



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 10:08 am BST

PDB ID : 2DL D
Title : D-LACTATE DEHYDROGENASE COMPLEXED WITH NADH AND OXAMATE
Authors : Dunn, C.R.; Holbrook, J.J.
Deposited on : 1995-10-28
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

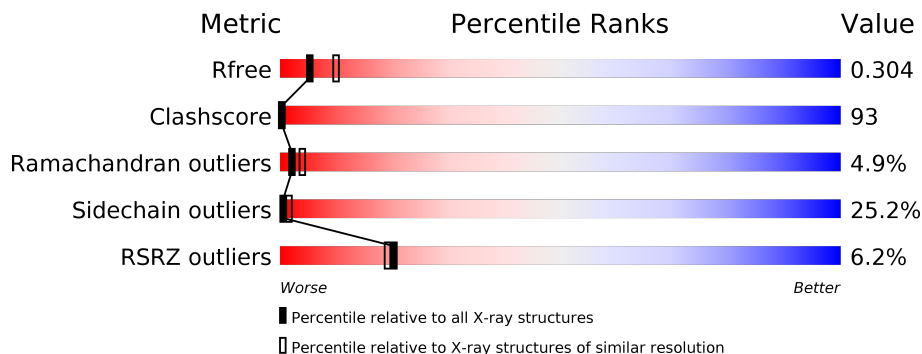
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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

Mol	Chain	Length	Quality of chain
1	A	337	
1	B	337	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAI	A	401	X	-	-	-
2	NAI	B	401	-	-	X	-
3	OXM	A	402	-	-	X	X
3	OXM	B	402	-	-	X	X

2 Entry composition i

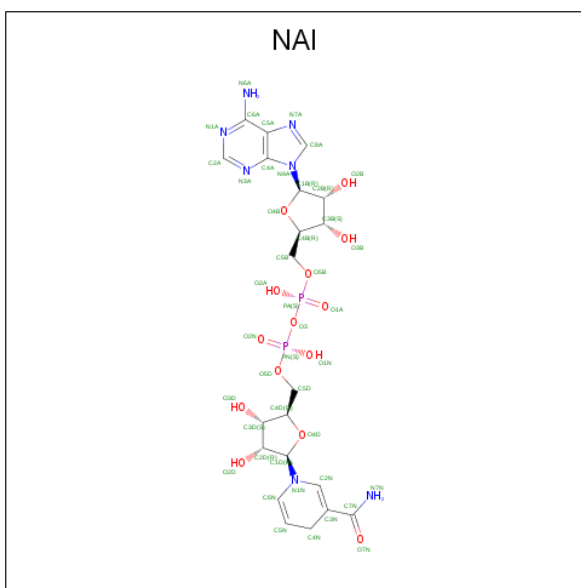
There are 3 unique types of molecules in this entry. The entry contains 5416 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 D-LACTATE DEHYDROGENASE.

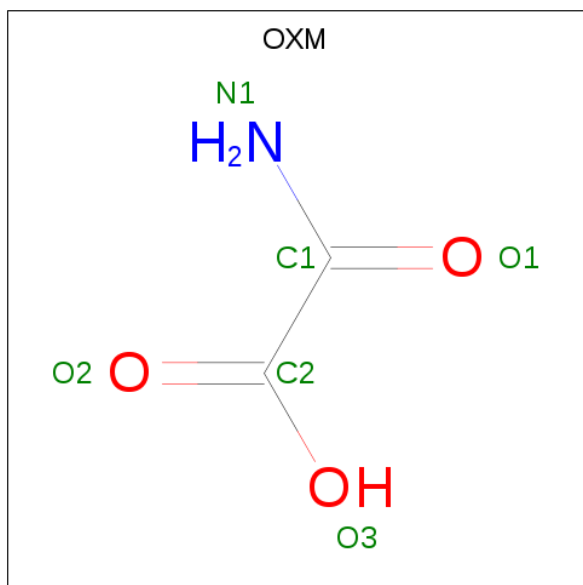
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	337	Total 2658	1684	458	504	12	0	0	0
1	B	337	Total 2658	1684	458	504	12	0	0	0

- Molecule 2 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (three-letter code: NAI) (formula: C₂₁H₂₉N₇O₁₄P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	Total 44	21	7	14	2	0	0
2	B	1	Total 44	21	7	14	2	0	0

- Molecule 3 is OXAMIC ACID (three-letter code: OXM) (formula: C₂H₃N₃O₃).

