	1.89	0.70
1:B:181:VAL:HB	1:B:185:ARG:HH22	1.56	0.70
1:F:1364:GLN:OE1	1:E:2047:LEU:HA	1.91	0.70
1:E:1120:VAL:HG11	1:E:1135:ASN:HB3	1.72	0.70
1:B:674:ASN:HB3	1:E:411:ILE:CD1	2.22	0.70
1:F:189:ALA:CB	1:E:2115:ASN:CB	2.68	0.70
1:F:1120:VAL:HG11	1:F:1135:ASN:HB3	1.74	0.70
1:F:1733:PHE:HB2	1:F:1740:ALA:HB3	1.74	0.70
1:A:181:VAL:HB	1:A:185:ARG:HH22	1.56	0.70
1:E:2139:ARG:HH21	1:E:2144:GLN:HB3	1.56	0.70
1:F:2124:ILE:CD1	1:E:204:ARG:NH2	2.55	0.70
1:D:1195:ASP:OD2	1:D:1211:ARG:NH1	2.22	0.69
1:C:323:ASN:HD21	1:E:316:ARG:NE	1.89	0.69
1:D:2124:ILE:CD1	1:C:204:ARG:NH2	2.55	0.69
1:D:189:ALA:HA	1:C:2112:MET:HA	1.74	0.69
1:B:2064:TYR:HB2	1:A:2150:PHE:HE1	1.55	0.69
1:F:189:ALA:HA	1:E:2112:MET:HA	1.74	0.69
1:F:1360:LEU:CD2	1:E:2047:LEU:HD13	2.18	0.69
1:B:1434:ASN:HD22	1:A:1302:LYS:HE3	1.53	0.69
1:B:2150:PHE:HE1	1:A:2064:TYR:HB2	1.55	0.69
1:F:196:GLU:HB3	1:E:2057:ASN:OD1	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2109:ALA:O	1:C:2112:MET:HG2	1.93	0.69
1:C:411:ILE:CD1	1:A:674:ASN:HB3	2.22	0.69
1:B:470:THR:HG22	1:B:472:ALA:H	1.57	0.69
1:A:470:THR:HG22	1:A:472:ALA:H	1.57	0.69
1:A:631:PRO:HD3	1:A:717:ILE:HD11	1.73	0.69
1:B:631:PRO:HD3	1:B:717:ILE:HD11	1.73	0.69
1:F:2147:ILE:HD11	1:E:2114:VAL:HG22	1.75	0.69
1:D:196:GLU:HB3	1:C:2057:ASN:OD1	1.92	0.68
1:D:1733:PHE:HB2	1:D:1740:ALA:HB3	1.74	0.68
1:A:1916:ILE:HG21	1:A:2039:ILE:HG21	1.74	0.68
1:D:1120:VAL:HG11	1:D:1135:ASN:HB3	1.74	0.68
1:E:2109:ALA:O	1:E:2112:MET:HG2	1.93	0.68
1:B:1916:ILE:HG21	1:B:2039:ILE:HG21	1.74	0.68
1:D:2147:ILE:HD11	1:C:2114:VAL:HG22	1.75	0.68
1:A:759:TYR:HB3	1:A:763:LEU:HD23	1.73	0.68
1:C:74:LEU:HA	1:C:77:LYS:HD3	1.76	0.68
1:F:1195:ASP:OD2	1:F:1211:ARG:NH1	2.22	0.68
1:D:204:ARG:NH1	1:C:2054:SER:HB2	2.10	0.67
1:C:421:THR:CG2	1:A:597:LEU:CD1	2.71	0.67
1:F:205:ALA:CB	1:E:2052:VAL:HG21	2.20	0.67
1:E:74:LEU:HA	1:E:77:LYS:HD3	1.76	0.67
1:D:1919:ARG:NH1	1:D:2085:THR:OG1	2.28	0.67
1:F:1919:ARG:NH1	1:F:2085:THR:OG1	2.28	0.67
1:A:1150:LEU:HD22	1:A:1155:ILE:HD11	1.75	0.67
1:E:1199:LEU:HD11	1:E:1394:THR:HG21	1.77	0.67
1:D:205:ALA:CB	1:C:2052:VAL:HG21	2.20	0.67
1:B:1150:LEU:HD22	1:B:1155:ILE:HD11	1.75	0.67
1:D:133:THR:O	1:D:137:GLN:NE2	2.28	0.67
1:C:1199:LEU:HD11	1:C:1394:THR:HG21	1.77	0.67
1:F:204:ARG:NH1	1:E:2054:SER:HB2	2.10	0.67
1:A:1633:ILE:HD12	1:A:1681:CYS:HB3	1.76	0.67
1:B:1439:ASN:HB3	1:B:2132:ARG:HD2	1.76	0.67
1:F:133:THR:O	1:F:137:GLN:NE2	2.28	0.67
1:B:597:LEU:CD1	1:E:421:THR:CG2	2.71	0.67
1:F:193:TYR:CD1	1:E:2116:LYS:NZ	2.61	0.67
1:E:1590:LEU:HA	1:E:1593:MET:HG3	1.77	0.67
1:B:1633:ILE:HD12	1:B:1681:CYS:HB3	1.76	0.66
1:F:189:ALA:HB2	1:E:2111:ASN:O	1.95	0.66
1:E:1400:SER:HB3	1:E:1402:LEU:HD12	1.77	0.66
1:B:1630:LYS:HG2	1:B:1863:ILE:HD12	1.76	0.66
1:D:2146:SER:HB3	1:C:2118:ILE:H	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:293:LEU:HD11	1:D:562:ILE:HG22	1.77	0.66
1:D:690:VAL:HG11	1:D:943:LEU:HD22	1.77	0.66
1:D:1321:THR:HG22	1:D:1322:PHE:H	1.60	0.66
1:F:293:LEU:HD11	1:F:562:ILE:HG22	1.77	0.66
1:A:679:PHE:HZ	1:A:1166:PRO:HD2	1.61	0.66
1:C:1590:LEU:HA	1:C:1593:MET:HG3	1.77	0.66
1:E:1675:ILE:HG22	1:E:1677:PRO:HD2	1.78	0.66
1:D:196:GLU:HG3	1:C:2056:VAL:HG23	1.73	0.66
1:B:1302:LYS:HE3	1:A:1434:ASN:HD22	1.53	0.66
1:D:164:ASP:CB	1:C:2107:ARG:HD2	2.26	0.65
1:D:189:ALA:HB2	1:C:2111:ASN:O	1.95	0.65
1:D:519:GLU:OE2	1:D:1405:ARG:NH1	2.30	0.65
1:A:1371:ILE:HG12	1:A:1524:THR:HG21	1.78	0.65
1:A:1630:LYS:HG2	1:A:1863:ILE:HD12	1.76	0.65
1:B:679:PHE:HZ	1:B:1166:PRO:HD2	1.61	0.65
1:F:690:VAL:HG11	1:F:943:LEU:HD22	1.77	0.65
1:F:1195:ASP:HB2	1:F:1398:MET:HE2	1.79	0.65
1:E:195:ARG:HG3	1:E:196:GLU:HG2	1.78	0.65
1:F:519:GLU:OE2	1:F:1405:ARG:NH1	2.30	0.65
1:F:2063:ARG:HG2	1:E:2150:PHE:CD1	2.32	0.65
1:C:1400:SER:HB3	1:C:1402:LEU:HD12	1.77	0.65
1:C:421:THR:CG2	1:A:597:LEU:HD12	2.27	0.65
1:C:1700:ALA:HA	1:C:1704:ALA:HB3	1.79	0.65
1:D:2063:ARG:HG2	1:C:2150:PHE:CD1	2.32	0.65
1:B:597:LEU:HD12	1:E:421:THR:CG2	2.27	0.65
1:B:985:PHE:HE2	1:B:1068:PHE:HB2	1.61	0.65
1:B:1921:LYS:NZ	1:B:1922:ILE:O	2.30	0.65
1:A:1868:TYR:CG	1:A:1898:GLU:HB2	2.32	0.65
1:D:117:VAL:HG13	1:D:160:ALA:HB3	1.79	0.65
1:F:1321:THR:HG22	1:F:1322:PHE:H	1.60	0.65
1:B:1868:TYR:CG	1:B:1898:GLU:HB2	2.32	0.64
1:C:1675:ILE:HG22	1:C:1677:PRO:HD2	1.78	0.64
1:A:1921:LYS:NZ	1:A:1922:ILE:O	2.30	0.64
1:F:196:GLU:HG3	1:E:2056:VAL:HG23	1.73	0.64
1:C:195:ARG:HG3	1:C:196:GLU:HG2	1.78	0.64
1:B:1371:ILE:HG12	1:B:1524:THR:HG21	1.78	0.64
1:F:117:VAL:HG13	1:F:160:ALA:HB3	1.79	0.64
1:A:1118:LEU:HG	1:A:1122:GLN:HE22	1.61	0.64
1:B:1118:LEU:HG	1:B:1122:GLN:HE22	1.61	0.64
1:C:1522:LEU:HD12	1:C:1528:PRO:HB3	1.79	0.64
1:F:164:ASP:CB	1:E:2107:ARG:HD2	2.26	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:188:GLN:CD	1:E:2108:GLU:HG3	2.18	0.64
1:D:480:ARG:HD3	1:D:1238:ARG:HH12	1.62	0.64
1:F:2146:SER:HB3	1:E:2118:ILE:H	1.61	0.64
1:D:1195:ASP:HB2	1:D:1398:MET:HE2	1.79	0.64
1:F:480:ARG:HD3	1:F:1238:ARG:HH12	1.62	0.64
1:A:626:LEU:HD22	1:A:720:VAL:HG21	1.80	0.64
1:E:1700:ALA:HA	1:E:1704:ALA:HB3	1.79	0.64
1:D:1514:THR:HB	1:C:2050:GLU:OE2	1.98	0.64
1:B:807:VAL:HG23	1:B:918:ASN:HD22	1.62	0.64
1:A:807:VAL:HG23	1:A:918:ASN:HD22	1.62	0.64
1:A:985:PHE:HE2	1:A:1068:PHE:HB2	1.61	0.64
1:E:619:LEU:HD22	1:E:660:ILE:HD12	1.80	0.64
1:F:196:GLU:CG	1:E:2056:VAL:CG2	2.61	0.63
1:F:854:ARG:NH2	1:F:1348:GLU:OE1	2.32	0.63
1:B:597:LEU:HD12	1:E:421:THR:HG22	1.79	0.63
1:B:626:LEU:HD22	1:B:720:VAL:HG21	1.80	0.63
1:B:1183:ILE:HD11	1:B:1187:LYS:HD3	1.81	0.63
1:D:193:TYR:CD1	1:C:2116:LYS:NZ	2.61	0.63
1:F:1192:SER:HA	1:F:1211:ARG:HD2	1.81	0.63
1:D:188:GLN:CD	1:C:2108:GLU:HG3	2.18	0.63
1:E:1522:LEU:HD12	1:E:1528:PRO:HB3	1.79	0.63
1:B:876:LYS:HE3	1:B:1014:LYS:HB3	1.81	0.63
1:F:1514:THR:HB	1:E:2050:GLU:OE2	1.98	0.63
1:D:196:GLU:CG	1:C:2056:VAL:CG2	2.61	0.63
1:D:201:THR:HB	1:C:2124:ILE:HD12	1.79	0.63
1:B:1675:ILE:HG22	1:B:1677:PRO:HD2	1.81	0.63
1:F:2047:LEU:CD1	1:E:1360:LEU:CD2	2.77	0.63
1:D:1192:SER:HA	1:D:1211:ARG:HD2	1.81	0.63
1:D:2047:LEU:CD1	1:C:1360:LEU:CD2	2.77	0.63
1:B:674:ASN:HD22	1:E:411:ILE:CD1	2.12	0.63
1:A:1636:TRP:CE3	1:A:1685:MET:HG3	2.34	0.63
1:D:854:ARG:NH2	1:D:1348:GLU:OE1	2.32	0.62
1:B:1302:LYS:NZ	1:A:1434:ASN:HD21	1.98	0.62
1:C:114:THR:O	1:C:162:ARG:HA	1.99	0.62
1:C:411:ILE:CD1	1:A:674:ASN:HD22	2.12	0.62
1:F:2146:SER:CB	1:E:2118:ILE:N	2.62	0.62
1:B:1514:THR:HB	1:B:1517:GLU:HB2	1.81	0.62
1:C:421:THR:HG22	1:A:597:LEU:HD13	1.81	0.62
1:D:42:MET:SD	1:D:180:VAL:HG11	2.40	0.62
1:B:1251:ALA:O	1:A:1302:LYS:N	2.29	0.62
1:B:1542:VAL:HG21	1:B:1550:ILE:HD11	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:619:LEU:HD22	1:C:660:ILE:HD12	1.80	0.62
1:F:2047:LEU:HD12	1:E:1360:LEU:HD21	1.82	0.62
1:A:1250:PRO:HG3	1:A:1266:GLY:O	1.99	0.62
1:D:2047:LEU:HD12	1:C:1360:LEU:HD21	1.82	0.62
1:B:1636:TRP:CE3	1:B:1685:MET:HG3	2.34	0.62
1:F:1414:MET:HG2	1:F:1415:LYS:H	1.64	0.62
1:D:1414:MET:HG2	1:D:1415:LYS:H	1.64	0.62
1:D:2146:SER:CB	1:C:2118:ILE:N	2.62	0.62
1:B:1250:PRO:HG3	1:B:1266:GLY:O	1.99	0.62
1:F:42:MET:SD	1:F:180:VAL:HG11	2.40	0.62
1:E:114:THR:O	1:E:162:ARG:HA	1.99	0.62
1:B:722:THR:HG23	1:B:1186:VAL:HG21	1.82	0.62
1:F:1384:VAL:O	1:F:1388:ASN:ND2	2.33	0.62
1:C:952:ILE:HG12	1:C:960:ILE:HB	1.81	0.62
1:C:967:MET:HG3	1:C:1166:PRO:HA	1.82	0.62
1:A:969:VAL:HG13	1:A:1164:VAL:HG12	1.82	0.62
1:D:16:PRO:HB3	1:D:197:HIS:CD2	2.36	0.61
1:A:1183:ILE:HD11	1:A:1187:LYS:HD3	1.81	0.61
1:E:967:MET:HG3	1:E:1166:PRO:HA	1.82	0.61
1:F:1863:ILE:HG13	1:F:1866:ILE:HD11	1.83	0.61
1:E:952:ILE:HG12	1:E:960:ILE:HB	1.81	0.61
1:B:1302:LYS:N	1:A:1251:ALA:O	2.29	0.61
1:A:1514:THR:HB	1:A:1517:GLU:HB2	1.81	0.61
1:A:1675:ILE:HG22	1:A:1677:PRO:HD2	1.81	0.61
1:A:830:LEU:HD11	1:A:1392:ILE:HG23	1.82	0.61
1:B:195:ARG:HH12	1:B:204:ARG:HH22	1.48	0.61
1:A:876:LYS:HE3	1:A:1014:LYS:HB3	1.81	0.61
1:B:52:ASP:N	1:B:52:ASP:OD1	2.34	0.61
1:A:1542:VAL:HG21	1:A:1550:ILE:HD11	1.81	0.61
1:D:184:MET:O	1:D:187:VAL:HG22	2.01	0.61
1:D:197:HIS:HE1	1:C:2119:CYS:H	1.48	0.61
1:D:293:LEU:HD22	1:D:566:ARG:HD3	1.82	0.61
1:B:1434:ASN:HD21	1:A:1302:LYS:NZ	1.98	0.61
1:F:197:HIS:HE1	1:E:2119:CYS:H	1.48	0.61
1:B:597:LEU:HD13	1:E:421:THR:HG22	1.81	0.60
1:B:975:LYS:NZ	1:B:976:TRP:O	2.33	0.60
1:C:456:GLN:HA	1:C:460:GLN:HB3	1.83	0.60
1:E:763:LEU:HD11	1:E:768:TYR:HB3	1.83	0.60
1:E:1682:ALA:HA	1:E:1685:MET:HG2	1.83	0.60
1:C:763:LEU:HD11	1:C:768:TYR:HB3	1.83	0.60
1:F:164:ASP:HB3	1:E:2107:ARG:CD	2.30	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1638:TRP:HZ2	1:F:2032:ILE:HD12	1.66	0.60
1:A:975:LYS:NZ	1:A:976:TRP:O	2.33	0.60
1:C:1784:GLU:HB2	1:C:1814:LYS:HE3	1.83	0.60
1:F:16:PRO:HB3	1:F:197:HIS:CD2	2.36	0.60
1:D:1384:VAL:O	1:D:1388:ASN:ND2	2.33	0.60
1:C:184:MET:HA	1:C:187:VAL:HG22	1.83	0.60
1:C:2060:LEU:HD12	1:C:2123:VAL:HG11	1.83	0.60
1:F:293:LEU:HD22	1:F:566:ARG:HD3	1.82	0.60
1:A:722:THR:HG23	1:A:1186:VAL:HG21	1.82	0.60
1:B:631:PRO:HA	1:B:634:THR:HG22	1.84	0.60
1:B:920:SER:HA	1:B:924:ILE:HB	1.84	0.60
1:F:184:MET:O	1:F:187:VAL:HG22	2.01	0.60
1:B:1657:ASP:OD1	1:B:1657:ASP:N	2.35	0.60
1:A:1640:LYS:NZ	1:A:1839:ASP:O	2.34	0.60
1:E:1784:GLU:HB2	1:E:1814:LYS:HE3	1.83	0.60
1:D:1863:ILE:HG13	1:D:1866:ILE:HD11	1.83	0.60
1:B:830:LEU:HD11	1:B:1392:ILE:HG23	1.82	0.60
1:F:329:PRO:HB3	1:F:381:GLU:HB3	1.84	0.60
1:A:1654:TRP:HB2	1:A:1874:VAL:HG23	1.83	0.60
1:D:1638:TRP:HZ2	1:D:2032:ILE:HD12	1.66	0.60
1:D:2124:ILE:CD1	1:C:204:ARG:HH21	2.14	0.60
1:B:969:VAL:HG13	1:B:1164:VAL:HG12	1.82	0.60
1:E:182:GLN:O	1:E:186:LEU:HG	2.02	0.60
1:B:1255:GLN:HE21	1:A:1302:LYS:HZ2	1.49	0.59
1:C:182:GLN:O	1:C:186:LEU:HG	2.02	0.59
1:C:1835:THR:HB	1:C:1844:ILE:HG13	1.83	0.59
1:D:329:PRO:HB3	1:D:381:GLU:HB3	1.84	0.59
1:D:2150:PHE:CZ	1:C:2120:PRO:HA	2.37	0.59
1:F:2150:PHE:CZ	1:E:2120:PRO:HA	2.37	0.59
1:E:348:ASP:OD2	1:E:364:ASN:ND2	2.35	0.59
1:D:189:ALA:HB1	1:C:2115:ASN:HB2	1.82	0.59
1:D:195:ARG:NH2	1:C:2108:GLU:OE2	2.36	0.59
1:F:201:THR:HB	1:E:2124:ILE:HD12	1.79	0.59
1:A:1286:LYS:NZ	1:A:1461:GLU:OE1	2.34	0.59
1:E:1835:THR:HB	1:E:1844:ILE:HG13	1.83	0.59
1:B:1286:LYS:NZ	1:B:1461:GLU:OE1	2.34	0.59
1:F:722:THR:HG23	1:F:1186:VAL:HG21	1.85	0.59
1:A:1339:LYS:N	1:A:1416:VAL:O	2.35	0.59
1:A:636:LEU:HD11	1:A:1166:PRO:HD2	1.84	0.59
1:E:456:GLN:HA	1:E:460:GLN:HB3	1.83	0.59
1:B:742:HIS:HB3	1:B:1040:PHE:HZ	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1654:TRP:HB2	1:B:1874:VAL:HG23	1.83	0.59
1:C:337:MET:HE1	1:C:511:PHE:HB3	1.85	0.59
1:D:722:THR:HG23	1:D:1186:VAL:HG21	1.85	0.59
1:C:1682:ALA:HA	1:C:1685:MET:HG2	1.83	0.59
1:B:861:HIS:HA	1:B:1376:ARG:HG2	1.84	0.59
1:C:421:THR:HG22	1:A:597:LEU:HD12	1.79	0.59
1:D:340:ARG:NH1	1:D:372:LYS:O	2.36	0.59
1:F:1514:THR:CG2	1:E:2050:GLU:OE2	2.51	0.59
1:A:195:ARG:HH12	1:A:204:ARG:HH22	1.48	0.59
1:A:920:SER:HA	1:A:924:ILE:HB	1.84	0.59
1:E:184:MET:HA	1:E:187:VAL:HG22	1.83	0.59
1:D:1514:THR:CG2	1:C:2050:GLU:OE2	2.51	0.58
1:E:2060:LEU:HD12	1:E:2123:VAL:HG11	1.83	0.58
1:D:954:LEU:HB2	1:D:958:LYS:HB2	1.85	0.58
1:F:487:ILE:HG21	1:F:1407:ARG:HE	1.68	0.58
1:B:1251:ALA:O	1:A:1301:GLN:HA	2.03	0.58
1:A:631:PRO:HA	1:A:634:THR:HG22	1.84	0.58
1:A:742:HIS:HB3	1:A:1040:PHE:HZ	1.67	0.58
1:D:196:GLU:CG	1:C:2056:VAL:HG21	2.16	0.58
1:F:51:LYS:NZ	1:F:99:TYR:O	2.33	0.58
1:F:340:ARG:NH1	1:F:372:LYS:O	2.36	0.58
1:E:337:MET:HE1	1:E:511:PHE:HB3	1.85	0.58
1:B:66:VAL:HG22	1:B:70:ILE:HD11	1.86	0.58
1:A:1700:ALA:HA	1:A:1704:ALA:HB3	1.85	0.58
1:B:1301:GLN:HA	1:A:1251:ALA:O	2.03	0.58
1:A:923:TYR:HE1	1:A:1074:LEU:HD11	1.69	0.58
1:D:1364:GLN:OE1	1:C:2047:LEU:CA	2.52	0.58
1:A:52:ASP:OD1	1:A:52:ASP:N	2.34	0.58
1:B:329:PRO:HA	1:B:332:TYR:HD2	1.69	0.58
1:B:836:GLN:O	1:B:838:GLN:NE2	2.36	0.58
1:F:195:ARG:NH2	1:E:2108:GLU:OE2	2.36	0.58
1:F:205:ALA:HB2	1:E:2052:VAL:CG2	2.24	0.58
1:F:599:TYR:HB2	1:F:707:ARG:HH22	1.69	0.58
1:B:118:ASP:OD1	1:B:119:LYS:N	2.37	0.58
1:B:636:LEU:HD11	1:B:1166:PRO:HD2	1.84	0.58
1:B:742:HIS:HB3	1:B:1040:PHE:CZ	2.39	0.58
1:C:348:ASP:OD2	1:C:364:ASN:ND2	2.35	0.58
1:C:985:PHE:O	1:C:989:THR:HG22	2.04	0.58
1:F:2124:ILE:CD1	1:E:204:ARG:HH21	2.14	0.58
1:B:670:ALA:HB1	1:E:411:ILE:HG13	1.85	0.58
1:B:1302:LYS:HZ2	1:A:1255:GLN:HE21	1.52	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:882:VAL:HG12	1:C:896:ILE:HG23	1.86	0.58
1:A:136:GLU:OE1	1:A:154:ILE:N	2.34	0.58
1:A:861:HIS:HA	1:A:1376:ARG:HG2	1.84	0.58
1:C:411:ILE:HG13	1:A:670:ALA:HB1	1.85	0.57
1:F:972:ASP:HA	1:F:1099:ASP:HA	1.86	0.57
1:A:980:ASP:OD1	1:A:984:LYS:NZ	2.37	0.57
1:F:884:LYS:HB2	1:F:887:ARG:HD3	1.85	0.57
1:F:954:LEU:HB2	1:F:958:LYS:HB2	1.85	0.57
1:A:1192:SER:HA	1:A:1211:ARG:HD3	1.86	0.57
1:C:117:VAL:HG13	1:C:160:ALA:HB3	1.87	0.57
1:B:1339:LYS:N	1:B:1416:VAL:O	2.35	0.57
1:F:792:LEU:O	1:F:796:GLU:HG2	2.04	0.57
1:A:66:VAL:HG22	1:A:70:ILE:HD11	1.86	0.57
1:A:119:LYS:HA	1:A:122:ARG:HE	1.70	0.57
1:B:923:TYR:HE1	1:B:1074:LEU:HD11	1.69	0.57
1:B:1192:SER:HA	1:B:1211:ARG:HD3	1.86	0.57
1:C:579:ILE:HD12	1:C:1193:LEU:HD11	1.85	0.57
1:D:487:ILE:HG21	1:D:1407:ARG:HE	1.68	0.57
1:D:972:ASP:HA	1:D:1099:ASP:HA	1.86	0.57
1:B:379:ARG:NH2	1:B:381:GLU:OE2	2.37	0.57
1:C:690:VAL:HG11	1:C:943:LEU:HD22	1.87	0.57
1:A:118:ASP:OD1	1:A:119:LYS:N	2.37	0.57
1:D:17:GLY:HA2	1:D:199:ILE:O	2.05	0.57
1:D:599:TYR:HB2	1:D:707:ARG:HH22	1.69	0.57
1:D:884:LYS:HB2	1:D:887:ARG:HD3	1.85	0.57
1:B:1700:ALA:HA	1:B:1704:ALA:HB3	1.85	0.57
1:F:196:GLU:CG	1:E:2056:VAL:HG21	2.16	0.57
1:F:1364:GLN:OE1	1:E:2047:LEU:CA	2.52	0.57
1:A:562:ILE:HD11	1:A:567:LEU:HD13	1.87	0.57
1:A:820:PRO:HB2	1:A:823:SER:HB3	1.87	0.57
1:D:1360:LEU:CD2	1:C:2047:LEU:CD1	2.80	0.57
1:A:329:PRO:HA	1:A:332:TYR:HD2	1.69	0.57
1:B:562:ILE:HD11	1:B:567:LEU:HD13	1.87	0.57
1:B:980:ASP:OD1	1:B:984:LYS:NZ	2.37	0.57
1:F:189:ALA:HB1	1:E:2115:ASN:HB2	1.82	0.57
1:A:836:GLN:O	1:A:838:GLN:NE2	2.36	0.57
1:E:728:GLU:HG3	1:E:730:GLY:H	1.69	0.57
1:E:842:HIS:CG	1:E:1021:ARG:HE	2.22	0.57
1:D:792:LEU:O	1:D:796:GLU:HG2	2.04	0.57
1:B:119:LYS:HA	1:B:122:ARG:HE	1.70	0.57
1:B:121:ILE:O	1:B:125:LYS:HB2	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:205:ALA:HB2	1:C:2052:VAL:CG2	2.24	0.56
1:D:1514:THR:OG1	1:D:1517:GLU:CG	2.53	0.56
1:C:621:ALA:O	1:C:625:ASN:ND2	2.37	0.56
1:C:986:ARG:HD3	1:C:1010:LYS:HG3	1.87	0.56
1:F:1360:LEU:CD2	1:E:2047:LEU:CD1	2.80	0.56
1:C:728:GLU:HG3	1:C:730:GLY:H	1.69	0.56
1:A:121:ILE:O	1:A:125:LYS:HB2	2.04	0.56
1:A:742:HIS:HB3	1:A:1040:PHE:CZ	2.39	0.56
1:A:1186:VAL:HG22	1:A:1190:LEU:HD23	1.87	0.56
1:A:1658:LYS:HD2	1:A:1662:GLU:HB3	1.87	0.56
1:E:882:VAL:HG12	1:E:896:ILE:HG23	1.86	0.56
1:D:1514:THR:OG1	1:D:1517:GLU:HG3	2.06	0.56
1:B:2110:GLN:HA	1:A:2151:TYR:OH	2.05	0.56
1:C:511:PHE:HB2	1:C:528:ILE:HG23	1.86	0.56
1:C:842:HIS:CG	1:C:1021:ARG:HE	2.22	0.56
1:C:1078:GLN:OE1	1:C:1082:ASN:ND2	2.37	0.56
1:F:17:GLY:HA2	1:F:199:ILE:O	2.05	0.56
1:F:1514:THR:OG1	1:F:1517:GLU:CG	2.53	0.56
1:A:379:ARG:NH2	1:A:381:GLU:OE2	2.37	0.56
1:A:1657:ASP:N	1:A:1657:ASP:OD1	2.35	0.56
1:E:985:PHE:O	1:E:989:THR:HG22	2.04	0.56
1:D:288:PRO:HB3	1:D:405:LEU:HD21	1.86	0.56
1:E:579:ILE:HD12	1:E:1193:LEU:HD11	1.85	0.56
1:D:649:GLU:HG3	1:D:650:ARG:HG3	1.88	0.56
1:B:1255:GLN:HE21	1:A:1302:LYS:NZ	2.03	0.56
1:F:288:PRO:HB3	1:F:405:LEU:HD21	1.86	0.56
1:F:1514:THR:OG1	1:F:1517:GLU:HG3	2.06	0.56
1:A:1453:LEU:HA	1:A:1457:THR:HG22	1.87	0.56
1:E:117:VAL:HG13	1:E:160:ALA:HB3	1.87	0.56
1:E:929:GLU:O	1:E:931:LYS:HG3	2.06	0.56
1:B:820:PRO:HB2	1:B:823:SER:HB3	1.87	0.56
1:B:1302:LYS:NZ	1:A:1255:GLN:HE21	2.03	0.56
1:C:407:ILE:O	1:C:413:GLN:NE2	2.39	0.56
1:C:2057:ASN:HA	1:C:2060:LEU:HG	1.88	0.56
1:E:511:PHE:HB2	1:E:528:ILE:HG23	1.86	0.56
1:E:621:ALA:O	1:E:625:ASN:ND2	2.37	0.56
1:B:1658:LYS:HD2	1:B:1662:GLU:HB3	1.87	0.56
1:B:2151:TYR:OH	1:A:2110:GLN:HA	2.05	0.56
1:A:229:ASP:OD1	1:A:1000:LYS:NZ	2.38	0.56
1:E:2057:ASN:HA	1:E:2060:LEU:HG	1.88	0.56
1:D:546:ILE:HD11	1:D:553:GLN:HB3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1084:PHE:HZ	1:D:1134:VAL:HG21	1.71	0.56
1:B:1640:LYS:NZ	1:B:1839:ASP:O	2.34	0.56
1:F:193:TYR:CG	1:E:2116:LYS:HD3	2.40	0.56
1:E:690:VAL:HG11	1:E:943:LEU:HD22	1.87	0.56
1:B:1453:LEU:HA	1:B:1457:THR:HG22	1.87	0.56
1:F:11:LEU:HD13	1:F:194:VAL:HG21	1.88	0.56
1:F:1084:PHE:HZ	1:F:1134:VAL:HG21	1.71	0.56
1:A:355:PRO:HD2	1:A:358:GLN:HG3	1.88	0.56
1:B:707:ARG:CB	1:E:417:VAL:HG11	2.19	0.56
1:F:381:GLU:O	1:F:385:MET:HG2	2.06	0.56
1:D:193:TYR:CG	1:C:2116:LYS:HD3	2.40	0.55
1:D:2147:ILE:CD1	1:C:2114:VAL:HG13	2.35	0.55
1:B:356:ARG:NH1	1:B:367:GLU:OE1	2.39	0.55
1:C:490:SER:HB2	1:C:518:LEU:HB2	1.87	0.55
1:C:1764:LYS:HA	1:C:1767:MET:SD	2.46	0.55
1:A:194:VAL:HG22	1:A:198:LEU:HD12	1.88	0.55
1:E:329:PRO:HB2	1:E:385:MET:HB2	1.88	0.55
1:E:883:ARG:HG3	1:E:884:LYS:H	1.71	0.55
1:E:2061:MET:N	1:E:2061:MET:SD	2.79	0.55
1:D:381:GLU:O	1:D:385:MET:HG2	2.06	0.55
1:B:2095:GLY:HA2	1:B:2098:VAL:HG22	1.88	0.55
1:C:929:GLU:O	1:C:931:LYS:HG3	2.06	0.55
1:F:649:GLU:HG3	1:F:650:ARG:HG3	1.88	0.55
1:B:880:ARG:NH1	1:B:881:ILE:O	2.40	0.55
1:B:971:ALA:HA	1:B:1162:THR:HG22	1.88	0.55
1:B:1186:VAL:HG22	1:B:1190:LEU:HD23	1.87	0.55
1:C:1544:ARG:HD2	1:C:1545:GLU:HG3	1.89	0.55
1:C:2061:MET:SD	1:C:2061:MET:N	2.79	0.55
1:F:2139:ARG:NH2	1:E:2121:GLU:OE2	2.39	0.55
1:D:164:ASP:HB3	1:C:2107:ARG:CD	2.30	0.55
1:D:2122:ASP:OD2	1:C:16:PRO:HB2	2.06	0.55
1:B:194:VAL:HG22	1:B:198:LEU:HD12	1.88	0.55
1:B:2132:ARG:HH11	1:B:2132:ARG:HB2	1.71	0.55
1:C:329:PRO:HB2	1:C:385:MET:HB2	1.88	0.55
1:C:1845:ALA:HB2	1:C:1856:LEU:HD22	1.89	0.55
1:F:459:THR:OG1	1:F:1223:GLN:OE1	2.25	0.55
1:A:356:ARG:NH1	1:A:367:GLU:OE1	2.39	0.55
1:E:36:HIS:NE2	1:E:111:VAL:O	2.36	0.55
1:E:490:SER:HB2	1:E:518:LEU:HB2	1.87	0.55
1:D:876:LYS:HE3	1:D:1014:LYS:HB3	1.89	0.55
1:B:136:GLU:OE1	1:B:154:ILE:N	2.34	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:ASP:OD1	1:B:1000:LYS:NZ	2.38	0.55
1:F:1115:ASP:OD1	1:F:1116:TRP:N	2.40	0.55
1:E:1509:TYR:HD2	1:E:1535:LEU:HD12	1.72	0.55
1:B:674:ASN:ND2	1:E:411:ILE:HD13	2.22	0.55
1:C:417:VAL:HG11	1:A:707:ARG:CB	2.19	0.55
1:C:584:TRP:NE1	1:C:719:GLU:OE2	2.39	0.55
1:E:407:ILE:O	1:E:413:GLN:NE2	2.39	0.55
1:B:812:ILE:O	1:B:817:TRP:NE1	2.34	0.55
1:F:2146:SER:CB	1:E:2117:GLY:CA	2.80	0.55
1:A:880:ARG:NH1	1:A:881:ILE:O	2.40	0.55
1:A:971:ALA:HA	1:A:1162:THR:HG22	1.88	0.55
1:A:1945:SER:OG	1:A:1946:GLY:N	2.39	0.55
1:E:833:MET:HG2	1:E:851:GLU:HG3	1.89	0.55
1:E:986:ARG:HD3	1:E:1010:LYS:HG3	1.87	0.55
1:E:1078:GLN:OE1	1:E:1082:ASN:ND2	2.37	0.55
1:B:1554:ASP:OD1	1:B:1554:ASP:N	2.39	0.55
1:D:2139:ARG:NH2	1:C:2121:GLU:OE2	2.39	0.55
1:B:1544:ARG:NH1	1:B:1545:GLU:OE2	2.40	0.55
1:F:189:ALA:CA	1:E:2112:MET:HA	2.37	0.55
1:A:925:SER:HG	1:A:932:ILE:N	2.05	0.55
1:E:1262:PRO:HB2	1:E:1265:LEU:HD12	1.89	0.55
1:C:883:ARG:HG3	1:C:884:LYS:H	1.71	0.55
1:C:1419:LEU:HG	1:C:1420:ASP:H	1.72	0.55
1:C:1509:TYR:HD2	1:C:1535:LEU:HD12	1.72	0.55
1:C:1789:VAL:HG12	1:C:1791:HIS:H	1.72	0.55
1:A:1115:ASP:OD1	1:A:1115:ASP:N	2.40	0.55
1:A:1544:ARG:NH1	1:A:1545:GLU:OE2	2.40	0.55
1:E:1764:LYS:HA	1:E:1767:MET:SD	2.46	0.55
1:B:148:ILE:HG13	1:B:149:PRO:HD2	1.90	0.54
1:F:546:ILE:HD11	1:F:553:GLN:HB3	1.87	0.54
1:F:2122:ASP:OD2	1:E:16:PRO:HB2	2.06	0.54
1:A:1076:PHE:HD1	1:A:1149:ILE:HD11	1.72	0.54
1:A:2095:GLY:HA2	1:A:2098:VAL:HG22	1.88	0.54
1:E:1926:LEU:HD21	1:E:2076:VAL:HG21	1.88	0.54
1:B:355:PRO:HD2	1:B:358:GLN:HG3	1.88	0.54
1:B:925:SER:HG	1:B:932:ILE:N	2.05	0.54
1:C:1659:THR:HG23	1:C:1662:GLU:H	1.72	0.54
1:F:1650:PHE:CD1	1:F:1660:PHE:HB3	2.43	0.54
1:A:1844:ILE:HG22	1:A:1855:LEU:HA	1.89	0.54
1:A:2108:GLU:O	1:A:2112:MET:HG2	2.08	0.54
1:E:1419:LEU:HG	1:E:1420:ASP:H	1.72	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1890:PRO:HB2	1:E:1916:ILE:HD11	1.89	0.54
1:E:2135:MET:SD	1:E:2135:MET:N	2.81	0.54
1:D:912:TYR:HA	1:D:915:ILE:HG22	1.89	0.54
1:C:36:HIS:NE2	1:C:111:VAL:O	2.36	0.54
1:C:1926:LEU:HD21	1:C:2076:VAL:HG21	1.88	0.54
1:C:2135:MET:N	1:C:2135:MET:SD	2.81	0.54
1:D:11:LEU:HD13	1:D:194:VAL:HG21	1.88	0.54
1:D:459:THR:OG1	1:D:1223:GLN:OE1	2.25	0.54
1:D:2095:GLY:O	1:D:2099:ILE:HG12	2.07	0.54
1:C:411:ILE:HD13	1:A:674:ASN:ND2	2.22	0.54
1:F:876:LYS:HE3	1:F:1014:LYS:HB3	1.89	0.54
1:F:1364:GLN:OE1	1:E:2047:LEU:HB2	2.08	0.54
1:A:148:ILE:HG13	1:A:149:PRO:HD2	1.90	0.54
1:D:1084:PHE:HB3	1:D:1087:LEU:HB2	1.90	0.54
1:D:1254:LEU:HD11	1:D:1265:LEU:HD23	1.90	0.54
1:B:1192:SER:O	1:B:1192:SER:OG	2.25	0.54
1:C:2100:ASP:OD1	1:C:2100:ASP:N	2.40	0.54
1:F:912:TYR:HA	1:F:915:ILE:HG22	1.89	0.54
1:E:1845:ALA:HB2	1:E:1856:LEU:HD22	1.89	0.54
1:E:1912:ALA:HA	1:E:1915:LEU:HD23	1.88	0.54
1:F:533:ILE:HD12	1:F:540:LYS:HE2	1.90	0.54
1:D:192:SER:HA	1:D:195:ARG:CZ	2.38	0.54
1:D:1364:GLN:OE1	1:C:2047:LEU:HB2	2.08	0.54
1:D:1617:LYS:O	1:D:1620:ILE:HG13	2.08	0.54
1:B:1945:SER:OG	1:B:1946:GLY:N	2.39	0.54
1:C:288:PRO:HB3	1:C:405:LEU:HD21	1.90	0.54
1:F:246:TYR:CD1	1:F:774:ARG:HG2	2.43	0.54
1:F:2095:GLY:O	1:F:2099:ILE:HG12	2.07	0.54
1:A:1686:ILE:O	1:A:1690:LYS:HB3	2.08	0.54
1:E:1544:ARG:HD2	1:E:1545:GLU:HG3	1.89	0.54
1:E:1697:GLN:NE2	1:E:1832:PHE:O	2.41	0.54
1:E:1943:ASP:N	1:E:1943:ASP:OD1	2.36	0.54
1:D:1115:ASP:OD1	1:D:1116:TRP:N	2.40	0.54
1:B:456:GLN:HA	1:B:460:GLN:HB3	1.90	0.54
1:B:2108:GLU:O	1:B:2112:MET:HG2	2.08	0.54
1:A:798:ASN:HA	1:A:801:LEU:HB2	1.90	0.54
1:E:562:ILE:HD11	1:E:567:LEU:HD13	1.89	0.54
1:D:533:ILE:HD12	1:D:540:LYS:HE2	1.90	0.54
1:B:798:ASN:HA	1:B:801:LEU:HB2	1.90	0.54
1:B:1076:PHE:HD1	1:B:1149:ILE:HD11	1.72	0.54
1:C:581:THR:HG23	1:C:604:VAL:HG23	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1912:ALA:HA	1:C:1915:LEU:HD23	1.88	0.54
1:F:39:VAL:O	1:F:42:MET:HG2	2.08	0.54
1:E:581:THR:HG23	1:E:604:VAL:HG23	1.90	0.54
1:E:634:THR:HG21	1:E:713:TYR:CE2	2.43	0.54
1:D:189:ALA:CA	1:C:2112:MET:HA	2.37	0.54
1:F:1254:LEU:HD11	1:F:1265:LEU:HD23	1.90	0.54
1:F:1617:LYS:O	1:F:1620:ILE:HG13	2.08	0.54
1:A:456:GLN:HA	1:A:460:GLN:HB3	1.90	0.54
1:E:1472:HIS:HB3	1:E:1602:LYS:HB3	1.90	0.54
1:C:562:ILE:HD11	1:C:567:LEU:HD13	1.89	0.53
1:C:694:THR:HG22	1:C:695:VAL:H	1.73	0.53
1:C:770:MET:HG3	1:C:774:ARG:HD2	1.91	0.53
1:C:1890:PRO:HB2	1:C:1916:ILE:HD11	1.89	0.53
1:E:1705:TYR:HB2	1:E:1736:GLY:H	1.73	0.53
1:D:362:THR:OG1	1:D:365:VAL:O	2.22	0.53
1:D:456:GLN:HA	1:D:460:GLN:HB3	1.89	0.53
1:D:1697:GLN:NE2	1:D:1832:PHE:O	2.41	0.53
1:B:334:ILE:HG23	1:B:511:PHE:CZ	2.44	0.53
1:C:833:MET:HG2	1:C:851:GLU:HG3	1.89	0.53
1:C:1705:TYR:HB2	1:C:1736:GLY:H	1.73	0.53
1:A:1135:ASN:N	1:A:1135:ASN:OD1	2.42	0.53
1:A:1192:SER:OG	1:A:1192:SER:O	2.25	0.53
1:E:366:ARG:HH21	1:E:372:LYS:HD2	1.74	0.53
1:D:246:TYR:CD1	1:D:774:ARG:HG2	2.43	0.53
1:D:2146:SER:CB	1:C:2117:GLY:CA	2.80	0.53
1:B:1538:MET:HA	1:B:1614:PHE:CE2	2.44	0.53
1:C:366:ARG:HH21	1:C:372:LYS:HD2	1.74	0.53
1:C:1696:LEU:HD22	1:C:1856:LEU:HD21	1.91	0.53
1:F:192:SER:HA	1:F:195:ARG:CZ	2.38	0.53
1:A:1123:GLN:OE1	1:A:1128:HIS:ND1	2.41	0.53
1:D:1493:ARG:NH1	1:D:1565:LYS:HB3	2.24	0.53
1:B:184:MET:HA	1:B:187:VAL:HG22	1.90	0.53
1:B:1686:ILE:O	1:B:1690:LYS:HB3	2.08	0.53
1:C:707:ARG:HH22	1:A:428:GLU:HB3	1.73	0.53
1:F:1650:PHE:HD1	1:F:1660:PHE:HB3	1.73	0.53
1:F:1697:GLN:NE2	1:F:1832:PHE:O	2.41	0.53
1:A:977:SER:OG	1:A:980:ASP:OD2	2.27	0.53
1:E:2034:GLU:HG3	1:E:2037:ARG:HH21	1.73	0.53
1:B:1106:TYR:HB2	1:B:1138:MET:SD	2.49	0.53
1:C:1697:GLN:NE2	1:C:1832:PHE:O	2.41	0.53
1:A:1106:TYR:HB2	1:A:1138:MET:SD	2.49	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2150:PHE:CD2	1:C:2113:VAL:HG23	2.44	0.53
1:B:428:GLU:HB3	1:E:707:ARG:HH22	1.73	0.53
1:B:584:TRP:NE1	1:B:710:TYR:OH	2.41	0.53
1:B:873:ARG:NE	1:B:1007:ASP:OD2	2.39	0.53
1:C:1262:PRO:HB2	1:C:1265:LEU:HD12	1.89	0.53
1:F:456:GLN:HA	1:F:460:GLN:HB3	1.89	0.53
1:F:1084:PHE:HB3	1:F:1087:LEU:HB2	1.90	0.53
1:F:1654:TRP:N	1:F:1872:ASP:O	2.39	0.53
1:E:1915:LEU:HD12	1:E:1919:ARG:HD3	1.91	0.53
1:E:2100:ASP:OD1	1:E:2100:ASP:N	2.40	0.53
1:D:39:VAL:O	1:D:42:MET:HG2	2.08	0.53
1:D:1522:LEU:HD22	1:D:1528:PRO:HB3	1.91	0.53
1:D:1650:PHE:CD1	1:D:1660:PHE:HB3	2.43	0.53
1:B:1365:HIS:O	1:B:1367:THR:N	2.41	0.53
1:B:1844:ILE:HG22	1:B:1855:LEU:HA	1.89	0.53
1:F:1364:GLN:OE1	1:E:2047:LEU:CB	2.57	0.53
1:A:19:LEU:HD12	1:A:198:LEU:HB3	1.91	0.53
1:A:1554:ASP:OD1	1:A:1554:ASP:N	2.39	0.53
1:A:1881:HIS:O	1:A:1884:VAL:HG12	2.09	0.53
1:E:694:THR:HG22	1:E:695:VAL:H	1.73	0.53
1:E:1034:ASP:O	1:E:1038:LYS:HB2	2.09	0.53
1:D:182:GLN:O	1:D:186:LEU:CD1	2.57	0.53
1:D:1650:PHE:HD1	1:D:1660:PHE:HB3	1.73	0.53
1:C:2034:GLU:HG3	1:C:2037:ARG:HH21	1.73	0.53
1:E:770:MET:HG3	1:E:774:ARG:HD2	1.91	0.53
1:C:204:ARG:O	1:C:208:GLU:HG2	2.08	0.53
1:F:2150:PHE:CD2	1:E:2113:VAL:HG23	2.44	0.53
1:A:1116:TRP:NE1	1:A:1135:ASN:O	2.39	0.53
1:E:204:ARG:O	1:E:208:GLU:HG2	2.08	0.53
1:B:127:LYS:HG3	1:B:128:TYR:CD1	2.40	0.53
1:B:1135:ASN:OD1	1:B:1135:ASN:N	2.42	0.53
1:B:1930:ASN:HA	1:B:1933:LEU:HD12	1.91	0.53
1:C:20:THR:HG22	1:C:21:ALA:H	1.74	0.53
1:C:1472:HIS:HB3	1:C:1602:LYS:HB3	1.90	0.53
1:C:1796:LYS:HB2	1:C:1813:TYR:HE1	1.74	0.53
1:F:1550:ILE:HG22	1:F:1559:ILE:HD11	1.91	0.53
1:A:341:TYR:HH	1:A:353:TYR:HH	1.56	0.53
1:A:1538:MET:HA	1:A:1614:PHE:CE2	2.44	0.53
1:E:1659:THR:HG23	1:E:1662:GLU:H	1.72	0.53
1:D:1364:GLN:OE1	1:C:2047:LEU:CB	2.57	0.52
1:B:1835:THR:HB	1:B:1844:ILE:HG13	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1298:HIS:CE1	1:F:1299:LYS:HB2	2.44	0.52
1:F:2147:ILE:CD1	1:E:2114:VAL:HG13	2.35	0.52
1:A:334:ILE:HG23	1:A:511:PHE:CZ	2.44	0.52
1:A:1675:ILE:O	1:A:1679:ILE:HG13	2.09	0.52
1:E:288:PRO:HB3	1:E:405:LEU:HD21	1.90	0.52
1:E:584:TRP:NE1	1:E:719:GLU:OE2	2.39	0.52
1:B:1123:GLN:OE1	1:B:1128:HIS:ND1	2.41	0.52
1:C:1:MET:HG2	1:C:38:ILE:HG22	1.91	0.52
1:C:927:GLY:HA2	1:C:931:LYS:HE2	1.91	0.52
1:E:1789:VAL:HG12	1:E:1791:HIS:H	1.72	0.52
1:C:634:THR:HG21	1:C:713:TYR:CE2	2.43	0.52
1:C:1034:ASP:O	1:C:1038:LYS:HB2	2.09	0.52
1:A:142:PHE:HE1	1:A:147:GLU:HB3	1.75	0.52
1:A:182:GLN:O	1:A:186:LEU:HG	2.09	0.52
1:D:1297:SER:O	1:D:1299:LYS:N	2.43	0.52
1:D:1514:THR:HG1	1:D:1517:GLU:CD	2.13	0.52
1:D:2063:ARG:HG2	1:C:2150:PHE:CE1	2.45	0.52
1:F:2063:ARG:HG2	1:E:2150:PHE:CE1	2.45	0.52
1:A:1217:ASP:HB2	1:A:1572:VAL:HG12	1.91	0.52
1:A:1365:HIS:O	1:A:1367:THR:N	2.41	0.52
1:A:1835:THR:HB	1:A:1844:ILE:HG13	1.91	0.52
1:B:1633:ILE:HD13	1:B:1685:MET:SD	2.50	0.52
1:F:764:VAL:HG22	1:F:784:LEU:HD21	1.91	0.52
1:A:584:TRP:NE1	1:A:710:TYR:OH	2.41	0.52
1:E:1696:LEU:HD22	1:E:1856:LEU:HD21	1.91	0.52
1:D:429:LEU:O	1:D:471:THR:OG1	2.24	0.52
1:D:1298:HIS:CE1	1:D:1299:LYS:HB2	2.44	0.52
1:B:19:LEU:HD12	1:B:198:LEU:HB3	1.91	0.52
1:B:1659:THR:HG22	1:B:1662:GLU:HG3	1.92	0.52
1:F:182:GLN:O	1:F:186:LEU:CD1	2.57	0.52
1:F:189:ALA:HB3	1:E:2115:ASN:HB2	1.86	0.52
1:A:1659:THR:HG22	1:A:1662:GLU:HG3	1.92	0.52
1:E:20:THR:HG22	1:E:21:ALA:H	1.74	0.52
1:E:836:GLN:OE1	1:E:854:ARG:NH1	2.43	0.52
1:D:764:VAL:HG22	1:D:784:LEU:HD21	1.91	0.52
1:D:1514:THR:HG22	1:C:2050:GLU:CD	2.30	0.52
1:B:809:ALA:HB2	1:B:995:GLY:HA3	1.92	0.52
1:B:2115:ASN:OD1	1:B:2116:LYS:N	2.43	0.52
1:C:931:LYS:HD2	1:C:932:ILE:HG13	1.91	0.52
1:F:524:PHE:HB3	1:F:561:SER:HB2	1.91	0.52
1:F:1368:TYR:OH	1:F:1516:GLU:OE1	2.28	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1509:TYR:CD2	1:E:1535:LEU:HD12	2.45	0.52
1:B:1675:ILE:O	1:B:1679:ILE:HG13	2.09	0.52
1:F:1493:ARG:NH1	1:F:1565:LYS:HB3	2.24	0.52
1:A:1930:ASN:HA	1:A:1933:LEU:HD12	1.91	0.52
1:E:927:GLY:HA2	1:E:931:LYS:HE2	1.91	0.52
1:D:1514:THR:CG2	1:C:2050:GLU:CG	2.75	0.52
1:B:1115:ASP:N	1:B:1115:ASP:OD1	2.40	0.52
1:F:2147:ILE:HG13	1:E:2114:VAL:HG22	1.91	0.52
1:E:1:MET:HG2	1:E:38:ILE:HG22	1.91	0.52
1:D:1555:VAL:O	1:D:1559:ILE:HG12	2.10	0.52
1:D:1640:LYS:NZ	1:D:1840:GLY:O	2.43	0.52
1:B:36:HIS:NE2	1:B:111:VAL:O	2.40	0.52
1:B:123:GLU:O	1:B:127:LYS:HG2	2.10	0.52
1:C:343:ASN:OD1	1:E:343:ASN:OD1	2.27	0.52
1:C:1741:ARG:NH2	1:C:1743:GLU:OE2	2.43	0.52
1:A:184:MET:HA	1:A:187:VAL:HG22	1.90	0.52
1:A:1633:ILE:HD13	1:A:1685:MET:SD	2.50	0.52
1:E:1741:ARG:NH2	1:E:1743:GLU:OE2	2.43	0.52
1:D:1928:MET:HB3	1:D:2095:GLY:HA3	1.93	0.51
1:C:792:LEU:O	1:C:796:GLU:HG2	2.10	0.51
1:F:189:ALA:CB	1:E:2112:MET:HA	2.40	0.51
1:A:429:LEU:O	1:A:471:THR:OG1	2.26	0.51
1:E:1796:LYS:HB2	1:E:1813:TYR:HE1	1.74	0.51
1:D:1405:ARG:O	1:D:1409:GLN:HG2	2.10	0.51
1:C:42:MET:SD	1:C:176:ARG:NH2	2.84	0.51
1:F:1297:SER:O	1:F:1299:LYS:N	2.43	0.51
1:F:1544:ARG:HH21	1:F:1620:ILE:HD13	1.75	0.51
1:A:117:VAL:HG13	1:A:160:ALA:HB3	1.93	0.51
1:A:127:LYS:HG3	1:A:128:TYR:CD1	2.40	0.51
1:A:1878:TRP:HB3	1:A:1885:LYS:HE2	1.93	0.51
1:A:2115:ASN:OD1	1:A:2116:LYS:N	2.43	0.51
1:E:931:LYS:HD2	1:E:932:ILE:HG13	1.91	0.51
1:E:1491:THR:O	1:E:1491:THR:OG1	2.28	0.51
1:D:189:ALA:HB3	1:C:2115:ASN:CB	2.39	0.51
1:B:117:VAL:HG13	1:B:160:ALA:HB3	1.93	0.51
1:B:142:PHE:HE1	1:B:147:GLU:HB3	1.75	0.51
1:B:1653:LEU:O	1:B:1659:THR:OG1	2.21	0.51
1:B:1881:HIS:O	1:B:1884:VAL:HG12	2.09	0.51
1:C:181:VAL:HA	1:C:184:MET:HG3	1.92	0.51
1:C:836:GLN:OE1	1:C:854:ARG:NH1	2.43	0.51
1:C:1915:LEU:HD12	1:C:1919:ARG:HD3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:1522:LEU:HD22	1:F:1528:PRO:HB3	1.91	0.51
1:A:123:GLU:O	1:A:127:LYS:HG2	2.10	0.51
1:A:809:ALA:HB2	1:A:995:GLY:HA3	1.92	0.51
1:D:189:ALA:CB	1:C:2112:MET:HA	2.40	0.51
1:D:880:ARG:NH1	1:D:881:ILE:O	2.43	0.51
1:D:1544:ARG:NH2	1:D:1620:ILE:HD13	2.26	0.51
1:B:182:GLN:O	1:B:186:LEU:HG	2.09	0.51
1:C:1702:ARG:O	1:C:1737:LEU:N	2.41	0.51
1:F:89:LYS:HG3	1:F:93:LYS:HE3	1.93	0.51
1:F:950:SER:HB2	1:F:964:ARG:HE	1.74	0.51
1:E:42:MET:SD	1:E:176:ARG:NH2	2.84	0.51
1:D:21:ALA:O	1:D:25:ILE:HG12	2.11	0.51
1:D:950:SER:HB2	1:D:964:ARG:HE	1.74	0.51
1:C:15:SER:O	1:C:18:THR:OG1	2.29	0.51
1:C:1509:TYR:CD2	1:C:1535:LEU:HD12	2.45	0.51
1:C:1539:LYS:HA	1:C:1550:ILE:HD11	1.93	0.51
1:F:830:LEU:HD11	1:F:1392:ILE:HG23	1.93	0.51
1:F:880:ARG:NH1	1:F:881:ILE:O	2.43	0.51
1:E:868:LEU:O	1:E:872:THR:OG1	2.28	0.51
1:E:1686:ILE:HG13	1:E:1695:VAL:HG21	1.93	0.51
1:D:197:HIS:CE1	1:C:2119:CYS:H	2.28	0.51
1:D:524:PHE:HB3	1:D:561:SER:HB2	1.91	0.51
1:D:1550:ILE:HG22	1:D:1559:ILE:HD11	1.91	0.51
1:D:1620:ILE:HD12	1:D:1624:LYS:NZ	2.26	0.51
1:D:2076:VAL:HG23	1:D:2079:LEU:HD12	1.93	0.51
1:F:21:ALA:O	1:F:25:ILE:HG12	2.11	0.51
1:F:1514:THR:CG2	1:E:2050:GLU:CG	2.75	0.51
1:F:1640:LYS:NZ	1:F:1840:GLY:O	2.43	0.51
1:F:2076:VAL:HG23	1:F:2079:LEU:HD12	1.93	0.51
1:A:770:MET:HE3	1:A:774:ARG:HB2	1.93	0.51
1:E:792:LEU:O	1:E:796:GLU:HG2	2.10	0.51
1:E:1311:PHE:O	1:E:1315:MET:HG3	2.11	0.51
1:D:1368:TYR:OH	1:D:1516:GLU:OE1	2.28	0.51
1:B:1217:ASP:HB2	1:B:1572:VAL:HG12	1.91	0.51
1:C:1686:ILE:HG13	1:C:1695:VAL:HG21	1.93	0.51
1:F:2124:ILE:HB	1:E:204:ARG:HH21	1.76	0.51
1:E:429:LEU:O	1:E:471:THR:OG1	2.29	0.51
1:E:1348:GLU:HG2	1:E:1349:PHE:CD2	2.46	0.51
1:D:2147:ILE:HG13	1:C:2114:VAL:HG22	1.91	0.51
1:B:977:SER:OG	1:B:980:ASP:OD2	2.27	0.51
1:C:116:ASP:N	1:C:116:ASP:OD1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:840:ASP:N	1:C:840:ASP:OD1	2.43	0.51
1:C:1348:GLU:HG2	1:C:1349:PHE:CD2	2.46	0.51
1:C:1669:ARG:HD3	1:C:1670:VAL:HG13	1.93	0.51
1:F:105:THR:HG22	1:F:153:LYS:HB3	1.93	0.51
1:F:197:HIS:CE1	1:E:2119:CYS:H	2.28	0.51
1:F:1514:THR:HG22	1:E:2050:GLU:CD	2.30	0.51
1:A:1145:LEU:O	1:A:1149:ILE:HG12	2.11	0.51
1:A:1311:PHE:O	1:A:1315:MET:HG3	2.11	0.51
1:A:1631:LEU:HD12	1:A:1866:ILE:HG23	1.93	0.51
1:D:89:LYS:HG3	1:D:93:LYS:HE3	1.93	0.51
1:D:1339:LYS:HE2	1:D:1423:TRP:CD2	2.46	0.51
1:D:1654:TRP:N	1:D:1872:ASP:O	2.39	0.51
1:D:2147:ILE:CG1	1:C:2114:VAL:HG22	2.41	0.51
1:B:640:PHE:CD2	1:B:641:PRO:HD3	2.46	0.51
1:B:1145:LEU:O	1:B:1149:ILE:HG12	2.11	0.51
1:F:429:LEU:O	1:F:471:THR:OG1	2.24	0.51
1:F:624:ASP:OD1	1:F:627:ARG:NH2	2.43	0.51
1:F:1544:ARG:NH2	1:F:1620:ILE:HD13	2.26	0.51
1:F:2124:ILE:HD13	1:E:201:THR:HB	1.93	0.51
1:A:640:PHE:CD2	1:A:641:PRO:HD3	2.46	0.51
1:A:2064:TYR:HE2	1:A:2068:THR:HG21	1.76	0.51
1:E:1917:MET:SD	1:E:1917:MET:N	2.84	0.51
1:D:624:ASP:OD1	1:D:627:ARG:NH2	2.43	0.51
1:D:1903:ASN:HA	1:D:2038:LEU:HD11	1.93	0.51
1:B:492:LEU:HB2	1:B:519:GLU:HG3	1.94	0.51
1:D:475:ILE:O	1:D:479:ILE:HG12	2.11	0.50
1:D:786:CYS:O	1:D:790:ILE:HG12	2.11	0.50
1:D:830:LEU:HD11	1:D:1392:ILE:HG23	1.93	0.50
1:B:1138:MET:O	1:B:1141:SER:OG	2.24	0.50
1:C:935:ILE:HD11	1:C:1096:HIS:HB2	1.93	0.50
1:F:1405:ARG:O	1:F:1409:GLN:HG2	2.10	0.50
1:E:1169:ALA:O	1:E:1173:SER:OG	2.23	0.50
1:D:1544:ARG:HH21	1:D:1620:ILE:HD13	1.75	0.50
1:B:951:PHE:HE1	1:B:961:ARG:HG2	1.76	0.50
1:B:1114:THR:O	1:B:1118:LEU:N	2.40	0.50
1:C:519:GLU:OE2	1:C:1405:ARG:HG2	2.11	0.50
1:A:584:TRP:HZ2	1:A:708:ILE:HD11	1.77	0.50
1:E:935:ILE:HD11	1:E:1096:HIS:HB2	1.93	0.50
1:E:1114:THR:HA	1:E:1117:PHE:HD1	1.76	0.50
1:B:110:GLU:OE2	1:B:124:LYS:NZ	2.45	0.50
1:B:1631:LEU:HD12	1:B:1866:ILE:HG23	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2132:ARG:NH1	1:A:1438:GLU:OE2	2.45	0.50
1:C:1114:THR:HA	1:C:1117:PHE:HD1	1.76	0.50
1:C:1311:PHE:O	1:C:1315:MET:HG3	2.11	0.50
1:F:1903:ASN:HA	1:F:2038:LEU:HD11	1.93	0.50
1:F:1928:MET:HB3	1:F:2095:GLY:HA3	1.93	0.50
1:A:1138:MET:O	1:A:1141:SER:OG	2.24	0.50
1:E:181:VAL:HA	1:E:184:MET:HG3	1.92	0.50
1:E:1669:ARG:HD3	1:E:1670:VAL:HG13	1.93	0.50
1:A:2:ASP:HA	1:A:5:ARG:HG2	1.94	0.50
1:A:110:GLU:OE2	1:A:124:LYS:NZ	2.45	0.50
1:A:1114:THR:O	1:A:1118:LEU:N	2.40	0.50
1:C:626:LEU:HA	1:C:629:LEU:HB2	1.94	0.50
1:C:868:LEU:O	1:C:872:THR:OG1	2.28	0.50
1:F:1717:THR:O	1:F:1726:GLU:N	2.43	0.50
1:E:1539:LYS:HA	1:E:1550:ILE:HD11	1.93	0.50
1:C:1917:MET:N	1:C:1917:MET:SD	2.84	0.50
1:F:768:TYR:CE1	1:F:786:CYS:HB2	2.47	0.50
1:F:1339:LYS:HE2	1:F:1423:TRP:CD2	2.46	0.50
1:F:1555:VAL:O	1:F:1559:ILE:HG12	2.10	0.50
1:F:1620:ILE:HD12	1:F:1624:LYS:NZ	2.26	0.50
1:F:2147:ILE:CG1	1:E:2114:VAL:HG22	2.41	0.50
1:A:985:PHE:O	1:A:989:THR:HG22	2.12	0.50
1:D:389:LEU:HD21	1:D:559:VAL:HG11	1.93	0.50
1:B:985:PHE:O	1:B:989:THR:HG22	2.12	0.50
1:B:1301:GLN:HG2	1:A:1251:ALA:HB1	1.94	0.50
1:C:411:ILE:CD1	1:A:674:ASN:ND2	2.74	0.50
1:F:19:LEU:HD12	1:F:198:LEU:CB	2.42	0.50
1:D:1271:MET:SD	1:D:1284:SER:HB2	2.52	0.50
1:B:1836:ILE:HG23	1:B:1840:GLY:HA2	1.94	0.50
1:B:1878:TRP:HB3	1:B:1885:LYS:HE2	1.93	0.50
1:B:2064:TYR:HE2	1:B:2068:THR:HG21	1.76	0.50
1:F:28:LEU:CD2	1:F:191:ILE:HG23	2.41	0.50
1:F:189:ALA:HB3	1:E:2115:ASN:CB	2.39	0.50
1:F:884:LYS:HB2	1:F:887:ARG:HH11	1.77	0.50
1:A:110:GLU:HB3	1:A:158:VAL:HG22	1.94	0.50
1:A:812:ILE:O	1:A:817:TRP:NE1	2.34	0.50
1:A:1666:ARG:O	1:A:1670:VAL:HG12	2.12	0.50
1:E:840:ASP:N	1:E:840:ASP:OD1	2.43	0.50
1:E:1549:ASP:OD2	1:E:1551:SER:OG	2.29	0.50
1:E:1727:GLY:O	1:E:1746:TRP:NE1	2.45	0.50
1:D:884:LYS:HB2	1:D:887:ARG:HH11	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1311:PHE:O	1:B:1315:MET:HG3	2.11	0.50
1:B:1666:ARG:O	1:B:1670:VAL:HG12	2.12	0.50
1:C:584:TRP:NE1	1:C:710:TYR:OH	2.45	0.50
1:F:1254:LEU:HD23	1:F:1434:ASN:HB2	1.94	0.50
1:E:1602:LYS:O	1:E:1602:LYS:NZ	2.33	0.50
1:D:105:THR:HG22	1:D:153:LYS:HB3	1.93	0.49
1:D:2124:ILE:HD13	1:C:201:THR:HB	1.93	0.49
1:B:584:TRP:HZ2	1:B:708:ILE:HD11	1.77	0.49
1:B:1510:LYS:HB2	1:B:1535:LEU:HD13	1.94	0.49
1:F:1636:TRP:O	1:F:1640:LYS:HG2	2.12	0.49
1:A:91:PHE:CE2	1:A:131:GLY:HA3	2.47	0.49
1:A:951:PHE:HE1	1:A:961:ARG:HG2	1.76	0.49
1:A:1634:GLU:OE1	1:A:1637:ARG:NH2	2.45	0.49
1:A:1653:LEU:O	1:A:1659:THR:OG1	2.21	0.49
1:E:15:SER:O	1:E:18:THR:OG1	2.29	0.49
1:D:618:LYS:HE3	1:D:622:ILE:HD11	1.93	0.49
1:B:1634:GLU:OE1	1:B:1637:ARG:NH2	2.45	0.49
1:C:418:SER:OG	1:A:708:ILE:HA	2.12	0.49
1:F:197:HIS:ND1	1:E:2118:ILE:HG23	2.28	0.49
1:F:475:ILE:O	1:F:479:ILE:HG12	2.11	0.49
1:F:1514:THR:OG1	1:F:1517:GLU:CD	2.51	0.49
1:A:748:TRP:CD1	1:A:978:PRO:HB2	2.48	0.49
1:A:1696:LEU:HD22	1:A:1856:LEU:HD21	1.94	0.49
1:B:2052:VAL:HG11	1:A:1428:GLU:OE1	2.13	0.49
1:C:1602:LYS:O	1:C:1602:LYS:NZ	2.33	0.49
1:D:1254:LEU:HD23	1:D:1434:ASN:HB2	1.94	0.49
1:D:1636:TRP:O	1:D:1640:LYS:HG2	2.12	0.49
1:B:1253:TYR:O	1:A:1302:LYS:HD2	2.13	0.49
1:F:389:LEU:HD21	1:F:559:VAL:HG11	1.93	0.49
1:F:1706:SER:OG	1:F:1707:GLY:N	2.46	0.49
1:A:271:PHE:HB3	1:A:665:LYS:HE3	1.95	0.49
1:A:492:LEU:HB2	1:A:519:GLU:HG3	1.94	0.49
1:A:1510:LYS:HB2	1:A:1535:LEU:HD13	1.94	0.49
1:E:1702:ARG:O	1:E:1737:LEU:N	2.41	0.49
1:D:299:ILE:HG23	1:D:300:THR:HG23	1.95	0.49
1:D:2124:ILE:HB	1:C:204:ARG:HH21	1.76	0.49
1:B:530:VAL:HG13	1:B:556:VAL:HG12	1.94	0.49
1:B:968:TYR:HE2	1:B:1167:THR:HA	1.78	0.49
1:B:1438:GLU:HG2	1:B:2132:ARG:HH21	1.76	0.49
1:C:1347:PHE:HB2	1:C:1350:ALA:HB2	1.94	0.49
1:F:194:VAL:HG22	1:F:198:LEU:HD12	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:299:ILE:HG23	1:F:300:THR:HG23	1.95	0.49
1:F:362:THR:OG1	1:F:365:VAL:O	2.22	0.49
1:A:16:PRO:HA	1:A:198:LEU:HD23	1.95	0.49
1:A:1942:LEU:HD23	1:A:2071:LEU:HB3	1.95	0.49
1:E:519:GLU:OE2	1:E:1405:ARG:HG2	2.11	0.49
1:E:1347:PHE:HB2	1:E:1350:ALA:HB2	1.94	0.49
1:D:768:TYR:CE1	1:D:786:CYS:HB2	2.47	0.49
1:D:1685:MET:O	1:D:1689:ILE:HG12	2.13	0.49
1:B:674:ASN:ND2	1:E:411:ILE:CD1	2.74	0.49
1:F:1271:MET:SD	1:F:1284:SER:HB2	2.52	0.49
1:F:1419:LEU:HB3	1:F:1424:VAL:HG11	1.93	0.49
1:E:584:TRP:NE1	1:E:710:TYR:OH	2.45	0.49
1:D:19:LEU:HD12	1:D:198:LEU:CB	2.42	0.49
1:D:1419:LEU:HB3	1:D:1424:VAL:HG11	1.93	0.49
1:D:2150:PHE:CE2	1:C:2118:ILE:HB	2.48	0.49
1:B:91:PHE:CE2	1:B:131:GLY:HA3	2.47	0.49
1:B:1139:TRP:HA	1:B:1142:MET:HG2	1.95	0.49
1:B:1696:LEU:HD22	1:B:1856:LEU:HD21	1.94	0.49
1:A:328:THR:O	1:A:331:SER:OG	2.24	0.49
1:A:797:LEU:HD21	1:A:1067:LEU:HD22	1.94	0.49
1:E:626:LEU:HA	1:E:629:LEU:HB2	1.94	0.49
1:B:16:PRO:HA	1:B:198:LEU:HD23	1.95	0.49
1:B:328:THR:O	1:B:331:SER:OG	2.24	0.49
1:B:429:LEU:O	1:B:471:THR:OG1	2.26	0.49
1:B:674:ASN:HD22	1:E:411:ILE:HD13	1.76	0.49
1:B:797:LEU:HD21	1:B:1067:LEU:HD22	1.94	0.49
1:B:802:ALA:O	1:B:805:SER:OG	2.31	0.49
1:F:618:LYS:HE3	1:F:622:ILE:HD11	1.93	0.49
1:A:36:HIS:NE2	1:A:111:VAL:O	2.40	0.49
1:A:530:VAL:HG13	1:A:556:VAL:HG12	1.94	0.49
1:E:637:TYR:HB2	1:E:1164:VAL:CG1	2.43	0.49
1:E:1640:LYS:NZ	1:E:1839:ASP:O	2.31	0.49
1:E:1666:ARG:O	1:E:1670:VAL:HG22	2.13	0.49
1:B:110:GLU:HB3	1:B:158:VAL:HG22	1.94	0.49
1:F:786:CYS:O	1:F:790:ILE:HG12	2.11	0.49
1:A:873:ARG:NE	1:A:1007:ASP:OD2	2.39	0.49
1:E:742:HIS:CE1	1:E:881:ILE:HD12	2.48	0.49
1:E:2144:GLN:NE2	1:E:2145:ASP:O	2.46	0.49
1:D:1514:THR:CB	1:C:2050:GLU:OE2	2.61	0.49
1:D:2047:LEU:HD23	1:D:2047:LEU:H	1.78	0.49
1:B:129:GLU:O	1:B:133:THR:OG1	2.29	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1899:ASN:HB2	1:B:2042:TRP:CZ2	2.48	0.49
1:C:1666:ARG:O	1:C:1670:VAL:HG22	2.13	0.49
1:C:2047:LEU:HD23	1:C:2047:LEU:H	1.78	0.49
1:A:1201:TYR:OH	1:A:1267:GLY:O	2.25	0.49
1:D:1056:TRP:HD1	1:D:1059:GLY:H	1.61	0.48
1:D:1514:THR:OG1	1:D:1517:GLU:CD	2.51	0.48
1:C:429:LEU:O	1:C:471:THR:OG1	2.29	0.48
1:F:2047:LEU:HD23	1:F:2047:LEU:H	1.78	0.48
1:E:2047:LEU:HD23	1:E:2047:LEU:H	1.78	0.48
1:D:28:LEU:CD2	1:D:191:ILE:HG23	2.41	0.48
1:D:923:TYR:HE2	1:D:1074:LEU:HD11	1.78	0.48
1:D:1260:ASP:OD1	1:D:1291:ARG:NH2	2.46	0.48
1:B:2:ASP:HA	1:B:5:ARG:HG2	1.94	0.48
1:B:597:LEU:HD12	1:B:599:TYR:HE1	1.78	0.48
1:B:1251:ALA:HB1	1:A:1301:GLN:HG2	1.94	0.48
1:B:2132:ARG:HB2	1:B:2132:ARG:NH1	2.29	0.48
1:C:1501:ASN:ND2	1:C:1527:PHE:O	2.41	0.48
1:F:2150:PHE:CE2	1:E:2118:ILE:HB	2.48	0.48
1:E:362:THR:O	1:E:366:ARG:NH1	2.46	0.48
1:E:756:GLU:HG2	1:E:761:GLU:HG2	1.95	0.48
1:D:16:PRO:HB2	1:C:2122:ASP:OD1	2.13	0.48
1:D:194:VAL:HG22	1:D:198:LEU:HD12	1.95	0.48
1:B:1253:TYR:O	1:A:1302:LYS:CD	2.61	0.48
1:C:319:SER:HB3	1:E:319:SER:HB3	1.95	0.48
1:C:1727:GLY:O	1:C:1746:TRP:NE1	2.45	0.48
1:F:480:ARG:CD	1:F:1238:ARG:HH12	2.24	0.48
1:F:1260:ASP:OD1	1:F:1291:ARG:NH2	2.46	0.48
1:A:77:LYS:HE2	1:A:77:LYS:HB2	1.53	0.48
1:A:1139:TRP:HA	1:A:1142:MET:HG2	1.95	0.48
1:A:1836:ILE:HG23	1:A:1840:GLY:HA2	1.94	0.48
1:D:197:HIS:ND1	1:C:2118:ILE:HG23	2.28	0.48
1:D:791:GLU:O	1:D:795:ILE:HG12	2.13	0.48
1:B:407:ILE:HD11	1:B:661:TYR:CD2	2.48	0.48
1:B:748:TRP:CD1	1:B:978:PRO:HB2	2.48	0.48
1:B:1302:LYS:HD2	1:A:1253:TYR:O	2.13	0.48
1:C:967:MET:HG3	1:C:1166:PRO:CA	2.44	0.48
1:C:1943:ASP:N	1:C:1943:ASP:OD1	2.36	0.48
1:F:16:PRO:HB2	1:E:2122:ASP:OD1	2.13	0.48
1:F:791:GLU:O	1:F:795:ILE:HG12	2.13	0.48
1:A:179:GLY:O	1:A:182:GLN:HG3	2.14	0.48
1:A:317:ALA:HB1	1:A:509:ILE:HD11	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:407:ILE:HD11	1:A:661:TYR:CD2	2.48	0.48
1:E:356:ARG:NH2	1:E:367:GLU:OE1	2.47	0.48
1:D:1201:TYR:OH	1:D:1267:GLY:O	2.29	0.48
1:B:708:ILE:HA	1:E:418:SER:OG	2.12	0.48
1:B:1428:GLU:OE1	1:A:2052:VAL:HG11	2.13	0.48
1:B:1942:LEU:HD23	1:B:2071:LEU:HB3	1.95	0.48
1:C:637:TYR:HB2	1:C:1164:VAL:CG1	2.43	0.48
1:C:1243:ALA:HB3	1:C:1246:MET:SD	2.54	0.48
1:F:923:TYR:HE2	1:F:1074:LEU:HD11	1.78	0.48
1:F:1685:MET:O	1:F:1689:ILE:HG12	2.13	0.48
1:F:2067:LYS:HZ3	1:F:2067:LYS:HB2	1.78	0.48
1:A:597:LEU:HD12	1:A:599:TYR:HE1	1.78	0.48
1:E:839:GLU:OE1	1:E:839:GLU:N	2.28	0.48
1:E:1243:ALA:HB3	1:E:1246:MET:SD	2.54	0.48
1:D:51:LYS:NZ	1:D:99:TYR:O	2.33	0.48
1:D:1458:PHE:CD2	1:D:1563:LEU:HB3	2.49	0.48
1:B:195:ARG:O	1:B:195:ARG:NH1	2.40	0.48
1:B:271:PHE:HB3	1:B:665:LYS:HE3	1.95	0.48
1:C:2139:ARG:NH2	1:C:2144:GLN:HB3	2.27	0.48
1:F:322:LEU:HD11	1:F:342:ILE:HG21	1.95	0.48
1:A:1590:LEU:O	1:A:1593:MET:HG3	2.13	0.48
1:D:1640:LYS:HD2	1:D:1646:TYR:CZ	2.48	0.48
1:B:640:PHE:CG	1:B:641:PRO:HD3	2.49	0.48
1:C:1325:GLU:OE1	1:C:1558:ARG:NH2	2.47	0.48
1:C:2144:GLN:NE2	1:C:2145:ASP:O	2.46	0.48
1:A:1070:VAL:O	1:A:1074:LEU:HD22	2.13	0.48
1:A:1899:ASN:HB2	1:A:2042:TRP:CZ2	2.48	0.48
1:E:843:LEU:HD23	1:E:880:ARG:HG2	1.96	0.48
1:D:1299:LYS:HD3	1:D:1300:ARG:N	2.28	0.48
1:D:1706:SER:OG	1:D:1707:GLY:N	2.46	0.48
1:D:2067:LYS:HZ3	1:D:2067:LYS:HB2	1.79	0.48
1:B:317:ALA:HB1	1:B:509:ILE:HD11	1.94	0.48
1:B:1302:LYS:CD	1:A:1253:TYR:O	2.61	0.48
1:C:681:SER:OG	1:C:682:LYS:N	2.47	0.48
1:F:186:LEU:HA	1:E:2115:ASN:CG	2.34	0.48
1:F:1640:LYS:HD2	1:F:1646:TYR:CZ	2.48	0.48
1:A:968:TYR:HE2	1:A:1167:THR:HA	1.78	0.48
1:A:1930:ASN:HD21	1:A:1942:LEU:HB2	1.79	0.48
1:E:52:ASP:N	1:E:52:ASP:OD1	2.45	0.48
1:E:786:CYS:O	1:E:790:ILE:HG12	2.13	0.48
1:D:322:LEU:HD11	1:D:342:ILE:HG21	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1216:LEU:HA	1:D:1220:ALA:HB3	1.96	0.48
1:B:1033:LEU:HD22	1:B:1036:HIS:CE1	2.49	0.48
1:C:356:ARG:NH2	1:C:367:GLU:OE1	2.47	0.48
1:C:967:MET:HE1	1:C:1139:TRP:CZ2	2.49	0.48
1:E:681:SER:OG	1:E:682:LYS:N	2.47	0.48
1:E:1325:GLU:OE1	1:E:1558:ARG:NH2	2.47	0.48
1:E:1553:PRO:O	1:E:1557:LYS:HB3	2.14	0.48
1:E:1698:LEU:O	1:E:1702:ARG:HG2	2.14	0.48
1:C:362:THR:O	1:C:366:ARG:NH1	2.46	0.48
1:C:861:HIS:HA	1:C:1376:ARG:HG2	1.95	0.48
1:C:1789:VAL:HB	1:C:1806:PRO:HD2	1.96	0.48
1:C:2109:ALA:HA	1:C:2112:MET:SD	2.54	0.48
1:F:1056:TRP:HD1	1:F:1059:GLY:H	1.61	0.48
1:A:192:SER:O	1:A:196:GLU:HG3	2.14	0.48
1:A:1033:LEU:HD22	1:A:1036:HIS:CE1	2.49	0.48
1:E:1789:VAL:HB	1:E:1806:PRO:HD2	1.96	0.48
1:B:1114:THR:HA	1:B:1117:PHE:HD1	1.79	0.47
1:C:1698:LEU:O	1:C:1702:ARG:HG2	2.14	0.47
1:F:19:LEU:HD12	1:F:198:LEU:HB3	1.96	0.47
1:F:1216:LEU:HA	1:F:1220:ALA:HB3	1.96	0.47
1:F:1299:LYS:HD3	1:F:1300:ARG:N	2.28	0.47
1:A:1080:TRP:HE1	1:A:1089:CYS:HB2	1.79	0.47
1:D:246:TYR:HD1	1:D:774:ARG:HG2	1.78	0.47
1:D:1843:ALA:O	1:D:1856:LEU:N	2.47	0.47
1:B:1520:ASP:O	1:B:1524:THR:HG22	2.14	0.47
1:B:1590:LEU:O	1:B:1593:MET:HG3	2.13	0.47
1:C:742:HIS:CE1	1:C:881:ILE:HD12	2.48	0.47
1:C:912:TYR:OH	1:C:989:THR:HB	2.14	0.47
1:C:1553:PRO:O	1:C:1557:LYS:HB3	2.14	0.47
1:F:1514:THR:CB	1:E:2050:GLU:OE2	2.61	0.47
1:D:1022:LYS:HZ2	1:D:1022:LYS:HB3	1.79	0.47
1:D:1222:PRO:HG2	1:D:1593:MET:HA	1.96	0.47
1:B:2083:ASP:HB2	1:B:2141:LEU:HD21	1.96	0.47
1:C:49:ASP:OD1	1:C:49:ASP:N	2.40	0.47
1:C:52:ASP:N	1:C:52:ASP:OD1	2.45	0.47
1:C:411:ILE:HD13	1:A:674:ASN:HD22	1.76	0.47
1:C:637:TYR:HB2	1:C:1164:VAL:HG13	1.96	0.47
1:C:756:GLU:HG2	1:C:761:GLU:HG2	1.95	0.47
1:F:1587:ARG:O	1:F:1591:LYS:HG3	2.14	0.47
1:A:637:TYR:HB2	1:A:1164:VAL:HG22	1.96	0.47
1:A:640:PHE:CG	1:A:641:PRO:HD3	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:956:ASN:O	1:A:958:LYS:NZ	2.39	0.47
1:A:2083:ASP:HB2	1:A:2141:LEU:HD21	1.96	0.47
1:E:1503:ILE:O	1:E:1507:ILE:HG12	2.14	0.47
1:E:2109:ALA:HA	1:E:2112:MET:SD	2.54	0.47
1:D:451:LEU:HD13	1:D:1593:MET:HG2	1.96	0.47
1:D:816:ASN:HB3	1:D:819:GLU:HG3	1.96	0.47
1:D:1680:GLN:HB2	1:D:1857:ALA:HB1	1.96	0.47
1:B:179:GLY:O	1:B:182:GLN:HG3	2.14	0.47
1:B:192:SER:O	1:B:196:GLU:HG3	2.14	0.47
1:B:1297:SER:OG	1:B:1298:HIS:N	2.47	0.47
1:C:267:VAL:HG23	1:C:669:VAL:HG22	1.97	0.47
1:A:340:ARG:HD3	1:A:377:MET:SD	2.55	0.47
1:A:860:ARG:O	1:A:1376:ARG:HD3	2.14	0.47
1:B:1070:VAL:O	1:B:1074:LEU:HD22	2.13	0.47
1:B:1208:ALA:HB1	1:B:1232:CYS:HB3	1.97	0.47
1:B:2035:PRO:O	1:B:2039:ILE:HG12	2.14	0.47
1:B:2083:ASP:OD2	1:B:2140:ARG:NH1	2.41	0.47
1:C:843:LEU:HD23	1:C:880:ARG:HG2	1.96	0.47
1:F:686:LEU:HD11	1:F:939:LEU:HD23	1.97	0.47
1:F:1079:VAL:O	1:F:1083:LEU:HD23	2.14	0.47
1:E:1501:ASN:ND2	1:E:1527:PHE:O	2.41	0.47
1:B:15:SER:O	1:B:18:THR:OG1	2.33	0.47
1:F:2146:SER:HB2	1:E:2118:ILE:H	1.80	0.47
1:A:1088:ASP:OD1	1:A:1088:ASP:N	2.44	0.47
1:A:1297:SER:OG	1:A:1298:HIS:N	2.47	0.47
1:E:2139:ARG:NH2	1:E:2144:GLN:HB3	2.27	0.47
1:D:19:LEU:HD12	1:D:198:LEU:HB3	1.96	0.47
1:D:243:LEU:HD22	1:D:1079:VAL:HG21	1.96	0.47
1:D:1197:PRO:O	1:D:1394:THR:HG21	2.14	0.47
1:D:1587:ARG:O	1:D:1591:LYS:HG3	2.14	0.47
1:D:2150:PHE:CZ	1:C:2120:PRO:CA	2.97	0.47
1:B:79:ILE:HA	1:B:134:TYR:CE2	2.50	0.47
1:B:201:THR:HA	1:B:204:ARG:HD3	1.96	0.47
1:B:340:ARG:HD3	1:B:377:MET:SD	2.55	0.47
1:B:1080:TRP:HE1	1:B:1089:CYS:HB2	1.79	0.47
1:B:1302:LYS:HZ1	1:A:1434:ASN:HD21	1.59	0.47
1:B:2078:LEU:HD23	1:B:2078:LEU:H	1.80	0.47