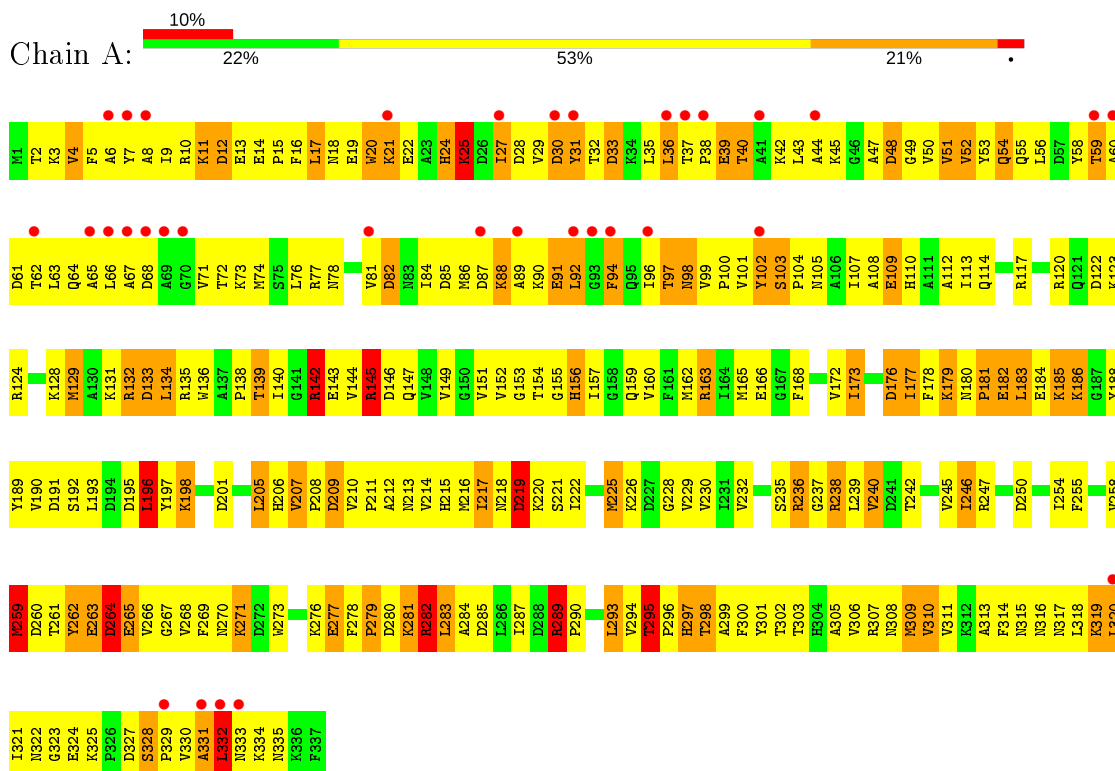


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	N			O
3	A	1	6	2	1	3	0	0
3	B	1	6	2	1	3	0	0

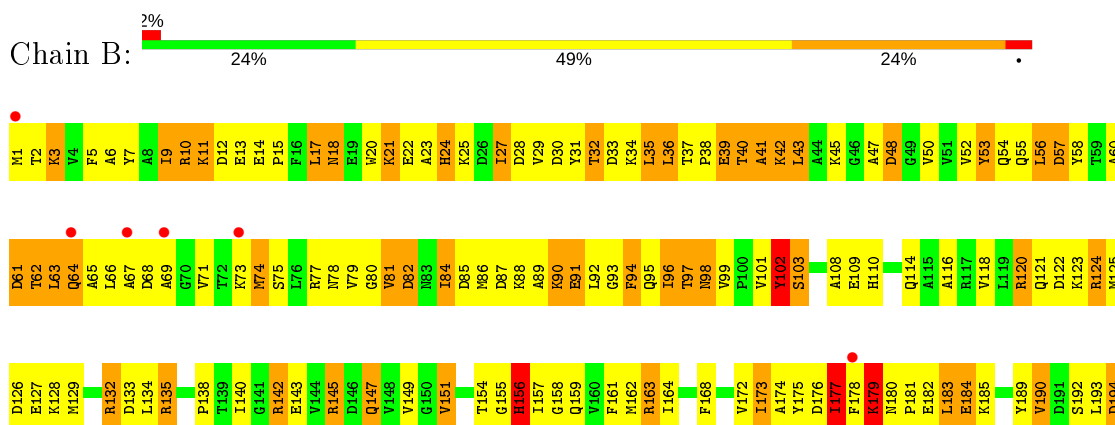
3 Residue-property plots [i](#)