1:F:1675:ILE:O	1:F:1679:ILE:HG12	2.15	0.47
1:F:2150:PHE:CZ	1:E:2120:PRO:CA	2.97	0.47
1:A:26:ASP:HA	1:A:29:ASP:OD2	2.14	0.47
1:A:79:ILE:HA	1:A:134:TYR:CE2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1114:THR:HA	1:A:1117:PHE:HD1	1.79	0.47
1:A:1297:SER:OG	1:A:1298:HIS:ND1	2.41	0.47
1:A:1520:ASP:O	1:A:1524:THR:HG22	2.14	0.47
1:A:2035:PRO:O	1:A:2039:ILE:HG12	2.14	0.47
1:E:637:TYR:HB2	1:E:1164:VAL:HG13	1.96	0.47
1:E:707:ARG:HA	1:E:707:ARG:HD2	1.50	0.47
1:E:748:TRP:CD1	1:E:978:PRO:HB2	2.50	0.47
1:E:861:HIS:HA	1:E:1376:ARG:HG2	1.95	0.47
1:D:1098:ASP:OD1	1:D:1098:ASP:N	2.48	0.47
1:D:1848:ASP:OD1	1:D:1851:SER:OG	2.26	0.47
1:B:26:ASP:HA	1:B:29:ASP:OD2	2.14	0.47
1:B:82:HIS:HD2	1:B:83:PRO:HD2	1.79	0.47
1:B:207:LEU:HD22	1:B:210:MET:HE1	1.97	0.47
1:B:288:PRO:HA	1:B:405:LEU:HD11	1.96	0.47
1:B:1587:ARG:HG3	1:B:1601:VAL:HG21	1.96	0.47
1:F:684:LYS:HA	1:F:689:THR:HA	1.97	0.47
1:F:816:ASN:HB3	1:F:819:GLU:HG3	1.96	0.47
1:A:240:ILE:HA	1:A:792:LEU:HD21	1.97	0.47
1:A:802:ALA:O	1:A:805:SER:OG	2.31	0.47
1:D:684:LYS:HA	1:D:689:THR:HA	1.97	0.47
1:D:742:HIS:CE1	1:D:881:ILE:HD12	2.50	0.47
1:B:1853:ARG:HD3	1:B:1853:ARG:HA	1.69	0.47
1:C:786:CYS:O	1:C:790:ILE:HG12	2.13	0.47
1:C:1549:ASP:OD2	1:C:1551:SER:OG	2.29	0.47
1:C:1763:LEU:HD13	1:C:1803:TRP:HE1	1.80	0.47
1:F:243:LEU:HD22	1:F:1079:VAL:HG21	1.96	0.47
1:F:246:TYR:HD1	1:F:774:ARG:HG2	1.78	0.47
1:F:1197:PRO:O	1:F:1394:THR:HG21	2.14	0.47
1:F:1458:PHE:CD2	1:F:1563:LEU:HB3	2.49	0.47
1:F:1702:ARG:O	1:F:1737:LEU:N	2.42	0.47
1:A:82:HIS:HD2	1:A:83:PRO:HD2	1.79	0.47
1:A:1578:VAL:HG13	1:A:1584:ALA:HB1	1.97	0.47
1:E:449:THR:OG1	1:E:450:VAL:N	2.47	0.47
1:E:1674:PRO:HA	1:E:1679:ILE:HD11	1.97	0.47
1:D:209:ALA:HB1	1:D:1522:LEU:HD12	1.97	0.47
1:C:1844:ILE:HG22	1:C:1855:LEU:HA	1.97	0.47
1:F:742:HIS:CE1	1:F:881:ILE:HD12	2.50	0.47
1:F:1222:PRO:HG2	1:F:1593:MET:HA	1.96	0.47
1:F:1249:HIS:ND1	1:F:1250:PRO:HD2	2.30	0.47
1:A:849:ILE:O	1:A:853:ILE:HD12	2.15	0.47
1:A:1638:TRP:CG	1:A:1901:MET:HG2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:480:ARG:CD	1:D:1238:ARG:HH12	2.24	0.46
1:D:912:TYR:OH	1:D:989:THR:HB	2.15	0.46
1:D:1645:PRO:HB2	1:D:1648:ASP:HB2	1.97	0.46
1:D:1675:ILE:O	1:D:1679:ILE:HG12	2.15	0.46
1:B:581:THR:HG23	1:B:604:VAL:HG23	1.97	0.46
1:B:849:ILE:O	1:B:853:ILE:HD12	2.15	0.46
1:B:1158:SER:OG	1:B:1160:LYS:O	2.33	0.46
1:B:1255:GLN:C	1:A:1303:SER:HB2	2.36	0.46
1:B:1930:ASN:HD21	1:B:1942:LEU:HB2	1.79	0.46
1:C:139:LEU:HD13	1:C:152:TYR:HB2	1.96	0.46
1:A:82:HIS:ND1	1:A:86:LYS:HB3	2.30	0.46
1:A:288:PRO:HA	1:A:405:LEU:HD11	1.96	0.46
1:E:912:TYR:OH	1:E:989:THR:HB	2.14	0.46
1:E:1035:PRO:O	1:E:1039:GLN:HG2	2.15	0.46
1:B:181:VAL:HA	1:B:184:MET:HG3	1.98	0.46
1:C:1090:PHE:CZ	1:C:1092:GLU:HG3	2.50	0.46
1:C:1503:ILE:O	1:C:1507:ILE:HG12	2.14	0.46
1:F:1640:LYS:HD2	1:F:1646:TYR:OH	2.15	0.46
1:A:1587:ARG:HG3	1:A:1601:VAL:HG21	1.96	0.46
1:E:1846:GLN:OE1	1:E:1853:ARG:NH1	2.48	0.46
1:D:186:LEU:HA	1:C:2115:ASN:CG	2.34	0.46
1:D:686:LEU:HD11	1:D:939:LEU:HD23	1.97	0.46
1:D:1249:HIS:ND1	1:D:1250:PRO:HD2	2.30	0.46
1:D:1640:LYS:HD2	1:D:1646:TYR:OH	2.15	0.46
1:C:898:THR:HG23	1:C:900:PRO:HD2	1.98	0.46
1:C:1685:MET:O	1:C:1689:ILE:HG12	2.16	0.46
1:C:2083:ASP:HB3	1:C:2137:LEU:HD11	1.97	0.46
1:F:912:TYR:OH	1:F:989:THR:HB	2.15	0.46
1:F:1634:GLU:OE1	1:F:1637:ARG:NH2	2.49	0.46
1:F:1843:ALA:O	1:F:1856:LEU:N	2.47	0.46
1:A:1530:SER:O	1:A:1530:SER:OG	2.27	0.46
1:E:139:LEU:HD13	1:E:152:TYR:HB2	1.96	0.46
1:E:1844:ILE:HG22	1:E:1855:LEU:HA	1.97	0.46
1:D:1079:VAL:O	1:D:1083:LEU:HD23	2.14	0.46
1:D:2128:LEU:O	1:D:2128:LEU:HD23	2.16	0.46
1:B:340:ARG:HD2	1:B:340:ARG:HA	1.83	0.46
1:B:1636:TRP:HH2	1:B:1684:LEU:HB3	1.80	0.46
1:C:449:THR:OG1	1:C:450:VAL:N	2.47	0.46
1:F:584:TRP:HD1	1:F:719:GLU:HG3	1.81	0.46
1:F:1451:GLN:O	1:F:1455:SER:N	2.48	0.46
1:E:267:VAL:HG23	1:E:669:VAL:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:357:ILE:HG23	1:E:358:GLN:HG3	1.98	0.46
1:E:967:MET:HE1	1:E:1139:TRP:CZ2	2.50	0.46
1:E:1919:ARG:HD2	1:E:1919:ARG:HA	1.53	0.46
1:B:329:PRO:HB2	1:B:385:MET:SD	2.56	0.46
1:B:956:ASN:O	1:B:958:LYS:NZ	2.39	0.46
1:B:1638:TRP:CD1	1:B:1901:MET:HG2	2.51	0.46
1:B:1931:ASP:O	1:B:1934:LYS:HG2	2.16	0.46
1:B:2111:ASN:HA	1:B:2114:VAL:HG22	1.97	0.46
1:C:748:TRP:CD1	1:C:978:PRO:HB2	2.50	0.46
1:C:839:GLU:H	1:C:839:GLU:CD	2.16	0.46
1:C:1674:PRO:HA	1:C:1679:ILE:HD11	1.97	0.46
1:C:1846:GLN:OE1	1:C:1853:ARG:NH1	2.48	0.46
1:F:293:LEU:HD22	1:F:566:ARG:CD	2.45	0.46
1:A:201:THR:HA	1:A:204:ARG:HD3	1.96	0.46
1:A:1636:TRP:HH2	1:A:1684:LEU:HB3	1.80	0.46
1:E:815:LYS:HA	1:E:815:LYS:HD2	1.84	0.46
1:E:1682:ALA:O	1:E:1686:ILE:HG12	2.16	0.46
1:D:1084:PHE:CZ	1:D:1134:VAL:HG21	2.51	0.46
1:D:1717:THR:O	1:D:1726:GLU:N	2.43	0.46
1:B:1116:TRP:NE1	1:B:1135:ASN:O	2.39	0.46
1:B:1434:ASN:HD21	1:A:1302:LYS:HZ1	1.62	0.46
1:C:1398:MET:HA	1:C:1403:GLN:HE22	1.81	0.46
1:F:451:LEU:HD13	1:F:1593:MET:HG2	1.96	0.46
1:F:1514:THR:CG2	1:E:2050:GLU:CD	2.84	0.46
1:F:1680:GLN:HB2	1:F:1857:ALA:HB1	1.96	0.46
1:F:2128:LEU:O	1:F:2128:LEU:HD23	2.16	0.46
1:A:207:LEU:HD22	1:A:210:MET:HE1	1.97	0.46
1:A:1158:SER:OG	1:A:1160:LYS:O	2.33	0.46
1:A:1208:ALA:HB1	1:A:1232:CYS:HB3	1.97	0.46
1:A:2111:ASN:HA	1:A:2114:VAL:HG22	1.97	0.46
1:D:2047:LEU:CD1	1:C:1360:LEU:HD23	2.46	0.46
1:D:2147:ILE:O	1:D:2151:TYR:N	2.49	0.46
1:B:77:LYS:HB2	1:B:77:LYS:HE2	1.53	0.46
1:B:637:TYR:HB2	1:B:1164:VAL:HG22	1.96	0.46
1:B:1201:TYR:OH	1:B:1267:GLY:O	2.25	0.46
1:B:1549:ASP:OD1	1:B:1551:SER:OG	2.22	0.46
1:F:1195:ASP:HB2	1:F:1398:MET:CE	2.46	0.46
1:F:1514:THR:HG1	1:F:1517:GLU:CD	2.19	0.46
1:A:3:LYS:NZ	1:A:1665:ASP:OD2	2.48	0.46
1:A:329:PRO:HB2	1:A:385:MET:SD	2.56	0.46
1:E:967:MET:HG3	1:E:1166:PRO:CA	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:9:ASN:HA	1:D:12:LYS:NZ	2.31	0.46
1:D:275:GLU:OE1	1:D:661:TYR:OH	2.32	0.46
1:D:796:GLU:HG3	1:D:1075:LEU:HA	1.98	0.46
1:D:1297:SER:HB2	1:C:1451:GLN:NE2	2.31	0.46
1:D:1514:THR:CG2	1:C:2050:GLU:CD	2.84	0.46
1:B:82:HIS:ND1	1:B:86:LYS:HB3	2.30	0.46
1:B:1084:PHE:HE1	1:B:1130:HIS:ND1	2.14	0.46
1:B:1297:SER:OG	1:B:1298:HIS:ND1	2.41	0.46
1:B:1638:TRP:CG	1:B:1901:MET:HG2	2.49	0.46
1:C:1706:SER:HA	1:C:1735:PHE:CE1	2.51	0.46
1:F:186:LEU:HD12	1:E:2115:ASN:HD21	1.81	0.46
1:A:2078:LEU:H	1:A:2078:LEU:HD23	1.80	0.46
1:E:1685:MET:O	1:E:1689:ILE:HG12	2.16	0.46
1:D:480:ARG:HD3	1:D:1238:ARG:NH1	2.30	0.46
1:D:584:TRP:HD1	1:D:719:GLU:HG3	1.81	0.46
1:B:240:ILE:HA	1:B:792:LEU:HD21	1.97	0.46
1:B:770:MET:HE3	1:B:774:ARG:HB2	1.97	0.46
1:B:860:ARG:O	1:B:1376:ARG:HD3	2.14	0.46
1:B:2120:PRO:HB3	1:A:2150:PHE:CZ	2.51	0.46
1:B:2150:PHE:CZ	1:A:2120:PRO:HB3	2.51	0.46
1:C:629:LEU:HD13	1:C:668:LEU:HD11	1.97	0.46
1:C:768:TYR:CE2	1:C:786:CYS:HB2	2.51	0.46
1:F:1457:THR:HG22	1:F:1565:LYS:HZ1	1.81	0.46
1:F:2147:ILE:O	1:F:2151:TYR:N	2.49	0.46
1:A:181:VAL:HA	1:A:184:MET:HG3	1.98	0.46
1:A:581:THR:HG23	1:A:604:VAL:HG23	1.97	0.46
1:A:600:ALA:O	1:A:604:VAL:HG13	2.16	0.46
1:A:756:GLU:OE1	1:A:761:GLU:HA	2.16	0.46
1:A:1638:TRP:CD1	1:A:1901:MET:HG2	2.51	0.46
1:D:16:PRO:HA	1:D:198:LEU:HD23	1.98	0.46
1:D:1583:GLU:HB2	1:D:1608:LEU:HD21	1.98	0.46
1:B:71:ILE:HG23	1:B:92:PHE:HE2	1.81	0.46
1:B:1351:ASP:OD1	1:B:1351:ASP:N	2.47	0.46
1:C:67:PRO:HD2	1:C:70:ILE:HD11	1.98	0.46
1:C:1846:GLN:HB2	1:C:1851:SER:HB2	1.98	0.46
1:A:134:TYR:O	1:A:137:GLN:HG2	2.16	0.46
1:E:1090:PHE:CZ	1:E:1092:GLU:HG3	2.50	0.46
1:D:31:LEU:HD13	1:D:191:ILE:HG12	1.98	0.45
1:D:186:LEU:HD12	1:C:2115:ASN:HD21	1.81	0.45
1:D:1659:THR:HG23	1:D:1662:GLU:H	1.81	0.45
1:B:845:SER:OG	1:B:880:ARG:NH1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:849:ILE:HG13	1:B:1383:LEU:HD12	1.98	0.45
1:B:918:ASN:OD1	1:B:918:ASN:N	2.49	0.45
1:C:311:GLN:OE1	1:C:315:ARG:NH2	2.49	0.45
1:C:1035:PRO:O	1:C:1039:GLN:HG2	2.15	0.45
1:F:1098:ASP:OD1	1:F:1098:ASP:N	2.48	0.45
1:F:1693:TYR:HE2	1:F:1836:ILE:HD11	1.82	0.45
1:A:71:ILE:HG23	1:A:92:PHE:HE2	1.81	0.45
1:A:630:ILE:HD13	1:A:716:LEU:HG	1.98	0.45
1:E:1398:MET:HA	1:E:1403:GLN:HE22	1.81	0.45
1:E:1587:ARG:NH2	1:E:1605:LYS:O	2.49	0.45
1:E:2083:ASP:HB3	1:E:2137:LEU:HD11	1.97	0.45
1:D:293:LEU:HD22	1:D:566:ARG:CD	2.45	0.45
1:D:759:TYR:OH	1:D:778:GLU:OE1	2.26	0.45
1:D:928:GLY:H	1:D:931:LYS:HD3	1.82	0.45
1:D:2146:SER:HB2	1:C:2118:ILE:H	1.80	0.45
1:B:630:ILE:HD13	1:B:716:LEU:HG	1.98	0.45
1:B:713:TYR:CE2	1:B:1170:GLU:HG2	2.52	0.45
1:C:1491:THR:O	1:C:1491:THR:OG1	2.28	0.45
1:C:1587:ARG:NH2	1:C:1605:LYS:O	2.49	0.45
1:F:16:PRO:HA	1:F:198:LEU:HD23	1.98	0.45
1:F:209:ALA:HB1	1:F:1522:LEU:HD12	1.97	0.45
1:A:845:SER:OG	1:A:880:ARG:NH1	2.50	0.45
1:A:1931:ASP:O	1:A:1934:LYS:HG2	2.16	0.45
1:E:1763:LEU:HD13	1:E:1803:TRP:HE1	1.80	0.45
1:D:2113:VAL:HG22	1:C:2146:SER:OG	2.16	0.45
1:B:134:TYR:O	1:B:137:GLN:HG2	2.16	0.45
1:B:786:CYS:O	1:B:790:ILE:HG12	2.16	0.45
1:B:1578:VAL:HG13	1:B:1584:ALA:HB1	1.97	0.45
1:C:842:HIS:CE1	1:C:1021:ARG:HA	2.52	0.45
1:C:989:THR:HG23	1:C:1006:ILE:HG12	1.99	0.45
1:C:1919:ARG:HD2	1:C:1919:ARG:HA	1.53	0.45
1:F:9:ASN:HA	1:F:12:LYS:NZ	2.31	0.45
1:F:277:ASN:HB3	1:F:281:ARG:HH21	1.82	0.45
1:F:278:HIS:HA	1:F:281:ARG:HG2	1.98	0.45
1:F:1340:ILE:HG22	1:F:1342:THR:HG22	1.97	0.45
1:A:952:ILE:HD11	1:A:960:ILE:HD12	1.99	0.45
1:A:1443:THR:HG23	1:A:1446:ASP:H	1.82	0.45
1:E:898:THR:HG23	1:E:900:PRO:HD2	1.98	0.45
1:E:1919:ARG:HH12	1:E:2084:LEU:HD23	1.81	0.45
1:B:453:LYS:HB2	1:B:453:LYS:HE2	1.70	0.45
1:B:600:ALA:O	1:B:604:VAL:HG13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:967:MET:HA	1:B:1166:PRO:HA	1.99	0.45
1:B:1303:SER:HB2	1:A:1255:GLN:C	2.36	0.45
1:C:626:LEU:HD22	1:C:664:ILE:HD11	1.99	0.45
1:F:1583:GLU:HB2	1:F:1608:LEU:HD21	1.98	0.45
1:F:1789:VAL:HG12	1:F:1791:HIS:H	1.81	0.45
1:F:2113:VAL:HG22	1:E:2146:SER:OG	2.16	0.45
1:E:105:THR:HG22	1:E:153:LYS:HB3	1.99	0.45
1:D:1340:ILE:HG22	1:D:1342:THR:HG22	1.97	0.45
1:D:1340:ILE:HD11	1:D:1390:PRO:HB3	1.98	0.45
1:D:1451:GLN:O	1:D:1455:SER:N	2.48	0.45
1:C:1682:ALA:O	1:C:1686:ILE:HG12	2.16	0.45
1:C:1730:ARG:HG2	1:C:1743:GLU:HG2	1.99	0.45
1:C:1932:LEU:HB2	1:C:2099:ILE:HD11	1.98	0.45
1:F:480:ARG:HD3	1:F:1238:ARG:NH1	2.30	0.45
1:F:712:HIS:HB2	1:F:714:ARG:HG2	1.98	0.45
1:A:15:SER:O	1:A:18:THR:OG1	2.33	0.45
1:A:82:HIS:CD2	1:A:83:PRO:HD2	2.52	0.45
1:A:285:SER:HB2	1:A:403:GLU:HB3	1.98	0.45
1:A:340:ARG:HG2	1:A:373:LEU:HD13	1.97	0.45
1:A:967:MET:HA	1:A:1166:PRO:HA	1.99	0.45
1:A:2115:ASN:OD1	1:A:2116:LYS:HG2	2.16	0.45
1:E:629:LEU:HD13	1:E:668:LEU:HD11	1.97	0.45
1:D:1634:GLU:OE1	1:D:1637:ARG:NH2	2.49	0.45
1:D:2052:VAL:CG2	1:C:205:ALA:HB2	2.43	0.45
1:B:285:SER:HB2	1:B:403:GLU:HB3	1.98	0.45
1:C:839:GLU:OE1	1:C:839:GLU:N	2.28	0.45
1:C:952:ILE:HD11	1:C:960:ILE:HD12	1.98	0.45
1:C:1919:ARG:HH12	1:C:2084:LEU:HD23	1.81	0.45
1:F:609:PHE:O	1:F:613:ILE:HG12	2.17	0.45
1:F:1645:PRO:HB2	1:F:1648:ASP:HB2	1.97	0.45
1:F:1659:THR:HG23	1:F:1662:GLU:H	1.81	0.45
1:A:52:ASP:OD2	1:A:1666:ARG:NE	2.50	0.45
1:E:623:PHE:O	1:E:627:ARG:HG3	2.16	0.45
1:B:38:ILE:HG13	1:B:39:VAL:N	2.32	0.45
1:B:340:ARG:HG2	1:B:373:LEU:HD13	1.97	0.45
1:C:311:GLN:HG3	1:C:353:TYR:CE2	2.52	0.45
1:F:928:GLY:H	1:F:931:LYS:HD3	1.82	0.45
1:F:1364:GLN:NE2	1:E:2047:LEU:HB2	2.31	0.45
1:A:786:CYS:O	1:A:790:ILE:HG12	2.16	0.45
1:A:1664:LEU:HD21	1:A:1685:MET:HE3	1.98	0.45
1:E:842:HIS:CE1	1:E:1021:ARG:HA	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1418:ARG:HB2	1:E:1423:TRP:CZ3	2.52	0.45
1:F:1418:ARG:NH2	1:F:1421:GLY:HA2	2.32	0.45
1:A:1205:LEU:HD21	1:A:1233:THR:HG23	1.98	0.45
1:E:116:ASP:N	1:E:116:ASP:OD1	2.43	0.45
1:E:1636:TRP:CH2	1:E:1640:LYS:HG3	2.52	0.45
1:E:1706:SER:HA	1:E:1735:PHE:CE1	2.51	0.45
1:D:712:HIS:HB2	1:D:714:ARG:HG2	1.98	0.45
1:D:1364:GLN:NE2	1:C:2047:LEU:HB2	2.31	0.45
1:D:1418:ARG:NH2	1:D:1421:GLY:HA2	2.32	0.45
1:C:357:ILE:HG23	1:C:358:GLN:HG3	1.98	0.45
1:C:421:THR:HG21	1:A:597:LEU:HD12	1.98	0.45
1:C:682:LYS:HE3	1:C:682:LYS:HB3	1.84	0.45
1:F:1297:SER:HB2	1:E:1451:GLN:NE2	2.31	0.45
1:A:713:TYR:CE2	1:A:1170:GLU:HG2	2.52	0.45
1:A:1371:ILE:HD12	1:A:1371:ILE:HA	1.80	0.45
1:E:1104:TYR:OH	1:E:1146:HIS:ND1	2.31	0.45
1:D:277:ASN:HB3	1:D:281:ARG:HH21	1.82	0.45
1:D:1014:LYS:NZ	1:D:1053:LYS:HD3	2.32	0.45
1:D:1693:TYR:HE2	1:D:1836:ILE:HD11	1.82	0.45
1:D:1868:TYR:CG	1:D:1898:GLU:HB2	2.52	0.45
1:B:1358:LEU:HD22	1:B:1385:ARG:HB2	1.99	0.45
1:C:298:LEU:HD21	1:C:302:TYR:HB2	1.99	0.45
1:C:834:SER:HB3	1:C:896:ILE:HG13	1.99	0.45
1:C:927:GLY:HA2	1:C:931:LYS:HG2	1.99	0.45
1:C:1418:ARG:HB2	1:C:1423:TRP:CZ3	2.52	0.45
1:F:31:LEU:HD13	1:F:191:ILE:HG12	1.98	0.45
1:F:1014:LYS:NZ	1:F:1053:LYS:HD3	2.32	0.45
1:F:1298:HIS:CG	1:F:1299:LYS:N	2.85	0.45
1:F:1879:PHE:HB3	1:F:1886:LEU:HB2	2.00	0.45
1:A:502:SER:OG	1:A:506:GLY:HA2	2.17	0.45
1:E:298:LEU:HD21	1:E:302:TYR:HB2	1.99	0.45
1:E:311:GLN:OE1	1:E:315:ARG:NH2	2.49	0.45
1:E:330:ALA:HB3	1:E:544:ASP:OD2	2.17	0.45
1:E:834:SER:HB3	1:E:896:ILE:HG13	1.99	0.45
1:E:937:GLY:O	1:E:941:LYS:HG3	2.17	0.45
1:E:1446:ASP:OD1	1:E:1446:ASP:N	2.50	0.45
1:D:1195:ASP:OD1	1:D:1195:ASP:N	2.51	0.44
1:B:1205:LEU:HD21	1:B:1233:THR:HG23	1.98	0.44
1:C:105:THR:HG22	1:C:153:LYS:HB3	1.99	0.44
1:C:307:THR:HG23	1:C:308:LEU:HD12	1.99	0.44
1:C:1918:ASN:O	1:C:1919:ARG:C	2.55	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:139:LEU:HD13	1:F:152:TYR:HB2	1.98	0.44
1:F:1915:LEU:HD11	1:F:2085:THR:HG23	1.98	0.44
1:F:2047:LEU:CD1	1:E:1360:LEU:HD23	2.46	0.44
1:F:2146:SER:HB2	1:E:2118:ILE:N	2.32	0.44
1:E:768:TYR:CE2	1:E:786:CYS:HB2	2.51	0.44
1:E:1672:VAL:HG21	1:E:1682:ALA:HB1	1.99	0.44
1:E:1846:GLN:HB2	1:E:1851:SER:HB2	1.98	0.44
1:E:1932:LEU:HB2	1:E:2099:ILE:HD11	1.98	0.44
1:D:278:HIS:HA	1:D:281:ARG:HG2	1.98	0.44
1:B:2115:ASN:OD1	1:B:2116:LYS:HG2	2.16	0.44
1:C:623:PHE:O	1:C:627:ARG:HG3	2.16	0.44
1:C:863:PRO:HG2	1:C:868:LEU:HB2	2.00	0.44
1:C:1636:TRP:CH2	1:C:1640:LYS:HG3	2.52	0.44
1:F:498:TRP:CH2	1:F:514:PRO:HG3	2.52	0.44
1:F:796:GLU:HG3	1:F:1075:LEU:HA	1.98	0.44
1:F:1022:LYS:HZ2	1:F:1022:LYS:HB3	1.82	0.44
1:A:1084:PHE:HE1	1:A:1130:HIS:ND1	2.14	0.44
1:A:1929:PHE:O	1:A:1933:LEU:HG	2.18	0.44
1:E:548:ILE:HD12	1:E:549:ASP:H	1.83	0.44
1:D:609:PHE:O	1:D:613:ILE:HG12	2.17	0.44
1:D:637:TYR:HB2	1:D:1164:VAL:CG1	2.47	0.44
1:D:1602:LYS:HB3	1:D:1603:PRO:HD3	1.99	0.44
1:B:52:ASP:O	1:B:1669:ARG:NH2	2.44	0.44
1:B:952:ILE:HD11	1:B:960:ILE:HD12	1.99	0.44
1:B:1078:GLN:O	1:B:1081:THR:OG1	2.35	0.44
1:B:1591:LYS:HA	1:B:1599:ILE:HB	2.00	0.44
1:B:1664:LEU:HD11	1:B:1685:MET:HE3	2.00	0.44
1:B:1929:PHE:O	1:B:1933:LEU:HG	2.18	0.44
1:B:2150:PHE:O	1:A:2063:ARG:HG2	2.18	0.44
1:C:967:MET:HE1	1:C:1139:TRP:CE2	2.52	0.44
1:F:1340:ILE:HD11	1:F:1390:PRO:HB3	1.98	0.44
1:E:311:GLN:HG3	1:E:353:TYR:CE2	2.52	0.44
1:E:626:LEU:HD22	1:E:664:ILE:HD11	1.99	0.44
1:E:952:ILE:HD11	1:E:960:ILE:HD12	1.98	0.44
1:D:498:TRP:CH2	1:D:514:PRO:HG3	2.52	0.44
1:D:1879:PHE:HB3	1:D:1886:LEU:HB2	2.00	0.44
1:D:2122:ASP:HB2	1:C:2132:ARG:HH22	1.82	0.44
1:B:52:ASP:OD2	1:B:1666:ARG:NE	2.50	0.44
1:B:502:SER:OG	1:B:506:GLY:HA2	2.17	0.44
1:C:428:GLU:O	1:C:602:ARG:NH1	2.50	0.44
1:C:937:GLY:O	1:C:941:LYS:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:ARG:O	1:A:195:ARG:NH1	2.40	0.44
1:E:108:PHE:CD2	1:E:154:ILE:HD11	2.53	0.44
1:E:125:LYS:HA	1:E:156:PHE:HE2	1.82	0.44
1:D:888:THR:HG22	1:D:890:ALA:H	1.83	0.44
1:D:1195:ASP:HB2	1:D:1398:MET:CE	2.46	0.44
1:B:82:HIS:CD2	1:B:83:PRO:HD2	2.52	0.44
1:B:1209:GLN:HB3	1:B:1276:LEU:HD22	1.99	0.44
1:C:227:ILE:H	1:C:227:ILE:HG13	1.68	0.44
1:C:964:ARG:NH2	1:C:1088:ASP:OD2	2.47	0.44
1:C:1370:TYR:OH	1:C:1557:LYS:O	2.34	0.44
1:F:1602:LYS:HB3	1:F:1603:PRO:HD3	1.99	0.44
1:A:1591:LYS:HA	1:A:1599:ILE:HB	2.00	0.44
1:A:1853:ARG:HD3	1:A:1853:ARG:HA	1.69	0.44
1:E:307:THR:HG23	1:E:308:LEU:HD12	1.99	0.44
1:B:756:GLU:OE1	1:B:761:GLU:HA	2.16	0.44
1:C:323:ASN:HD21	1:E:316:ARG:HH21	1.66	0.44
1:C:330:ALA:HB3	1:C:544:ASP:OD2	2.17	0.44
1:C:746:VAL:HG21	1:C:1040:PHE:CD1	2.53	0.44
1:C:863:PRO:HB2	1:C:867:LYS:HB3	2.00	0.44
1:C:909:GLU:OE1	1:C:1063:LYS:HG2	2.17	0.44
1:C:1602:LYS:HB3	1:C:1603:PRO:HD3	2.00	0.44
1:F:2122:ASP:HB2	1:E:2132:ARG:HH22	1.82	0.44
1:A:50:ASN:HB3	1:A:1670:VAL:HG23	2.00	0.44
1:A:1341:PHE:O	1:A:1342:THR:OG1	2.28	0.44
1:E:27:TYR:O	1:E:31:LEU:HG	2.18	0.44
1:E:909:GLU:OE1	1:E:1063:LYS:HG2	2.17	0.44
1:E:1083:LEU:HD23	1:E:1083:LEU:HA	1.81	0.44
1:E:1837:LYS:HA	1:E:1837:LYS:HD3	1.75	0.44
1:D:139:LEU:HD13	1:D:152:TYR:HB2	1.98	0.44
1:D:337:MET:SD	1:D:511:PHE:HD2	2.41	0.44
1:D:971:ALA:HA	1:D:1162:THR:HG22	2.00	0.44
1:D:2113:VAL:HG11	1:C:2150:PHE:CD2	2.53	0.44
1:B:10:LYS:HD2	1:B:10:LYS:HA	1.83	0.44
1:B:792:LEU:O	1:B:796:GLU:HG2	2.18	0.44
1:B:1070:VAL:HG13	1:B:1093:PHE:CZ	2.53	0.44
1:B:1365:HIS:C	1:B:1367:THR:H	2.21	0.44
1:B:1531:LEU:HD23	1:B:1531:LEU:HA	1.84	0.44
1:C:108:PHE:CD2	1:C:154:ILE:HD11	2.53	0.44
1:C:613:ILE:HD13	1:C:613:ILE:HA	1.81	0.44
1:F:968:TYR:CE2	1:F:1172:LEU:HD21	2.53	0.44
1:F:1586:CYS:O	1:F:1590:LEU:HD23	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1078:GLN:O	1:A:1081:THR:OG1	2.35	0.44
1:A:1209:GLN:HB3	1:A:1276:LEU:HD22	1.99	0.44
1:A:1337:GLN:OE1	1:A:1418:ARG:HD2	2.18	0.44
1:A:1908:ILE:HG12	1:A:2042:TRP:HB3	1.99	0.44
1:E:746:VAL:HG21	1:E:1040:PHE:CD1	2.53	0.44
1:E:856:LEU:HD21	1:E:862:ASN:HB3	2.00	0.44
1:E:863:PRO:HG2	1:E:868:LEU:HB2	2.00	0.44
1:E:912:TYR:HA	1:E:915:ILE:HG22	1.99	0.44
1:E:927:GLY:HA2	1:E:931:LYS:HG2	1.99	0.44
1:D:968:TYR:CE2	1:D:1172:LEU:HD21	2.53	0.44
1:D:1789:VAL:HG12	1:D:1791:HIS:H	1.81	0.44
1:B:1443:THR:HG23	1:B:1446:ASP:H	1.82	0.44
1:C:148:ILE:HG13	1:C:149:PRO:HD2	2.00	0.44
1:F:637:TYR:HB2	1:F:1164:VAL:CG1	2.47	0.44
1:F:1868:TYR:CG	1:F:1898:GLU:HB2	2.52	0.44
1:E:67:PRO:HD2	1:E:70:ILE:HD11	1.98	0.44
1:E:1730:ARG:HG2	1:E:1743:GLU:HG2	1.99	0.44
1:E:1766:MET:N	1:E:1766:MET:SD	2.91	0.44
1:D:431:ILE:HD11	1:D:471:THR:HG23	1.99	0.44
1:D:1586:CYS:O	1:D:1590:LEU:HD23	2.18	0.44
1:B:1079:VAL:O	1:B:1083:LEU:N	2.49	0.44
1:C:27:TYR:O	1:C:31:LEU:HG	2.18	0.44
1:C:114:THR:OG1	1:C:116:ASP:OD1	2.26	0.44
1:F:888:THR:HG22	1:F:890:ALA:H	1.83	0.44
1:A:183:TYR:O	1:A:187:VAL:HG13	2.18	0.44
1:A:792:LEU:O	1:A:796:GLU:HG2	2.18	0.44
1:A:1664:LEU:HD11	1:A:1685:MET:HE3	2.00	0.44
1:D:1298:HIS:CG	1:D:1299:LYS:N	2.85	0.43
1:B:1908:ILE:HG12	1:B:2042:TRP:HB3	1.99	0.43
1:C:356:ARG:HD2	1:C:1414:MET:HE3	1.98	0.43
1:C:1672:VAL:HG21	1:C:1682:ALA:HB1	1.99	0.43
1:A:849:ILE:HG13	1:A:1383:LEU:HD12	1.98	0.43
1:A:1358:LEU:HD22	1:A:1385:ARG:HB2	1.99	0.43
1:A:1531:LEU:HD23	1:A:1531:LEU:HA	1.84	0.43
1:A:1555:VAL:O	1:A:1559:ILE:HG22	2.18	0.43
1:A:1865:ASP:O	1:A:1867:ARG:NH1	2.51	0.43
1:E:1838:ASP:OD2	1:E:1842:ARG:NE	2.51	0.43
1:E:1901:MET:HG3	1:E:1902:LYS:HE3	1.99	0.43
1:D:52:ASP:OD1	1:D:52:ASP:N	2.51	0.43
1:B:295:GLN:HE22	1:B:539:ASP:HB3	1.83	0.43
1:C:125:LYS:HA	1:C:156:PHE:HE2	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:640:PHE:CG	1:C:641:PRO:HD3	2.53	0.43
1:F:971:ALA:HA	1:F:1162:THR:HG22	2.00	0.43
1:A:317:ALA:HB1	1:A:509:ILE:CD1	2.49	0.43
1:A:860:ARG:O	1:A:860:ARG:HD3	2.18	0.43
1:A:1868:TYR:O	1:A:1871:VAL:HG12	2.19	0.43
1:E:756:GLU:HA	1:E:764:VAL:HG21	2.01	0.43
1:D:1080:TRP:HE1	1:D:1089:CYS:HB2	1.83	0.43
1:D:1250:PRO:HG3	1:D:1266:GLY:O	2.18	0.43
1:B:1341:PHE:O	1:B:1342:THR:OG1	2.28	0.43
1:B:1555:VAL:O	1:B:1559:ILE:HG22	2.18	0.43
1:B:1868:TYR:O	1:B:1871:VAL:HG12	2.19	0.43
1:C:298:LEU:HD11	1:C:478:LEU:HD22	2.00	0.43
1:C:912:TYR:HA	1:C:915:ILE:HG22	1.99	0.43
1:C:1581:THR:O	1:C:1585:ILE:HG12	2.18	0.43
1:C:1702:ARG:HG3	1:C:1703:ARG:N	2.34	0.43
1:F:255:ARG:HA	1:F:255:ARG:HD3	1.70	0.43
1:F:1084:PHE:CZ	1:F:1134:VAL:HG21	2.51	0.43
1:A:911:TYR:CD1	1:A:1005:VAL:HG21	2.53	0.43
1:E:428:GLU:O	1:E:602:ARG:NH1	2.50	0.43
1:E:518:LEU:HD23	1:E:518:LEU:HA	1.87	0.43
1:E:1702:ARG:HG3	1:E:1703:ARG:N	2.34	0.43
1:D:43:ILE:HD11	1:D:172:TRP:CD2	2.53	0.43
1:D:1915:LEU:HD11	1:D:2085:THR:HG23	1.98	0.43
1:D:2150:PHE:HZ	1:C:2120:PRO:HA	1.80	0.43
1:B:860:ARG:O	1:B:860:ARG:HD3	2.18	0.43
1:B:2063:ARG:HG2	1:A:2150:PHE:O	2.18	0.43
1:C:252:SER:HB2	1:C:1129:LEU:HB3	2.00	0.43
1:C:1650:PHE:CD1	1:C:1660:PHE:HB3	2.53	0.43
1:C:1766:MET:SD	1:C:1766:MET:N	2.91	0.43
1:C:1901:MET:HG3	1:C:1902:LYS:HE3	1.99	0.43
1:C:1940:ASN:ND2	1:C:2066:SER:O	2.52	0.43
1:A:1645:PRO:HG2	1:A:1649:TRP:CD1	2.53	0.43
1:E:2065:ILE:HG23	1:E:2069:PHE:HD2	1.83	0.43
1:D:1223:GLN:NE2	1:D:1593:MET:O	2.51	0.43
1:B:597:LEU:HD12	1:E:421:THR:HG21	1.98	0.43
1:B:1501:ASN:OD1	1:B:1501:ASN:N	2.52	0.43
1:C:1349:PHE:HD1	1:C:1352:MET:SD	2.41	0.43
1:C:1838:ASP:OD2	1:C:1842:ARG:NE	2.51	0.43
1:F:52:ASP:OD1	1:F:52:ASP:N	2.51	0.43
1:F:312:ILE:HD12	1:F:312:ILE:HA	1.92	0.43
1:F:2113:VAL:HG11	1:E:2150:PHE:CD2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:35:ARG:O	1:A:39:VAL:HG23	2.19	0.43
1:A:240:ILE:O	1:A:244:VAL:HG23	2.19	0.43
1:A:1070:VAL:HG13	1:A:1093:PHE:CZ	2.53	0.43
1:A:1351:ASP:OD1	1:A:1351:ASP:N	2.47	0.43
1:E:356:ARG:HD2	1:E:1414:MET:HE3	2.00	0.43
1:E:461:LYS:HG2	1:E:462:TYR:CD2	2.54	0.43
1:E:1650:PHE:CD1	1:E:1660:PHE:HB3	2.53	0.43
1:E:1794:LEU:HB2	1:E:1803:TRP:CZ3	2.54	0.43
1:D:1514:THR:HG22	1:C:2050:GLU:HG2	1.91	0.43
1:D:1837:LYS:HD3	1:D:1837:LYS:HA	1.84	0.43
1:B:35:ARG:O	1:B:39:VAL:HG23	2.19	0.43
1:B:1910:PRO:HG3	1:B:2048:SER:HB3	2.01	0.43
1:B:2091:VAL:HA	1:B:2094:TRP:CD1	2.54	0.43
1:C:425:SER:O	1:C:429:LEU:HD13	2.18	0.43
1:C:548:ILE:HD12	1:C:549:ASP:H	1.83	0.43
1:C:1794:LEU:HB2	1:C:1803:TRP:CZ3	2.54	0.43
1:C:2065:ILE:HG23	1:C:2069:PHE:HD2	1.83	0.43
1:F:1195:ASP:OD1	1:F:1195:ASP:N	2.51	0.43
1:F:1940:ASN:ND2	1:F:2066:SER:O	2.52	0.43
1:A:38:ILE:HG13	1:A:39:VAL:N	2.32	0.43
1:A:918:ASN:OD1	1:A:918:ASN:N	2.49	0.43
1:E:734:ASN:OD1	1:E:735:MET:N	2.52	0.43
1:E:989:THR:HG23	1:E:1006:ILE:HG12	1.99	0.43
1:E:1906:ALA:HB3	1:E:2042:TRP:CD2	2.53	0.43
1:B:56:ALA:O	1:B:60:VAL:HG23	2.19	0.43
1:B:905:LEU:HD13	1:B:905:LEU:HA	1.89	0.43
1:B:1366:VAL:O	1:B:1366:VAL:HG22	2.19	0.43
1:C:316:ARG:HH21	1:E:323:ASN:HD21	1.66	0.43
1:C:1188:ILE:H	1:C:1188:ILE:HD12	1.83	0.43
1:C:1906:ALA:HB3	1:C:2042:TRP:CD2	2.53	0.43
1:F:204:ARG:HH11	1:E:2054:SER:HB2	1.83	0.43
1:F:316:ARG:HG2	1:F:320:TYR:CZ	2.54	0.43
1:F:1223:GLN:NE2	1:F:1593:MET:O	2.51	0.43
1:A:67:PRO:O	1:A:71:ILE:HG12	2.19	0.43
1:A:295:GLN:OE1	1:A:539:ASP:N	2.46	0.43
1:A:1079:VAL:O	1:A:1083:LEU:N	2.49	0.43
1:E:252:SER:HB2	1:E:1129:LEU:HB3	2.00	0.43
1:D:855:TYR:OH	1:D:871:GLU:OE1	2.34	0.43
1:B:540:LYS:HA	1:B:543:LEU:HD12	2.01	0.43
1:B:1010:LYS:HE2	1:B:1010:LYS:HB3	1.59	0.43
1:B:1645:PRO:HG2	1:B:1649:TRP:CD1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1664:LEU:HD21	1:B:1685:MET:HE3	2.00	0.43
1:C:427:LEU:HD23	1:C:427:LEU:HA	1.85	0.43
1:C:1324:HIS:HE2	1:C:1369:ASP:CG	2.22	0.43
1:C:1446:ASP:N	1:C:1446:ASP:OD1	2.50	0.43
1:F:1283:MET:HG3	1:F:1287:ASN:HD21	1.84	0.43
1:E:293:LEU:HD23	1:E:570:LEU:HD11	2.00	0.43
1:E:449:THR:HG21	1:E:1272:SER:HB2	2.01	0.43
1:E:863:PRO:HB2	1:E:867:LYS:HB3	2.00	0.43
1:E:1283:MET:SD	1:E:1461:GLU:HB3	2.59	0.43
1:E:1602:LYS:HB3	1:E:1603:PRO:HD3	2.00	0.43
1:D:195:ARG:HH21	1:C:2056:VAL:HG21	1.84	0.43
1:D:840:ASP:OD1	1:D:840:ASP:N	2.52	0.43
1:D:1462:TYR:CD1	1:D:1608:LEU:HD22	2.54	0.43
1:B:183:TYR:O	1:B:187:VAL:HG13	2.18	0.43
1:B:1080:TRP:HA	1:B:1083:LEU:HB2	2.00	0.43
1:C:449:THR:HG21	1:C:1272:SER:HB2	2.01	0.43
1:C:856:LEU:HD21	1:C:862:ASN:HB3	2.00	0.43
1:F:337:MET:SD	1:F:511:PHE:HD2	2.41	0.43
1:F:470:THR:HG22	1:F:602:ARG:HD3	2.01	0.43
1:A:10:LYS:HD2	1:A:10:LYS:HA	1.83	0.43
1:A:498:TRP:CD1	1:A:498:TRP:N	2.87	0.43
1:A:601:ILE:HD13	1:A:601:ILE:HA	1.90	0.43
1:A:769:MET:N	1:A:772:GLU:OE2	2.47	0.43
1:A:905:LEU:HD13	1:A:905:LEU:HA	1.89	0.43
1:E:640:PHE:CG	1:E:641:PRO:HD3	2.53	0.43
1:D:316:ARG:HG2	1:D:320:TYR:CZ	2.54	0.43
1:D:628:TYR:CE2	1:D:1161:LYS:HE3	2.54	0.43
1:D:1364:GLN:HE22	1:C:2047:LEU:HB2	1.84	0.43
1:D:1699:GLN:HE22	1:D:1703:ARG:HB3	1.84	0.43
1:B:3:LYS:NZ	1:B:1665:ASP:OD2	2.48	0.43
1:C:293:LEU:HD23	1:C:570:LEU:HD11	2.00	0.43
1:C:461:LYS:HG2	1:C:462:TYR:CD2	2.54	0.43
1:C:734:ASN:OD1	1:C:735:MET:N	2.52	0.43
1:C:1283:MET:SD	1:C:1461:GLU:HB3	2.59	0.43
1:C:1640:LYS:NZ	1:C:1839:ASP:O	2.31	0.43
1:F:1292:ALA:HB1	1:F:1308:LEU:HD12	2.01	0.43
1:F:1333:ILE:HG13	1:F:1453:LEU:HD22	2.01	0.43
1:A:334:ILE:HD12	1:A:511:PHE:CD1	2.54	0.43
1:A:1114:THR:HA	1:A:1117:PHE:CD1	2.54	0.43
1:A:1565:LYS:HB2	1:A:1565:LYS:HE2	1.86	0.43
1:E:425:SER:O	1:E:429:LEU:HD13	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1177:GLU:O	1:E:1181:VAL:HG12	2.19	0.43
1:E:1347:PHE:CZ	1:E:1393:VAL:HG13	2.54	0.43
1:E:1569:SER:O	1:E:1569:SER:OG	2.35	0.43
1:D:1471:ILE:HD12	1:D:1603:PRO:HG2	2.00	0.42
1:D:1620:ILE:HD12	1:D:1624:LYS:HZ1	1.83	0.42
1:D:2146:SER:HB2	1:C:2118:ILE:N	2.32	0.42
1:B:42:MET:HG2	1:B:180:VAL:HG21	2.01	0.42
1:B:240:ILE:O	1:B:244:VAL:HG23	2.19	0.42
1:B:1076:PHE:CD1	1:B:1149:ILE:HD11	2.52	0.42
1:B:2151:TYR:HA	1:A:2067:LYS:HE3	2.01	0.42
1:C:673:GLN:HB3	1:A:422:LYS:HZ2	1.84	0.42
1:C:809:ALA:HB2	1:C:995:GLY:HA3	2.01	0.42
1:C:1795:PHE:HB3	1:C:1812:VAL:HG22	2.01	0.42
1:F:1514:THR:HG1	1:F:1517:GLU:HG3	1.82	0.42
1:A:295:GLN:HE22	1:A:539:ASP:HB3	1.83	0.42
1:A:1539:LYS:HE3	1:A:1539:LYS:HB3	1.84	0.42
1:D:255:ARG:HA	1:D:255:ARG:HD3	1.70	0.42
1:D:1333:ILE:HG13	1:D:1453:LEU:HD22	2.01	0.42
1:D:1514:THR:HG1	1:D:1517:GLU:HG3	1.83	0.42
1:B:50:ASN:HB3	1:B:1670:VAL:HG23	2.00	0.42
1:B:67:PRO:O	1:B:71:ILE:HG12	2.19	0.42
1:B:334:ILE:HD12	1:B:511:PHE:CD1	2.54	0.42
1:B:911:TYR:CD1	1:B:1005:VAL:HG21	2.53	0.42
1:B:912:TYR:OH	1:B:989:THR:HB	2.19	0.42
1:B:1337:GLN:OE1	1:B:1418:ARG:HD2	2.18	0.42
1:C:489:HIS:NE2	1:C:497:TYR:O	2.44	0.42
1:F:43:ILE:HD11	1:F:172:TRP:CD2	2.53	0.42
1:F:195:ARG:HH21	1:E:2056:VAL:HG21	1.84	0.42
1:F:431:ILE:HD11	1:F:471:THR:HG23	1.99	0.42
1:F:798:ASN:HD21	1:F:993:HIS:H	1.68	0.42
1:F:1835:THR:HB	1:F:1844:ILE:HG13	2.01	0.42
1:A:4:TYR:HA	1:A:7:ILE:HG22	2.01	0.42
1:E:809:ALA:HB2	1:E:995:GLY:HA3	2.01	0.42
1:B:317:ALA:HB1	1:B:509:ILE:CD1	2.49	0.42
1:B:1263:ILE:HG12	1:B:1285:ASP:OD1	2.19	0.42
1:C:707:ARG:HA	1:C:707:ARG:HD2	1.50	0.42
1:F:193:TYR:OH	1:F:198:LEU:HD21	2.19	0.42
1:A:739:ALA:O	1:A:743:LEU:HG	2.20	0.42
1:A:1366:VAL:HG22	1:A:1366:VAL:O	2.19	0.42
1:A:2086:GLU:O	1:A:2090:ILE:HG13	2.20	0.42
1:E:1188:ILE:H	1:E:1188:ILE:HD12	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:1349:PHE:HD1	1:E:1352:MET:SD	2.41	0.42
1:D:748:TRP:CD1	1:D:978:PRO:HB2	2.55	0.42
1:D:798:ASN:HD21	1:D:993:HIS:H	1.68	0.42
1:B:985:PHE:CE2	1:B:1068:PHE:HB2	2.48	0.42
1:C:756:GLU:HA	1:C:764:VAL:HG21	2.01	0.42
1:C:823:SER:O	1:C:823:SER:OG	2.38	0.42
1:F:748:TRP:CD1	1:F:978:PRO:HB2	2.55	0.42
1:F:1080:TRP:HE1	1:F:1089:CYS:HB2	1.83	0.42
1:F:1250:PRO:HG3	1:F:1266:GLY:O	2.18	0.42
1:A:682:LYS:HE3	1:A:683:VAL:HG12	2.02	0.42
1:A:1076:PHE:CD1	1:A:1149:ILE:HD11	2.52	0.42
1:A:1080:TRP:HA	1:A:1083:LEU:HB2	2.00	0.42
1:A:1365:HIS:C	1:A:1367:THR:H	2.21	0.42
1:A:1518:MET:HA	1:A:1521:VAL:HG12	2.01	0.42
1:A:1910:PRO:HG3	1:A:2048:SER:HB3	2.01	0.42
1:E:298:LEU:HD11	1:E:478:LEU:HD22	2.00	0.42
1:E:489:HIS:NE2	1:E:497:TYR:O	2.44	0.42
1:E:1940:ASN:ND2	1:E:2066:SER:O	2.52	0.42
1:D:901:THR:O	1:D:905:LEU:HD23	2.20	0.42
1:B:867:LYS:O	1:B:871:GLU:HG2	2.19	0.42
1:B:1518:MET:HA	1:B:1521:VAL:HG12	2.01	0.42
1:C:1104:TYR:HD1	1:C:1142:MET:HE2	1.85	0.42
1:C:1345:SER:OG	1:C:1346:GLU:OE1	2.38	0.42
1:C:1347:PHE:CZ	1:C:1393:VAL:HG13	2.54	0.42
1:F:646:LYS:HD2	1:F:1160:LYS:HD2	2.01	0.42
1:F:1462:TYR:CD1	1:F:1608:LEU:HD22	2.54	0.42
1:F:1471:ILE:HD12	1:F:1603:PRO:HG2	2.00	0.42
1:F:1616:ARG:O	1:F:1620:ILE:HG12	2.20	0.42
1:F:1699:GLN:HE22	1:F:1703:ARG:HB3	1.84	0.42
1:A:422:LYS:HD3	1:A:422:LYS:HA	1.46	0.42
1:E:1913:TYR:O	1:E:1917:MET:HG2	2.20	0.42
1:E:1915:LEU:O	1:E:1919:ARG:HB2	2.20	0.42
1:D:193:TYR:OH	1:D:198:LEU:HD21	2.19	0.42
1:D:1299:LYS:HD3	1:D:1300:ARG:H	1.85	0.42
1:B:44:LYS:NZ	1:B:51:LYS:H	2.18	0.42
1:B:255:ARG:HA	1:B:255:ARG:HD3	1.88	0.42
1:B:422:LYS:HZ2	1:E:673:GLN:HB3	1.85	0.42
1:B:579:ILE:HD12	1:B:1193:LEU:HD11	2.01	0.42
1:B:1684:LEU:HD21	1:B:1841:LEU:HA	2.02	0.42
1:C:234:GLU:OE1	1:C:234:GLU:N	2.53	0.42
1:F:746:VAL:HG21	1:F:1040:PHE:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:901:THR:O	1:F:905:LEU:HD23	2.20	0.42
1:E:244:VAL:HG13	1:E:1083:LEU:HD23	2.01	0.42
1:E:925:SER:OG	1:E:931:LYS:HB2	2.19	0.42
1:E:1581:THR:O	1:E:1585:ILE:HG12	2.18	0.42
1:D:291:PHE:HB3	1:D:654:SER:HB2	2.02	0.42
1:D:1616:ARG:O	1:D:1620:ILE:HG12	2.20	0.42
1:D:1846:GLN:HB2	1:D:1851:SER:HB2	2.02	0.42
1:B:739:ALA:O	1:B:743:LEU:HG	2.20	0.42
1:B:770:MET:HE1	1:B:774:ARG:HE	1.85	0.42
1:B:1139:TRP:HA	1:B:1142:MET:CG	2.50	0.42
1:C:374:THR:O	1:C:377:MET:HE2	2.20	0.42
1:C:1169:ALA:O	1:C:1173:SER:OG	2.23	0.42
1:F:19:LEU:CD1	1:F:198:LEU:HB3	2.50	0.42
1:F:1104:TYR:OH	1:F:1146:HIS:ND1	2.41	0.42
1:A:579:ILE:HD12	1:A:1193:LEU:HD11	2.01	0.42
1:A:1243:ALA:HB3	1:A:1246:MET:HE1	2.02	0.42
1:A:2064:TYR:CE2	1:A:2068:THR:HG21	2.55	0.42
1:A:2141:LEU:HD23	1:A:2141:LEU:HA	1.89	0.42
1:E:148:ILE:HG13	1:E:149:PRO:HD2	2.00	0.42
1:E:1345:SER:OG	1:E:1346:GLU:OE1	2.38	0.42
1:D:293:LEU:HD23	1:D:570:LEU:HD11	2.02	0.42
1:D:470:THR:HG22	1:D:602:ARG:HD3	2.01	0.42
1:D:1581:THR:O	1:D:1585:ILE:HG12	2.20	0.42
1:D:1940:ASN:ND2	1:D:2066:SER:O	2.52	0.42
1:B:588:TYR:CE2	1:B:708:ILE:HD12	2.55	0.42
1:F:309:SER:HA	1:F:312:ILE:HG22	2.01	0.42
1:F:1607:VAL:HG12	1:F:1609:GLN:HE22	1.85	0.42
1:F:1608:LEU:HD23	1:F:1608:LEU:HA	1.90	0.42
1:A:56:ALA:O	1:A:60:VAL:HG23	2.19	0.42
1:A:540:LYS:HA	1:A:543:LEU:HD12	2.01	0.42
1:A:985:PHE:CE2	1:A:1068:PHE:HB2	2.48	0.42
1:A:2091:VAL:HA	1:A:2094:TRP:CD1	2.54	0.42
1:E:1286:LYS:O	1:E:1462:TYR:OH	2.34	0.42
1:D:646:LYS:HD2	1:D:1160:LYS:HD2	2.01	0.42
1:D:746:VAL:HG21	1:D:1040:PHE:CE1	2.54	0.42
1:D:974:THR:HG21	1:D:1066:SER:HA	2.02	0.42
1:D:1607:VAL:HG12	1:D:1609:GLN:HE22	1.85	0.42
1:B:856:LEU:O	1:B:1376:ARG:NH1	2.53	0.42
1:B:923:TYR:CE1	1:B:1074:LEU:HD11	2.51	0.42
1:B:963:LYS:HD3	1:B:964:ARG:N	2.35	0.42
1:B:1865:ASP:O	1:B:1867:ARG:NH1	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1943:ASP:N	1:B:1943:ASP:OD1	2.53	0.42
1:C:1367:THR:HG21	1:C:1517:GLU:HB3	2.02	0.42
1:F:291:PHE:HB3	1:F:654:SER:HB2	2.02	0.42
1:F:628:TYR:CE2	1:F:1161:LYS:HE3	2.54	0.42
1:F:1544:ARG:NH2	1:F:1620:ILE:HG21	2.35	0.42
1:A:420:ILE:HG21	1:A:659:TYR:CD1	2.55	0.42
1:A:640:PHE:O	1:A:644:ILE:HG12	2.20	0.42
1:A:856:LEU:O	1:A:1376:ARG:NH1	2.53	0.42
1:A:1149:ILE:HA	1:A:1152:LEU:HG	2.02	0.42
1:A:1356:LYS:H	1:A:1356:LYS:HG2	1.61	0.42
1:A:1501:ASN:OD1	1:A:1501:ASN:N	2.52	0.42
1:E:234:GLU:OE1	1:E:234:GLU:N	2.53	0.42
1:D:1283:MET:HG3	1:D:1287:ASN:HD21	1.84	0.42
1:D:1658:LYS:HE3	1:D:1662:GLU:HB3	2.02	0.42
1:D:2103:GLU:OE1	1:D:2103:GLU:HA	2.20	0.42
1:B:640:PHE:O	1:B:644:ILE:HG12	2.20	0.42
1:B:676:LYS:HG3	1:B:677:ALA:H	1.85	0.42
1:B:2064:TYR:CE2	1:B:2068:THR:HG21	2.55	0.42
1:C:2147:ILE:HG13	1:C:2151:TYR:HD2	1.85	0.42
1:F:972:ASP:OD1	1:F:972:ASP:N	2.47	0.42
1:F:1299:LYS:HD3	1:F:1300:ARG:H	1.85	0.42
1:F:1846:GLN:OE1	1:F:1853:ARG:NH1	2.53	0.42
1:A:1943:ASP:OD1	1:A:1943:ASP:N	2.53	0.42
1:E:1324:HIS:HE2	1:E:1369:ASP:CG	2.22	0.42
1:E:2147:ILE:HG13	1:E:2151:TYR:HD2	1.85	0.42
1:D:197:HIS:NE2	1:C:2122:ASP:HB3	2.36	0.41
1:D:707:ARG:HD3	1:D:707:ARG:H	1.86	0.41
1:B:267:VAL:HG12	1:B:640:PHE:CE1	2.55	0.41
1:B:324:LEU:HD22	1:B:547:LEU:HB3	2.02	0.41
1:B:682:LYS:HE3	1:B:683:VAL:HG12	2.02	0.41
1:B:798:ASN:OD1	1:B:993:HIS:HB3	2.20	0.41
1:B:1414:MET:O	1:B:1416:VAL:HG22	2.20	0.41
1:B:2086:GLU:O	1:B:2090:ILE:HG13	2.20	0.41
1:C:925:SER:OG	1:C:931:LYS:HB2	2.19	0.41
1:C:1177:GLU:O	1:C:1181:VAL:HG12	2.19	0.41
1:C:1658:LYS:HB3	1:C:1663:TRP:NE1	2.34	0.41
1:C:1877:VAL:N	1:C:1889:ASN:OD1	2.39	0.41
1:F:302:TYR:OH	1:F:481:ASP:OD2	2.26	0.41
1:F:840:ASP:N	1:F:840:ASP:OD1	2.52	0.41
1:F:1763:LEU:O	1:F:1767:MET:HG2	2.20	0.41
1:A:255:ARG:HA	1:A:255:ARG:HD3	1.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:298:LEU:HD23	1:A:298:LEU:HA	1.83	0.41
1:A:1263:ILE:HG12	1:A:1285:ASP:OD1	2.19	0.41
1:A:1414:MET:O	1:A:1416:VAL:HG22	2.20	0.41
1:E:1658:LYS:HB3	1:E:1663:TRP:NE1	2.34	0.41
1:D:19:LEU:CD1	1:D:198:LEU:HB3	2.50	0.41
1:D:584:TRP:CE3	1:D:604:VAL:HG21	2.55	0.41
1:D:1564:TYR:C	1:D:1565:LYS:HD3	2.41	0.41
1:D:1763:LEU:O	1:D:1767:MET:HG2	2.20	0.41
1:D:1846:GLN:OE1	1:D:1853:ARG:NH1	2.53	0.41
1:B:1111:ASP:OD1	1:B:1111:ASP:N	2.43	0.41
1:B:1149:ILE:HA	1:B:1152:LEU:HG	2.02	0.41
1:B:2067:LYS:HE3	1:A:2151:TYR:HA	2.01	0.41
1:C:796:GLU:HG3	1:C:1075:LEU:HA	2.02	0.41
1:F:186:LEU:HD12	1:E:2115:ASN:ND2	2.36	0.41
1:F:197:HIS:NE2	1:E:2122:ASP:HB3	2.36	0.41
1:F:1456:CYS:HB2	1:F:1613:ILE:HD13	2.02	0.41
1:F:1611:VAL:HG23	1:F:1615:ASN:HD22	1.85	0.41
1:F:2113:VAL:CG2	1:E:2146:SER:OG	2.69	0.41
1:F:2147:ILE:HA	1:E:2113:VAL:HG22	2.02	0.41
1:A:867:LYS:O	1:A:871:GLU:HG2	2.19	0.41
1:A:1070:VAL:HG13	1:A:1093:PHE:HZ	1.85	0.41
1:E:340:ARG:HH21	1:E:364:ASN:HB3	1.85	0.41
1:E:389:LEU:HD23	1:E:389:LEU:HA	1.89	0.41
1:E:880:ARG:NH2	1:E:881:ILE:O	2.53	0.41
1:E:964:ARG:NH2	1:E:1088:ASP:OD2	2.47	0.41
1:E:1367:THR:HG21	1:E:1517:GLU:HB3	2.02	0.41
1:E:1631:LEU:HD21	1:E:1867:ARG:H	1.86	0.41
1:B:863:PRO:HG2	1:B:868:LEU:HD22	2.02	0.41
1:B:1070:VAL:HG13	1:B:1093:PHE:HZ	1.85	0.41
1:F:257:PHE:CE2	1:F:259:PHE:HB2	2.56	0.41
1:F:2056:VAL:O	1:F:2059:ILE:HG22	2.20	0.41
1:A:44:LYS:NZ	1:A:51:LYS:H	2.18	0.41
1:A:863:PRO:HG2	1:A:868:LEU:HD22	2.02	0.41
1:A:963:LYS:HD3	1:A:964:ARG:N	2.35	0.41
1:A:2111:ASN:HB3	1:A:2112:MET:CE	2.50	0.41
1:E:843:LEU:HB3	1:E:880:ARG:HD2	2.02	0.41
1:E:1014:LYS:HE2	1:E:1014:LYS:HB3	1.85	0.41
1:E:1115:ASP:N	1:E:1115:ASP:OD1	2.53	0.41
1:D:383:LYS:HE3	1:D:383:LYS:HB2	1.89	0.41
1:D:1637:ARG:HH22	1:D:1863:ILE:HG12	1.86	0.41
1:D:2147:ILE:HA	1:C:2113:VAL:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4:TYR:HA	1:B:7:ILE:HG22	2.01	0.41
1:B:420:ILE:HG21	1:B:659:TYR:CD1	2.55	0.41
1:B:1083:LEU:HD12	1:B:1084:PHE:CE1	2.56	0.41
1:B:1161:LYS:HE2	1:B:1161:LYS:HB2	1.90	0.41
1:B:1539:LYS:HE3	1:B:1539:LYS:HB3	1.84	0.41
1:C:498:TRP:CE3	1:C:514:PRO:HD3	2.55	0.41
1:C:854:ARG:NH2	1:C:1348:GLU:OE2	2.53	0.41
1:C:1415:LYS:HD2	1:C:1424:VAL:HA	2.02	0.41
1:C:1507:ILE:HD12	1:C:1556:MET:SD	2.61	0.41
1:F:26:ASP:OD2	1:F:27:TYR:N	2.53	0.41
1:F:1006:ILE:HG22	1:F:1010:LYS:NZ	2.35	0.41
1:F:1364:GLN:HE22	1:E:2047:LEU:HB2	1.84	0.41
1:A:324:LEU:HD22	1:A:547:LEU:HB3	2.02	0.41
1:A:923:TYR:CE1	1:A:1074:LEU:HD11	2.51	0.41
1:E:854:ARG:NH2	1:E:1348:GLU:OE2	2.53	0.41
1:D:309:SER:HA	1:D:312:ILE:HG22	2.01	0.41
1:D:487:ILE:O	1:D:490:SER:OG	2.28	0.41
1:D:1006:ILE:HG22	1:D:1010:LYS:NZ	2.35	0.41
1:D:1292:ALA:HB1	1:D:1308:LEU:HD12	2.01	0.41
1:D:1611:VAL:HG23	1:D:1615:ASN:HD22	1.85	0.41
1:B:89:LYS:HE3	1:B:89:LYS:HB3	1.76	0.41
1:B:329:PRO:HB3	1:B:381:GLU:HB3	2.03	0.41
1:B:1114:THR:HA	1:B:1117:PHE:CD1	2.54	0.41
1:C:640:PHE:CD1	1:C:641:PRO:HD3	2.56	0.41
1:C:880:ARG:NH2	1:C:881:ILE:O	2.53	0.41
1:F:855:TYR:OH	1:F:871:GLU:OE1	2.34	0.41
1:F:1658:LYS:HE3	1:F:1662:GLU:HB3	2.02	0.41
1:A:1:MET:HA	1:A:1690:LYS:NZ	2.35	0.41
1:A:643:LEU:HD23	1:A:643:LEU:HA	1.92	0.41
1:A:912:TYR:OH	1:A:989:THR:HB	2.19	0.41
1:A:2101:GLN:O	1:A:2105:LEU:HD23	2.21	0.41
1:E:982:SER:HB3	1:E:1056:TRP:HE3	1.85	0.41
1:D:186:LEU:HD12	1:C:2115:ASN:ND2	2.36	0.41
1:D:1544:ARG:NH2	1:D:1620:ILE:HG21	2.35	0.41
1:B:363:GLN:HA	1:B:366:ARG:HH12	1.86	0.41
1:B:943:LEU:HD12	1:B:943:LEU:HA	1.88	0.41
1:B:1243:ALA:HB3	1:B:1246:MET:HE1	2.03	0.41
1:B:1283:MET:HG3	1:B:1287:ASN:ND2	2.36	0.41
1:B:1467:PHE:O	1:B:1471:ILE:HG12	2.21	0.41
1:B:2111:ASN:HB3	1:B:2112:MET:CE	2.50	0.41
1:C:355:PRO:HB2	1:C:357:ILE:HG22	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:932:ILE:HG13	1:C:932:ILE:H	1.66	0.41
1:C:1115:ASP:OD1	1:C:1115:ASP:N	2.53	0.41
1:C:2056:VAL:O	1:C:2060:LEU:HG	2.21	0.41
1:F:10:LYS:HD2	1:F:10:LYS:HA	1.83	0.41
1:F:293:LEU:HD23	1:F:570:LEU:HD11	2.02	0.41
1:A:329:PRO:HB3	1:A:381:GLU:HB3	2.03	0.41
1:A:363:GLN:HA	1:A:366:ARG:HH12	1.86	0.41
1:A:676:LYS:HG3	1:A:677:ALA:H	1.85	0.41
1:A:958:LYS:HA	1:A:958:LYS:HD3	1.91	0.41
1:A:1501:ASN:ND2	1:A:1527:PHE:O	2.52	0.41
1:E:682:LYS:HB3	1:E:682:LYS:HE3	1.84	0.41
1:E:1404:LEU:O	1:E:1408:MET:HG3	2.21	0.41
1:E:1468:LEU:HD23	1:E:1468:LEU:HA	1.88	0.41
1:D:640:PHE:CG	1:D:641:PRO:HD3	2.56	0.41
1:D:1036:HIS:HA	1:D:1039:GLN:HG2	2.03	0.41
1:D:2091:VAL:O	1:D:2091:VAL:HG12	2.20	0.41
1:D:2113:VAL:CG2	1:C:2146:SER:OG	2.69	0.41
1:B:1629:LEU:HD11	1:B:1672:VAL:HG13	2.03	0.41
1:B:1639:CYS:HB3	1:B:1644:ALA:HB3	2.03	0.41
1:C:1308:LEU:HD23	1:C:1308:LEU:HA	1.92	0.41
1:F:1581:THR:O	1:F:1585:ILE:HG12	2.20	0.41
1:A:125:LYS:HD3	1:A:125:LYS:HA	1.93	0.41
1:A:267:VAL:HG12	1:A:640:PHE:CE1	2.55	0.41
1:A:1283:MET:HG3	1:A:1287:ASN:ND2	2.36	0.41
1:E:361:GLN:OE1	1:E:366:ARG:HD3	2.21	0.41
1:E:1027:ILE:HA	1:E:1027:ILE:HD12	1.81	0.41
1:E:2056:VAL:O	1:E:2060:LEU:HG	2.21	0.41
1:D:1703:ARG:HA	1:D:1736:GLY:HA3	2.02	0.41
1:D:1835:THR:HB	1:D:1844:ILE:HG13	2.01	0.41
1:B:106:ILE:HB	1:B:154:ILE:HD12	2.03	0.41
1:B:498:TRP:CD1	1:B:498:TRP:N	2.87	0.41
1:B:876:LYS:NZ	1:B:1016:ASP:OD1	2.47	0.41
1:C:244:VAL:HG13	1:C:1083:LEU:HD23	2.01	0.41
1:C:1274:MET:HE2	1:C:1274:MET:HB3	1.95	0.41
1:C:1631:LEU:HD21	1:C:1867:ARG:H	1.86	0.41
1:C:1900:PHE:HD1	1:C:2038:LEU:HD22	1.86	0.41
1:F:1846:GLN:HB2	1:F:1851:SER:HB2	2.02	0.41
1:F:2091:VAL:O	1:F:2091:VAL:HG12	2.20	0.41
1:F:2103:GLU:HA	1:F:2103:GLU:OE1	2.20	0.41
1:A:56:ALA:HB1	1:A:92:PHE:O	2.21	0.41
1:A:106:ILE:HB	1:A:154:ILE:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:911:TYR:CD2	1:E:1005:VAL:HG21	2.56	0.41
1:E:1104:TYR:HD1	1:E:1142:MET:HE2	1.85	0.41
1:E:1795:PHE:HB3	1:E:1812:VAL:HG22	2.01	0.41
1:D:189:ALA:HB1	1:C:2112:MET:HA	2.03	0.41
1:D:257:PHE:CE2	1:D:259:PHE:HB2	2.56	0.41
1:D:543:LEU:HD23	1:D:543:LEU:HA	1.93	0.41
1:D:1283:MET:HG3	1:D:1287:ASN:ND2	2.36	0.41
1:D:2056:VAL:O	1:D:2059:ILE:HG22	2.20	0.41
1:B:1:MET:HA	1:B:1690:LYS:NZ	2.35	0.41
1:B:244:VAL:O	1:B:248:LYS:HG3	2.21	0.41
1:B:308:LEU:O	1:B:312:ILE:HG12	2.21	0.41
1:B:674:ASN:HD22	1:E:411:ILE:HD12	1.83	0.41
1:B:1472:HIS:NE2	1:B:1602:LYS:HD3	2.36	0.41
1:B:2141:LEU:HD23	1:B:2141:LEU:HA	1.89	0.41
1:C:451:LEU:HA	1:C:1593:MET:CE	2.51	0.41
1:C:728:GLU:CG	1:C:730:GLY:H	2.34	0.41
1:C:843:LEU:HB3	1:C:880:ARG:HD2	2.02	0.41
1:C:911:TYR:CD2	1:C:1005:VAL:HG21	2.56	0.41
1:C:968:TYR:CD1	1:C:1103:ILE:HG12	2.56	0.41
1:C:982:SER:HB3	1:C:1056:TRP:HE3	1.85	0.41
1:C:1312:LYS:HA	1:C:1312:LYS:HD3	1.96	0.41
1:C:1557:LYS:HG3	1:C:1558:ARG:N	2.36	0.41
1:F:161:VAL:HG11	1:F:168:ILE:HD12	2.03	0.41
1:F:188:GLN:OE1	1:E:2108:GLU:HG3	2.20	0.41
1:F:581:THR:HG23	1:F:604:VAL:HG23	2.03	0.41
1:F:640:PHE:CG	1:F:641:PRO:HD3	2.56	0.41
1:F:707:ARG:H	1:F:707:ARG:HD3	1.86	0.41
1:F:1177:GLU:HG3	1:F:1485:LYS:HD2	2.02	0.41
1:F:1637:ARG:HH22	1:F:1863:ILE:HG12	1.86	0.41
1:F:2124:ILE:HD12	1:E:204:ARG:HH21	1.68	0.41
1:F:2150:PHE:HD2	1:E:2113:VAL:HG23	1.85	0.41
1:A:42:MET:HG2	1:A:180:VAL:HG21	2.01	0.41
1:A:636:LEU:HD11	1:A:679:PHE:CZ	2.56	0.41
1:A:960:ILE:HD13	1:A:1115:ASP:HB2	2.03	0.41
1:E:498:TRP:CE3	1:E:514:PRO:HD3	2.55	0.41
1:E:1002:LYS:O	1:E:1006:ILE:HG13	2.21	0.41
1:E:1087:LEU:HD23	1:E:1087:LEU:HA	1.92	0.41
1:E:1370:TYR:OH	1:E:1557:LYS:O	2.34	0.41
1:E:1900:PHE:HD1	1:E:2038:LEU:HD22	1.86	0.41
1:D:317:ALA:HB1	1:D:509:ILE:HG12	2.03	0.41
1:D:578:LEU:HD23	1:D:1231:LEU:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1009:LEU:HA	1:D:1012:VAL:HG22	2.03	0.41
1:B:82:HIS:CE1	1:B:86:LYS:HB3	2.56	0.41
1:B:636:LEU:HD12	1:B:636:LEU:H	1.86	0.41
1:B:764:VAL:HG23	1:B:784:LEU:HD23	2.03	0.41
1:B:770:MET:HE1	1:B:774:ARG:NE	2.35	0.41
1:C:199:ILE:HG23	1:C:204:ARG:NH1	2.36	0.41
1:C:498:TRP:CD1	1:C:498:TRP:N	2.89	0.41
1:C:1690:LYS:HD3	1:C:1690:LYS:HA	1.85	0.41
1:F:584:TRP:CE3	1:F:604:VAL:HG21	2.55	0.41
1:F:1918:ASN:C	1:F:1920:ALA:H	2.24	0.41
1:F:2052:VAL:CG2	1:E:205:ALA:HB2	2.43	0.41
1:F:2150:PHE:HZ	1:E:2120:PRO:HA	1.80	0.41
1:A:470:THR:HG22	1:A:472:ALA:N	2.30	0.41
1:A:636:LEU:H	1:A:636:LEU:HD12	1.86	0.41
1:A:797:LEU:HD22	1:A:1071:ALA:HB2	2.02	0.41
1:A:1036:HIS:O	1:A:1039:GLN:HG2	2.21	0.41
1:A:1467:PHE:O	1:A:1471:ILE:HG12	2.21	0.41
1:A:1472:HIS:NE2	1:A:1602:LYS:HD3	2.36	0.41
1:E:374:THR:O	1:E:377:MET:HE2	2.20	0.41
1:E:1300:ARG:HD2	1:E:1300:ARG:HA	1.84	0.41
1:D:461:LYS:HE2	1:D:461:LYS:HB2	1.86	0.40
1:D:717:ILE:HD13	1:D:717:ILE:HA	1.90	0.40
1:D:1177:GLU:HG3	1:D:1485:LYS:HD2	2.02	0.40
1:D:1490:PHE:HB2	1:D:1585:ILE:HG13	2.02	0.40
1:D:1514:THR:HG1	1:D:1517:GLU:CG	2.33	0.40
1:B:1645:PRO:HB2	1:B:1648:ASP:HB2	2.03	0.40
1:B:2101:GLN:O	1:B:2105:LEU:HD23	2.21	0.40
1:C:755:LYS:NZ	1:C:783:GLN:OE1	2.39	0.40
1:C:1468:LEU:HD23	1:C:1468:LEU:HA	1.88	0.40
1:F:317:ALA:HB1	1:F:509:ILE:HG12	2.03	0.40
1:F:1300:ARG:HH12	1:E:1546:LEU:HA	1.86	0.40
1:F:1490:PHE:HB2	1:F:1585:ILE:HG13	2.02	0.40
1:A:38:ILE:O	1:A:42:MET:HG3	2.21	0.40
1:A:248:LYS:O	1:A:1130:HIS:HB3	2.21	0.40
1:A:453:LYS:HB2	1:A:453:LYS:HE2	1.70	0.40
1:A:588:TYR:CE2	1:A:708:ILE:HD12	2.55	0.40
1:A:798:ASN:OD1	1:A:993:HIS:HB3	2.20	0.40
1:A:1139:TRP:HA	1:A:1142:MET:CG	2.50	0.40
1:E:728:GLU:CG	1:E:730:GLY:H	2.34	0.40
1:E:796:GLU:HG3	1:E:1075:LEU:HA	2.02	0.40
1:D:1457:THR:HG22	1:D:1565:LYS:HZ1	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2100:ASP:OD1	1:D:2101:GLN:N	2.54	0.40
1:D:2126:ASP:OD1	1:D:2129:PHE:HB2	2.21	0.40
1:B:951:PHE:CE1	1:B:961:ARG:HG2	2.56	0.40
1:C:340:ARG:HH21	1:C:364:ASN:HB3	1.85	0.40
1:C:502:SER:OG	1:C:506:GLY:HA2	2.22	0.40
1:C:1106:TYR:HB2	1:C:1138:MET:CG	2.52	0.40
1:C:1913:TYR:O	1:C:1917:MET:HG2	2.20	0.40
1:F:189:ALA:HB1	1:E:2112:MET:HA	2.03	0.40
1:F:275:GLU:OE1	1:F:661:TYR:OH	2.32	0.40
1:F:1201:TYR:OH	1:F:1267:GLY:O	2.29	0.40
1:A:903:CYS:O	1:A:907:ILE:HG13	2.21	0.40
1:A:1638:TRP:CD2	1:A:1901:MET:HG2	2.56	0.40
1:E:199:ILE:HG23	1:E:204:ARG:NH1	2.36	0.40
1:E:1415:LYS:HD2	1:E:1424:VAL:HA	2.02	0.40
1:E:1557:LYS:HG3	1:E:1558:ARG:N	2.36	0.40
1:D:26:ASP:OD2	1:D:27:TYR:N	2.53	0.40
1:D:581:THR:HG23	1:D:604:VAL:HG23	2.03	0.40
1:D:809:ALA:HB2	1:D:995:GLY:HA3	2.04	0.40
1:D:1456:CYS:HB2	1:D:1613:ILE:HD13	2.02	0.40
1:D:2150:PHE:HD2	1:C:2113:VAL:HG23	1.85	0.40
1:B:56:ALA:HB1	1:B:92:PHE:O	2.21	0.40
1:B:145:LYS:HB2	1:B:145:LYS:HE3	1.77	0.40
1:B:1036:HIS:O	1:B:1039:GLN:HG2	2.21	0.40
1:B:1529:ASP:OD1	1:B:1530:SER:N	2.55	0.40
1:B:1565:LYS:HE2	1:B:1565:LYS:HB2	1.86	0.40
1:C:607:ASN:HB3	1:C:705:MET:HE2	2.03	0.40
1:C:2079:LEU:HD22	1:C:2141:LEU:HD22	2.03	0.40
1:C:2147:ILE:O	1:C:2151:TYR:N	2.52	0.40
1:F:148:ILE:HD12	1:F:149:PRO:HD2	2.04	0.40
1:F:809:ALA:HB2	1:F:995:GLY:HA3	2.04	0.40
1:F:1036:HIS:HA	1:F:1039:GLN:HG2	2.03	0.40
1:F:1283:MET:HG3	1:F:1287:ASN:ND2	2.36	0.40
1:F:1838:ASP:OD2	1:F:1842:ARG:NE	2.54	0.40
1:A:1033:LEU:HG	1:A:1035:PRO:HD2	2.03	0.40
1:A:1684:LEU:HD21	1:A:1841:LEU:HA	2.02	0.40
1:E:115:ALA:HA	1:E:162:ARG:HG3	2.03	0.40
1:E:355:PRO:HB2	1:E:357:ILE:HG22	2.03	0.40
1:E:502:SER:OG	1:E:506:GLY:HA2	2.22	0.40
1:E:961:ARG:HB2	1:E:1110:VAL:HG11	2.03	0.40
1:E:968:TYR:CD1	1:E:1103:ILE:HG12	2.56	0.40
1:E:982:SER:HB3	1:E:1056:TRP:CE3	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:196:GLU:HB3	1:C:2057:ASN:CG	2.41	0.40
1:B:1438:GLU:CG	1:B:2132:ARG:HH21	2.34	0.40
1:C:89:LYS:HG3	1:C:93:LYS:HE3	2.03	0.40
1:C:383:LYS:HE3	1:C:383:LYS:HB2	1.92	0.40
1:C:411:ILE:HD12	1:A:674:ASN:HD22	1.83	0.40
1:C:1002:LYS:O	1:C:1006:ILE:HG13	2.21	0.40
1:F:684:LYS:HE2	1:F:684:LYS:HB2	1.92	0.40
1:F:1564:TYR:C	1:F:1565:LYS:HD3	2.41	0.40
1:F:1703:ARG:HA	1:F:1736:GLY:HA3	2.02	0.40
1:A:52:ASP:O	1:A:1669:ARG:NH2	2.44	0.40
1:A:82:HIS:CE1	1:A:86:LYS:HB3	2.56	0.40
1:A:1084:PHE:CZ	1:A:1134:VAL:HG21	2.57	0.40
1:A:1639:CYS:HB3	1:A:1644:ALA:HB3	2.03	0.40
1:E:640:PHE:CD1	1:E:641:PRO:HD3	2.56	0.40
1:E:948:GLY:O	1:E:964:ARG:HD2	2.21	0.40
1:E:1877:VAL:N	1:E:1889:ASN:OD1	2.39	0.40
1:D:49:ASP:HB2	1:D:51:LYS:HZ2	1.86	0.40
1:B:679:PHE:CZ	1:B:1166:PRO:HD2	2.50	0.40
1:B:960:ILE:HD13	1:B:1115:ASP:HB2	2.03	0.40
1:B:1550:ILE:HD13	1:B:1550:ILE:HA	1.87	0.40
1:B:1638:TRP:CD2	1:B:1901:MET:HG2	2.56	0.40
1:B:1655:PHE:CE2	1:B:1656:GLU:HG3	2.57	0.40
1:B:1930:ASN:HD21	1:B:1942:LEU:HD12	1.87	0.40
1:F:584:TRP:CD1	1:F:719:GLU:HG3	2.57	0.40
1:F:2100:ASP:OD1	1:F:2101:GLN:N	2.54	0.40
1:A:742:HIS:ND1	1:A:1023:LEU:HD22	2.37	0.40
1:A:1930:ASN:HD21	1:A:1942:LEU:HD12	1.87	0.40
1:A:2133:HIS:ND1	1:A:2133:HIS:N	2.69	0.40
1:E:580:ALA:HB2	1:E:726:LEU:HD21	2.03	0.40
1:E:932:ILE:HG13	1:E:932:ILE:H	1.66	0.40
1:E:1205:LEU:HD23	1:E:1205:LEU:HA	1.88	0.40
1:E:1308:LEU:HD23	1:E:1308:LEU:HA	1.92	0.40
1:E:1318:SER:HB3	1:E:1334:GLY:HA2	2.02	0.40
1:E:2147:ILE:O	1:E:2151:TYR:N	2.52	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	1853/2173 (85%)	1754 (95%)	98 (5%)	1 (0%)	51 83
1	B	1853/2173 (85%)	1754 (95%)	98 (5%)	1 (0%)	51 83
1	C	1977/2173 (91%)	1890 (96%)	87 (4%)	0	100 100
1	D	2016/2173 (93%)	1947 (97%)	69 (3%)	0	100 100
1	E	1977/2173 (91%)	1890 (96%)	87 (4%)	0	100 100
1	F	2016/2173 (93%)	1947 (97%)	69 (3%)	0	100 100
All	All	11692/13038 (90%)	11182 (96%)	508 (4%)	2 (0%)	100 100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1366	VAL
1	A	1366	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	1668/1941 (86%)	1621 (97%)	47 (3%)	43 72
1	B	1668/1941 (86%)	1622 (97%)	46 (3%)	43 72
1	C	1781/1941 (92%)	1732 (97%)	49 (3%)	43 72
1	D	1809/1941 (93%)	1804 (100%)	5 (0%)	92 97
1	E	1781/1941 (92%)	1732 (97%)	49 (3%)	43 72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	F	1809/1941 (93%)	1804 (100%)	5 (0%)	92 97
All	All	10516/11646 (90%)	10315 (98%)	201 (2%)	59 80