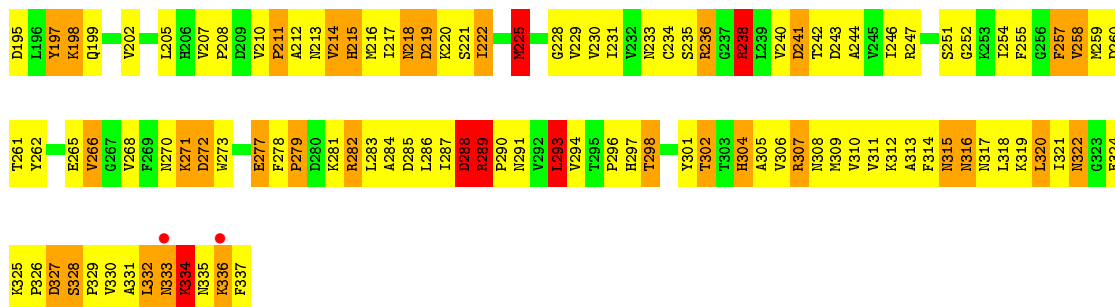
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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 dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: D-LACTATE DEHYDROGENASE



• Molecule 1: D-LACTATE DEHYDROGENASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	86.20Å 62.10Å 77.40Å 90.00° 113.20° 90.00°	Depositor
Resolution (Å)	10.00 – 2.70 10.00 – 2.72	Depositor EDS
% Data completeness (in resolution range)	82.0 (10.00-2.70) 88.8 (10.00-2.72)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 2.71Å)	Xtrriage
Refinement program	PROLSQ	Depositor
R, R_{free}	0.195 , 0.297 0.211 , 0.304	Depositor DCC
R_{free} test set	1411 reflections (7.89%)	wwPDB-VP
Wilson B-factor (Å ²)	35.8	Xtrriage
Anisotropy	0.117	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.15 , 74.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	5416	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.16% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: OXM, NAI

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	0.97	1/2707 (0.0%)	1.60	31/3661 (0.8%)
1	B	1.01	2/2707 (0.1%)	1.59	30/3661 (0.8%)
All	All	0.99	3/5414 (0.1%)	1.60	61/7322 (0.8%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	142	ARG	CA-CB	-5.40	1.42	1.53
1	B	279	PRO	N-CA	-5.13	1.38	1.47
1	A	279	PRO	N-CA	-5.08	1.38	1.47