All (201) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	707	ARG
1	D	1298	HIS
1	D	1483	ARG
1	D	1669	ARG
1	D	2112	MET
1	B	42	MET
1	B	134	TYR
1	B	183	TYR
1	B	210	MET
1	B	233	MET
1	B	284	MET
1	B	308	LEU
1	B	358	GLN
1	B	360	LYS
1	B	422	LYS
1	B	566	ARG
1	B	594	GLN
1	B	666	SER
1	B	679	PHE
1	B	680	TYR
1	B	747	GLU
1	B	959	PHE
1	B	980	ASP
1	B	991	MET
1	B	1064	CYS
1	B	1084	PHE
1	B	1119	PHE
1	B	1154	SER
1	B	1161	LYS
1	B	1222	PRO
1	B	1316	LYS
1	B	1376	ARG
1	B	1377	ASP
1	B	1398	MET
1	B	1427	ARG
1	B	1439	ASN

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Mol	Chain	Res	Type
1	B	1493	ARG
1	B	1501	ASN
1	B	1548	LEU
1	B	1549	ASP
1	B	1562	MET
1	B	1612	SER
1	B	1833	MET
1	B	1841	LEU
1	B	1872	ASP
1	B	1899	ASN
1	B	1913	TYR
1	B	1947	LEU
1	B	2064	TYR
1	B	2083	ASP
1	B	2122	ASP
1	C	86	LYS
1	C	183	TYR
1	C	226	TYR
1	C	253	ARG
1	C	286	ARG
1	C	418	SER
1	C	425	SER
1	C	532	ARG
1	C	707	ARG
1	C	867	LYS
1	C	903	CYS
1	C	931	LYS
1	C	957	HIS
1	C	962	MET
1	C	975	LYS
1	C	980	ASP
1	C	1019	MET
1	C	1034	ASP
1	C	1048	HIS
1	C	1112	ASP
1	C	1160	LYS
1	C	1203	ASP
1	C	1285	ASP
1	C	1297	SER
1	C	1330	PHE
1	C	1356	LYS
1	C	1376	ARG

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Mol	Chain	Res	Type
1	C	1405	ARG
1	C	1465	LYS
1	C	1467	PHE
1	C	1516	GLU
1	C	1544	ARG
1	C	1558	ARG
1	C	1564	TYR
1	C	1568	LYS
1	C	1583	GLU
1	C	1605	LYS
1	C	1669	ARG
1	C	1699	GLN
1	C	1705	TYR
1	C	1833	MET
1	C	1915	LEU
1	C	1919	ARG
1	C	1943	ASP
1	C	2064	TYR
1	C	2078	LEU
1	C	2092	ARG
1	C	2132	ARG
1	C	2145	ASP
1	F	707	ARG
1	F	1298	HIS
1	F	1483	ARG
1	F	1669	ARG
1	F	2112	MET
1	A	42	MET
1	A	134	TYR
1	A	183	TYR
1	A	210	MET
1	A	233	MET
1	A	284	MET
1	A	308	LEU
1	A	358	GLN
1	A	360	LYS
1	A	422	LYS
1	A	566	ARG
1	A	594	GLN
1	A	666	SER
1	A	679	PHE
1	A	680	TYR

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Mol	Chain	Res	Type
1	A	747	GLU
1	A	959	PHE
1	A	980	ASP
1	A	991	MET
1	A	1064	CYS
1	A	1084	PHE
1	A	1119	PHE
1	A	1154	SER
1	A	1161	LYS
1	A	1222	PRO
1	A	1316	LYS
1	A	1376	ARG
1	A	1377	ASP
1	A	1398	MET
1	A	1427	ARG
1	A	1439	ASN
1	A	1493	ARG
1	A	1501	ASN
1	A	1548	LEU
1	A	1549	ASP
1	A	1562	MET
1	A	1612	SER
1	A	1833	MET
1	A	1841	LEU
1	A	1872	ASP
1	A	1899	ASN
1	A	1913	TYR
1	A	1947	LEU
1	A	2064	TYR
1	A	2083	ASP
1	A	2122	ASP
1	A	2132	ARG
1	E	86	LYS
1	E	183	TYR
1	E	226	TYR
1	E	253	ARG
1	E	286	ARG
1	E	418	SER
1	E	425	SER
1	E	532	ARG
1	E	707	ARG
1	E	867	LYS