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	289	ARG	CD-NE-CZ	14.60	144.04	123.60
1	B	288	ASP	CB-CG-OD1	11.48	128.63	118.30
1	A	282	ARG	NE-CZ-NH1	-11.46	114.57	120.30
1	A	142	ARG	NE-CZ-NH1	11.07	125.83	120.30
1	A	293	LEU	CA-CB-CG	10.70	139.92	115.30
1	A	289	ARG	NE-CZ-NH1	9.51	125.06	120.30
1	A	122	ASP	CB-CG-OD1	-9.17	110.05	118.30
1	A	142	ARG	CD-NE-CZ	9.04	136.25	123.60
1	B	124	ARG	NE-CZ-NH1	8.95	124.78	120.30
1	B	142	ARG	CA-CB-CG	8.58	132.28	113.40
1	A	219	ASP	CA-CB-CG	8.50	132.10	113.40
1	A	219	ASP	CB-CG-OD1	8.45	125.90	118.30
1	B	53	TYR	CA-CB-CG	8.00	128.60	113.40
1	A	263	GLU	CA-CB-CG	7.95	130.88	113.40
1	B	135	ARG	NE-CZ-NH2	-7.90	116.35	120.30
1	A	124	ARG	NE-CZ-NH1	-7.89	116.36	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	262	TYR	CB-CG-CD1	7.82	125.69	121.00
1	B	282	ARG	NE-CZ-NH1	-7.46	116.57	120.30
1	A	262	TYR	CA-CB-CG	7.28	127.23	113.40
1	B	10	ARG	NE-CZ-NH1	7.23	123.91	120.30
1	B	156	HIS	CA-CB-CG	7.18	125.81	113.60
1	B	124	ARG	NE-CZ-NH2	-7.13	116.73	120.30
1	B	238	ARG	NE-CZ-NH1	-7.09	116.75	120.30
1	B	304	HIS	CA-CB-CG	7.08	125.63	113.60
1	B	241	ASP	CB-CG-OD1	6.76	124.39	118.30
1	B	236	ARG	NE-CZ-NH1	-6.66	116.97	120.30
1	A	129	MET	CA-CB-CG	6.49	124.33	113.30
1	A	133	ASP	CB-CG-OD2	-6.39	112.55	118.30
1	B	194	ASP	CB-CG-OD1	6.38	124.04	118.30
1	A	264	ASP	CB-CA-C	6.37	123.13	110.40
1	A	120	ARG	NE-CZ-NH1	-6.29	117.15	120.30
1	B	163	ARG	CD-NE-CZ	6.24	132.34	123.60
1	A	24	HIS	C-N-CA	6.20	137.21	121.70
1	B	102	TYR	CB-CG-CD1	6.12	124.67	121.00
1	A	142	ARG	NH1-CZ-NH2	-6.10	112.69	119.40
1	A	259	MET	CA-CB-CG	6.01	123.53	113.30
1	B	272	ASP	CB-CG-OD1	6.00	123.70	118.30
1	B	120	ARG	NE-CZ-NH2	5.98	123.29	120.30
1	B	293	LEU	N-CA-CB	5.96	122.33	110.40
1	B	135	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	A	282	ARG	CD-NE-CZ	-5.89	115.36	123.60
1	B	288	ASP	OD1-CG-OD2	-5.81	112.25	123.30
1	B	102	TYR	CA-CB-CG	5.79	124.40	113.40
1	B	163	ARG	NE-CZ-NH2	-5.68	117.46	120.30
1	A	295	THR	N-CA-CB	5.64	121.02	110.30
1	A	216	MET	CA-CB-CG	5.53	122.70	113.30
1	B	10	ARG	CD-NE-CZ	5.53	131.34	123.60
1	A	112	ALA	CB-CA-C	-5.45	101.93	110.10
1	B	257	PHE	N-CA-CB	-5.40	100.88	110.60
1	A	265	GLU	OE1-CD-OE2	-5.33	116.91	123.30
1	A	209	ASP	CB-CG-OD1	-5.31	113.52	118.30
1	A	265	GLU	CA-CB-CG	5.29	125.04	113.40
1	B	289	ARG	CD-NE-CZ	5.27	130.98	123.60
1	B	127	GLU	CA-CB-CG	5.17	124.78	113.40
1	A	120	ARG	NE-CZ-NH2	5.15	122.88	120.30
1	B	288	ASP	CA-CB-CG	5.11	124.64	113.40
1	B	163	ARG	NE-CZ-NH1	5.11	122.85	120.30
1	A	207	VAL	CB-CA-C	5.07	121.04	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	196	LEU	CA-CB-CG	5.07	126.96	115.30
1	A	236	ARG	NE-CZ-NH1	5.05	122.83	120.30
1	B	173	ILE	CB-CA-C	-5.01	101.58	111.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2658	0	2661	519	0
1	B	2658	0	2661	511	0
2	A	44	0	24	15	0
2	B	44	0	25	28	0
3	A	6	0	2	4	0
3	B	6	0	2	11	0
All	All	5416	0	5375	1004	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 93.