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Mol	Chain	Res	Type
1	E	903	CYS
1	E	931	LYS
1	E	957	HIS
1	E	962	MET
1	E	975	LYS
1	E	980	ASP
1	E	1019	MET
1	E	1034	ASP
1	E	1048	HIS
1	E	1112	ASP
1	E	1160	LYS
1	E	1203	ASP
1	E	1285	ASP
1	E	1297	SER
1	E	1330	PHE
1	E	1356	LYS
1	E	1376	ARG
1	E	1405	ARG
1	E	1465	LYS
1	E	1467	PHE
1	E	1516	GLU
1	E	1544	ARG
1	E	1558	ARG
1	E	1564	TYR
1	E	1568	LYS
1	E	1583	GLU
1	E	1605	LYS
1	E	1669	ARG
1	E	1699	GLN
1	E	1705	TYR
1	E	1833	MET
1	E	1915	LEU
1	E	1919	ARG
1	E	1943	ASP
1	E	2064	TYR
1	E	2078	LEU
1	E	2092	ARG
1	E	2132	ARG
1	E	2145	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	137	GLN
1	D	1298	HIS
1	D	1615	ASN
1	B	674	ASN
1	B	1036	HIS
1	B	1255	GLN
1	B	1434	ASN
1	C	323	ASN
1	C	625	ASN
1	C	842	HIS
1	C	1036	HIS
1	C	1082	ASN
1	C	1287	ASN
1	C	1451	GLN
1	F	137	GLN
1	F	1123	GLN
1	F	1298	HIS
1	F	1615	ASN
1	A	674	ASN
1	A	1036	HIS
1	A	1255	GLN
1	A	1434	ASN
1	E	323	ASN
1	E	625	ASN
1	E	842	HIS
1	E	1036	HIS
1	E	1287	ASN
1	E	1403	GLN
1	E	1451	GLN

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 [\(i\)](#)

There are no chain breaks in this entry.

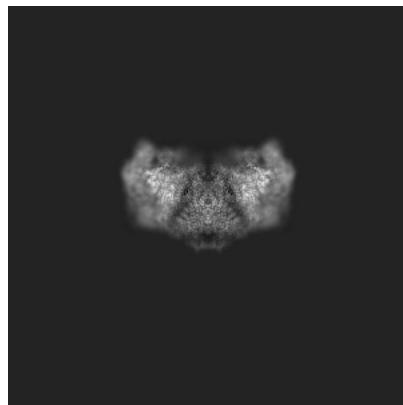
6 Map visualisation i

This section contains visualisations of the EMDB entry EMD-18408. These allow visual inspection of the internal detail of the map and identification of artifacts.

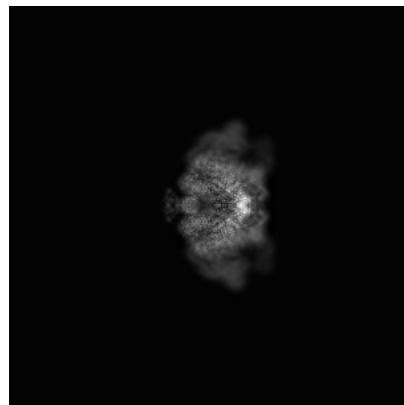
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections i

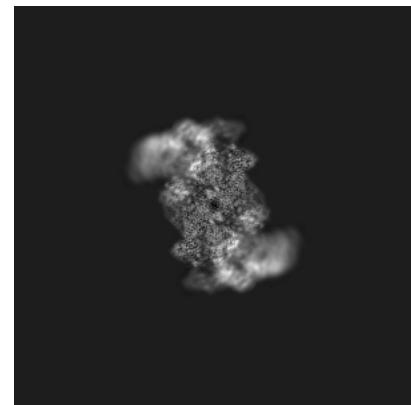
6.1.1 Primary map



X



Y

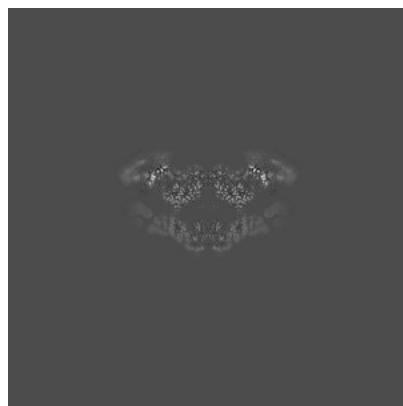


Z

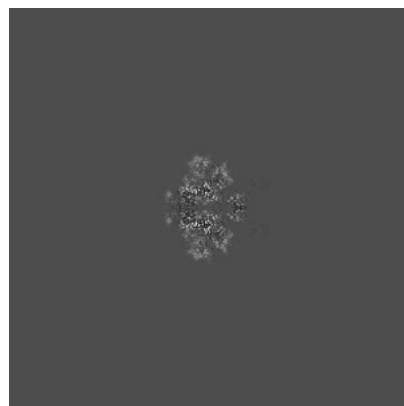
The images above show the map projected in three orthogonal directions.

6.2 Central slices i

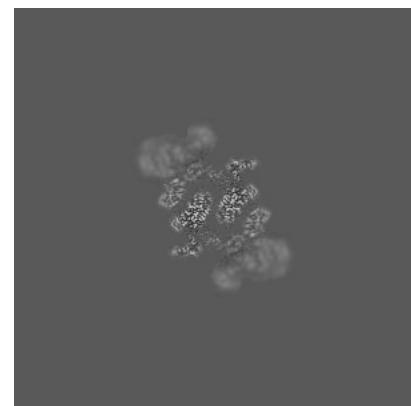
6.2.1 Primary map



X Index: 350



Y Index: 350



Z Index: 350

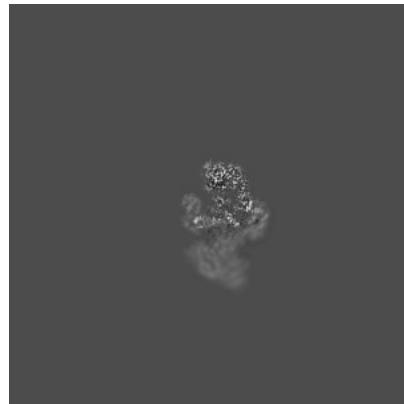
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [\(i\)](#)

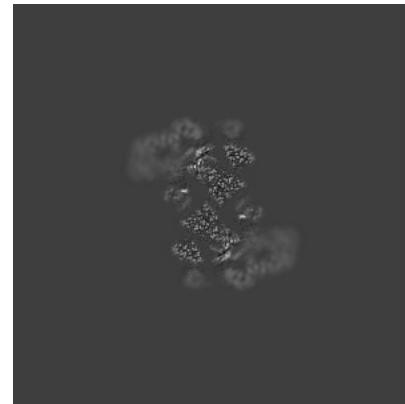
6.3.1 Primary map



X Index: 317



Y Index: 424

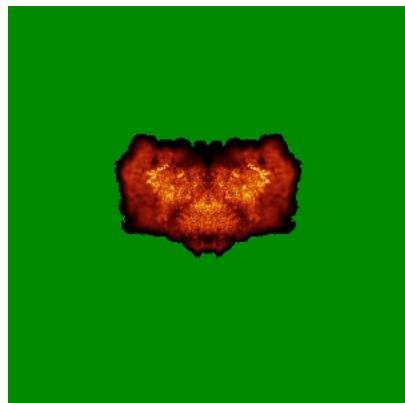


Z Index: 385

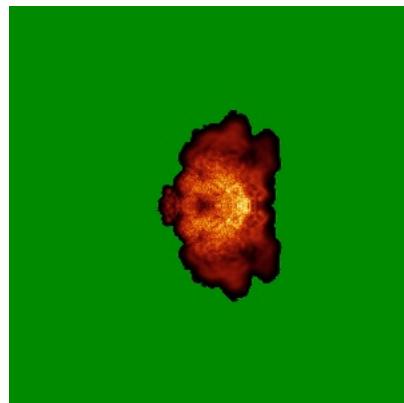
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [\(i\)](#)

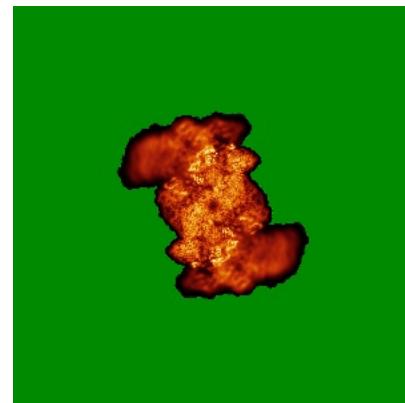
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [\(i\)](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.305. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

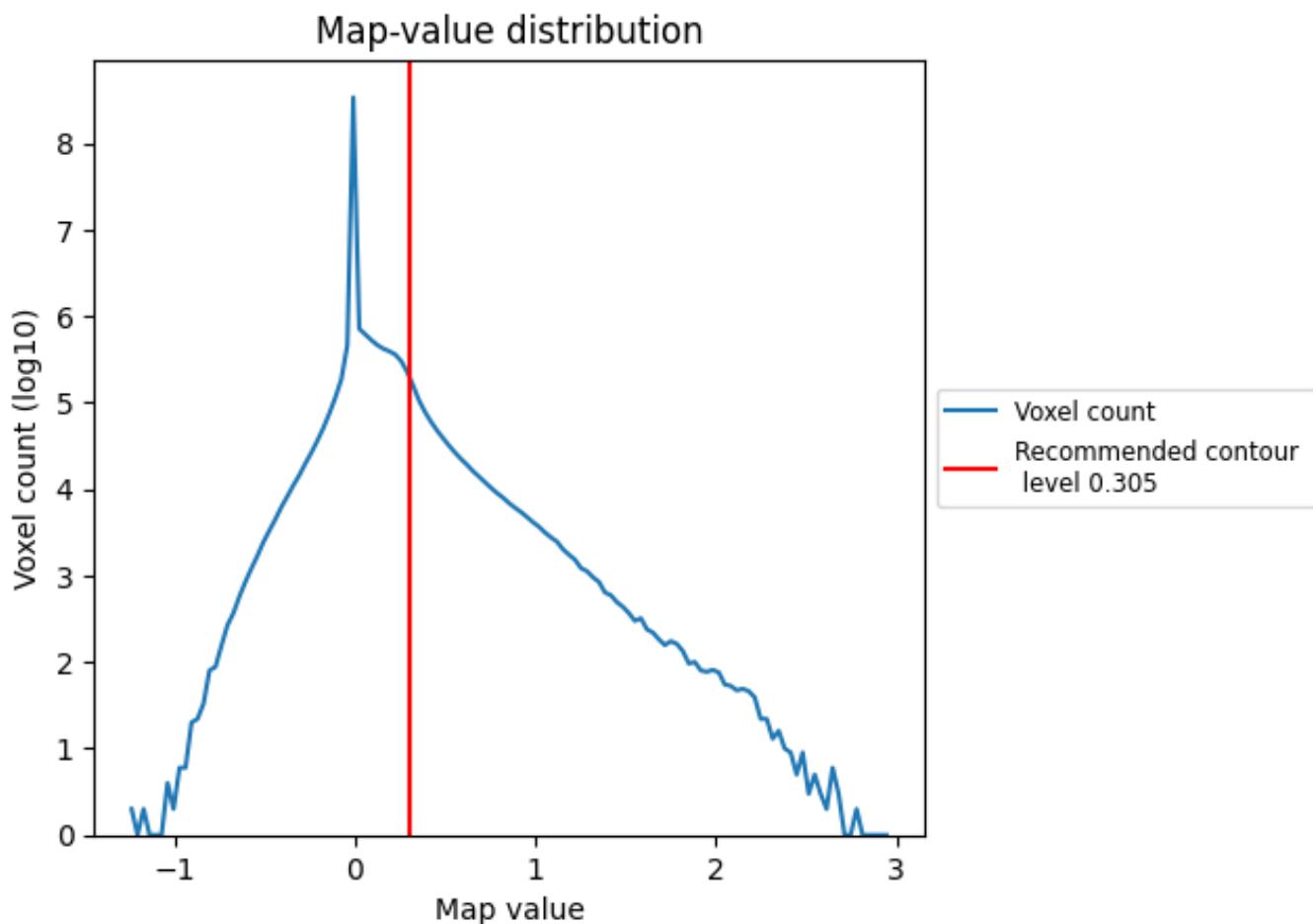
6.6 Mask visualisation [\(i\)](#)

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

7 Map analysis (i)

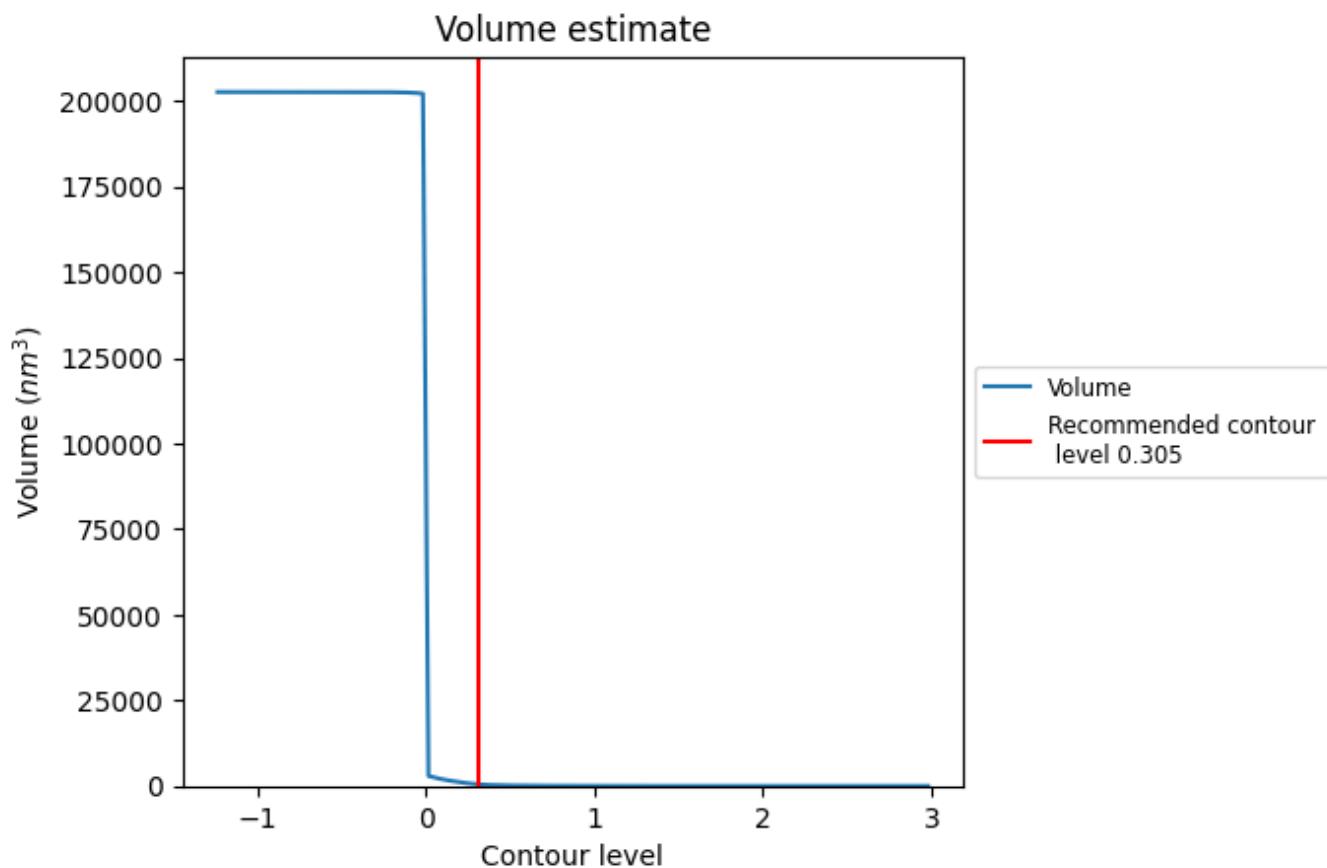
This section contains the results of statistical analysis of the map.

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.

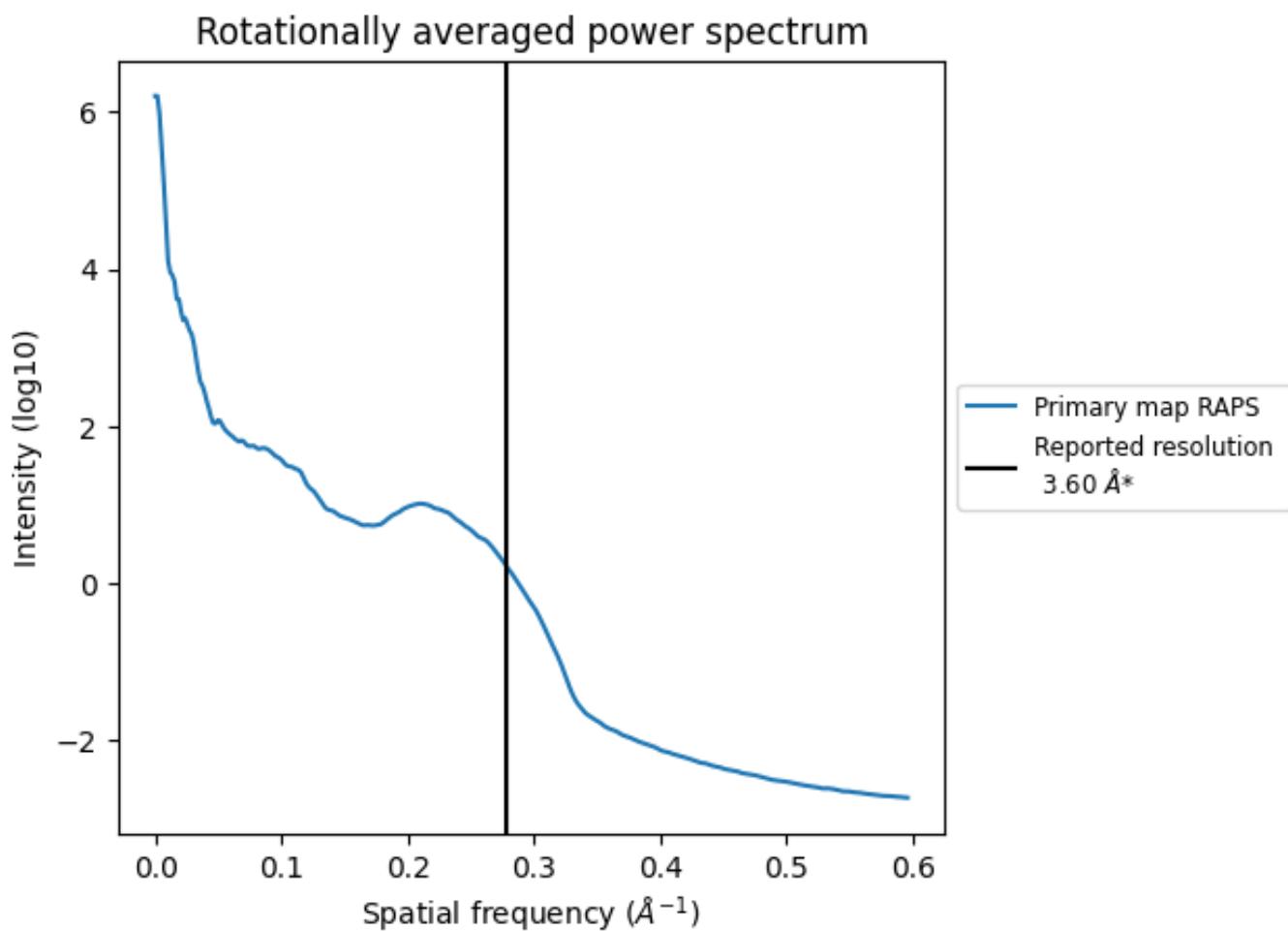
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 485 nm³; this corresponds to an approximate mass of 438 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 0.278 \AA^{-1}

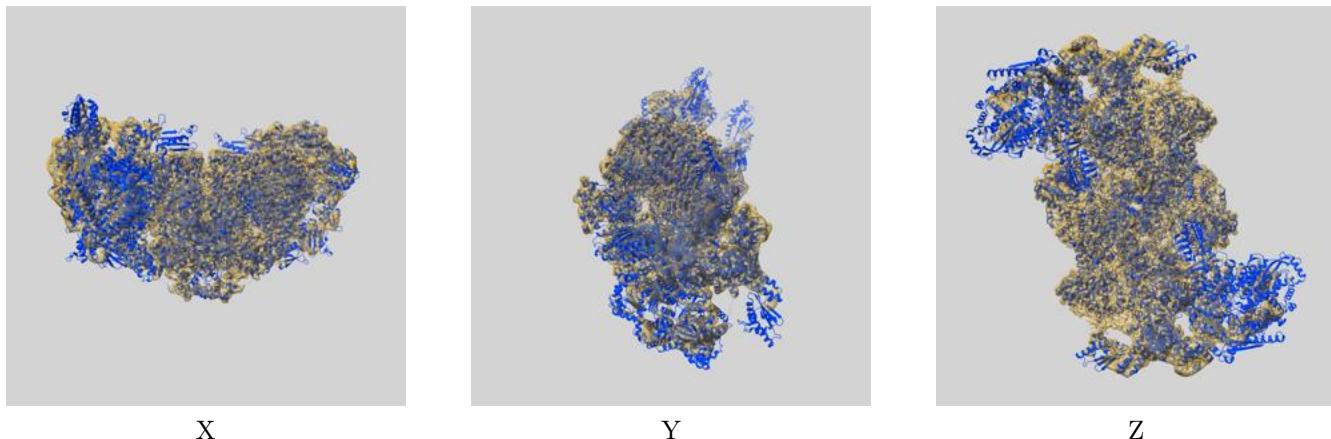
8 Fourier-Shell correlation

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

9 Map-model fit i

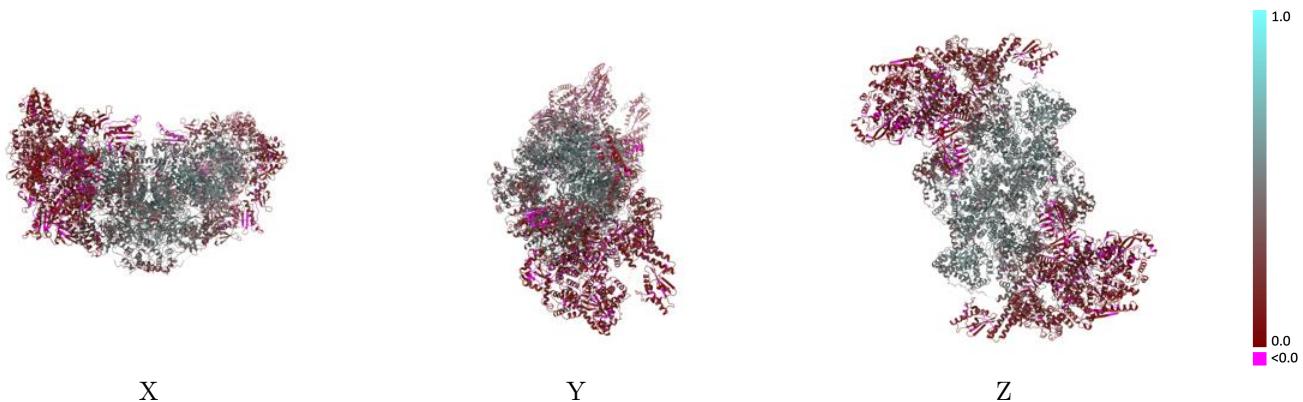
This section contains information regarding the fit between EMDB map EMD-18408 and PDB model 8QHD. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay i



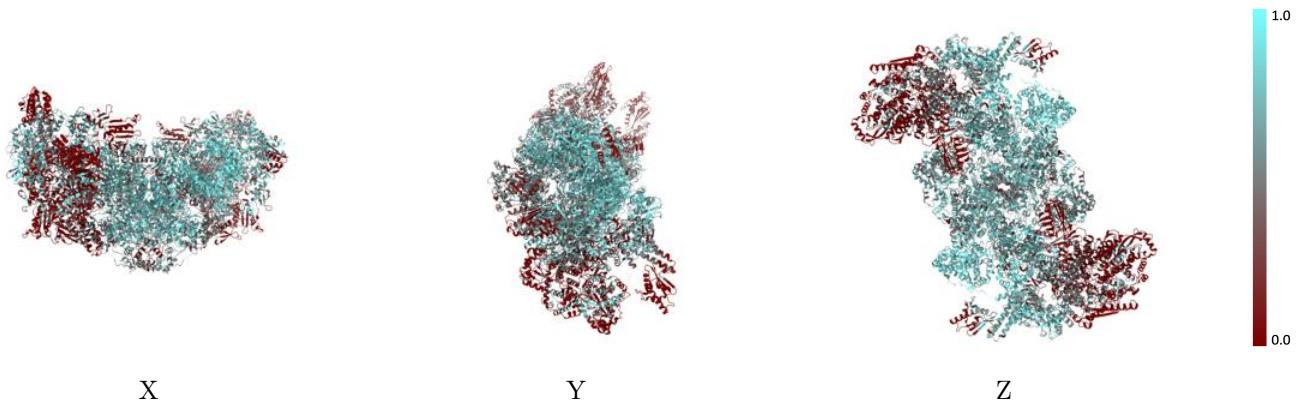
The images above show the 3D surface view of the map at the recommended contour level 0.305 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



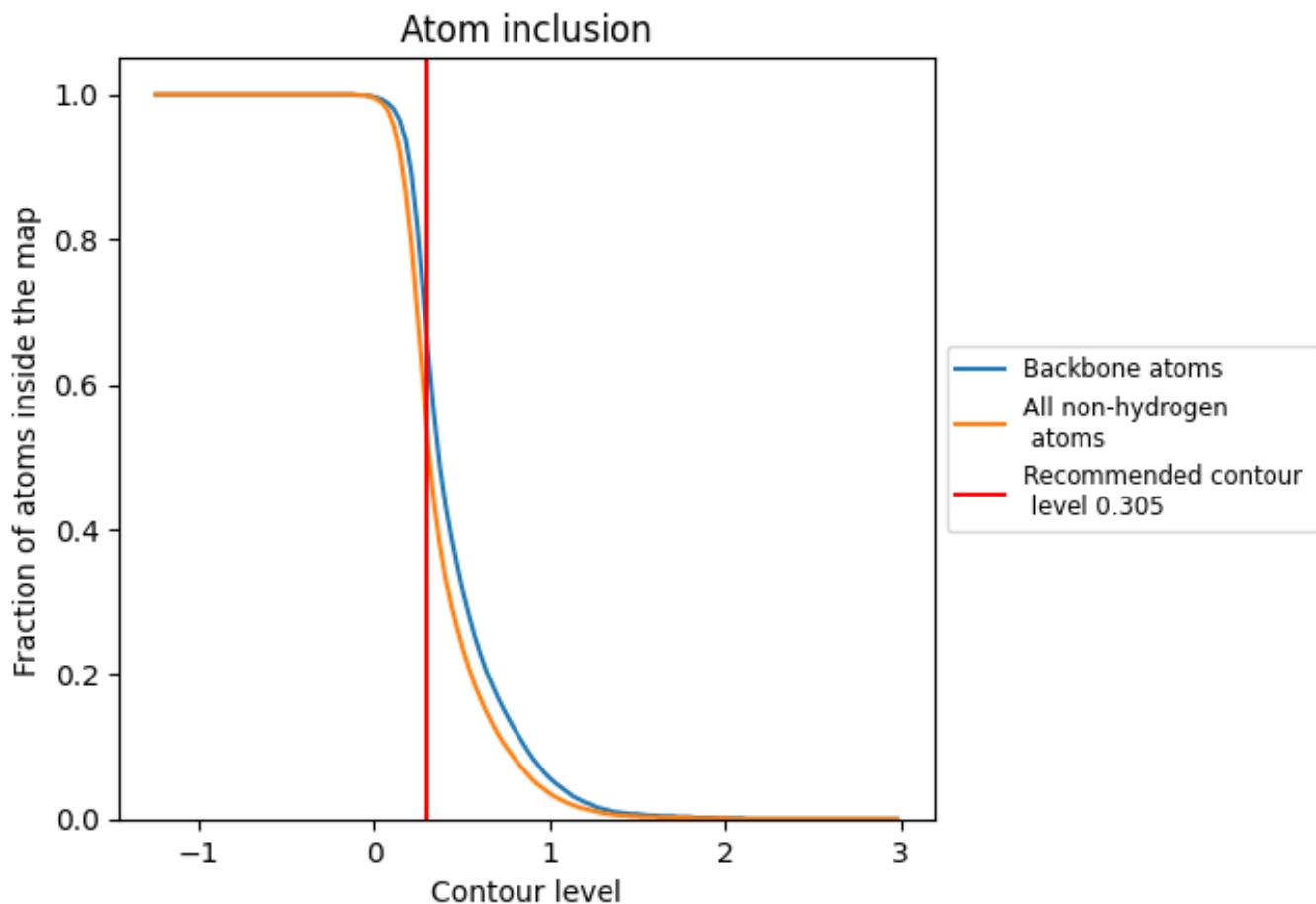
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.305).

9.4 Atom inclusion [\(i\)](#)



At the recommended contour level, 66% of all backbone atoms, 52% 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 (0.305) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.5250	0.3180
A	0.5990	0.4250
B	0.6380	0.4430
C	0.7090	0.4060
D	0.2710	0.1310
E	0.6900	0.3960
F	0.2650	0.1300