All (1004) 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)
2:B:401:NAI:H5N	3:B:402:OXM:N1	1.31	1.44
1:A:53:TYR:CE1	1:A:78:ASN:HB3	1.54	1.40
1:A:25:LYS:CA	1:A:25:LYS:HZ3	1.44	1.29
1:B:86:MET:CE	1:B:332:LEU:HA	1.67	1.24
1:A:85:ASP:OD2	1:A:88:LYS:HB2	1.37	1.24
1:A:96:ILE:CG2	1:A:330:VAL:HG21	1.69	1.21
1:A:53:TYR:CE1	1:A:78:ASN:CB	2.26	1.18
1:B:81:VAL:HG12	1:B:84:ILE:HD11	1.25	1.18
1:A:96:ILE:HG22	1:A:330:VAL:CG2	1.76	1.15
1:A:157:ILE:HD12	2:A:401:NAI:H51N	1.28	1.15
1:B:48:ASP:OD1	1:B:73:LYS:NZ	1.80	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:LYS:HB3	1:A:47:ALA:HA	1.29	1.14
1:A:19:GLU:HA	1:A:22:GLU:OE1	1.48	1.13
1:B:81:VAL:HG11	1:B:330:VAL:HG11	1.28	1.13
1:A:3:LYS:HG2	1:A:47:ALA:CB	1.77	1.13
1:A:3:LYS:HG2	1:A:47:ALA:HB1	1.26	1.12
1:A:25:LYS:CA	1:A:25:LYS:NZ	2.12	1.12
1:A:38:PRO:HA	1:A:62:THR:HG23	1.26	1.11
1:B:85:ASP:OD2	1:B:88:LYS:HB2	1.51	1.11
1:B:316:ASN:ND2	1:B:327:ASP:O	1.85	1.10
1:A:306:VAL:HA	1:A:309:MET:HG3	1.14	1.10
1:A:96:ILE:HG22	1:A:330:VAL:HG21	1.09	1.09
1:A:3:LYS:HD3	1:A:47:ALA:HB2	1.35	1.08
1:A:9:ILE:HD12	1:A:77:ARG:NH1	1.69	1.07
1:A:21:LYS:HA	1:A:21:LYS:HE2	1.09	1.07
1:B:90:LYS:HB2	1:B:332:LEU:HD12	1.36	1.07
1:B:222:ILE:O	1:B:225:MET:HB2	1.54	1.06
1:B:74:MET:O	1:B:96:ILE:HG23	1.55	1.06
1:A:84:ILE:CD1	1:A:86:MET:SD	2.44	1.04
1:A:245:VAL:HG13	1:A:254:ILE:CD1	1.87	1.04
1:B:66:LEU:HD23	1:B:94:PHE:HZ	1.22	1.04
2:B:401:NAI:C5N	3:B:402:OXM:C1	2.35	1.04
1:A:7:TYR:HB2	1:A:52:VAL:HB	1.04	1.03
1:A:25:LYS:HA	1:A:25:LYS:NZ	1.72	1.03
1:B:1:MET:HG3	1:B:2:THR:N	1.66	1.03
1:A:310:VAL:O	1:A:313:ALA:HB3	1.57	1.03
1:A:277:GLU:OE1	1:A:277:GLU:HA	1.51	1.03
1:B:218:ASN:ND2	1:B:220:LYS:H	1.56	1.03
1:B:218:ASN:HD22	1:B:219:ASP:N	1.56	1.02
1:A:5:PHE:O	1:A:50:VAL:HG13	1.59	1.02
1:B:2:THR:HB	1:B:27:ILE:HG23	1.38	1.02
1:B:36:LEU:HD12	1:B:37:THR:N	1.76	1.00
1:B:18:ASN:N	1:B:18:ASN:HD22	1.45	1.00
1:A:84:ILE:HD13	1:A:86:MET:SD	2.02	1.00
1:B:54:GLN:NE2	1:B:56:LEU:HB3	1.77	0.99
1:B:157:ILE:HD12	2:B:401:NAI:H51N	1.44	0.99
1:A:38:PRO:CA	1:A:62:THR:HG23	1.93	0.99
1:A:21:LYS:CA	1:A:21:LYS:HE2	1.88	0.99
1:A:270:ASN:O	1:A:270:ASN:OD1	1.79	0.99
1:A:210:VAL:HG22	1:A:211:PRO:HD2	1.43	0.98
1:B:63:LEU:HD12	1:B:63:LEU:N	1.75	0.98
1:B:86:MET:HE2	1:B:332:LEU:HA	1.43	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:21:LYS:CA	1:B:21:LYS:HE2	1.92	0.98
1:B:35:LEU:HD23	1:B:35:LEU:N	1.75	0.98
1:A:25:LYS:HA	1:A:25:LYS:HZ3	0.84	0.97
1:B:66:LEU:HD23	1:B:94:PHE:CZ	1.99	0.97
1:A:18:ASN:O	1:A:22:GLU:N	1.98	0.96
1:A:190:VAL:HG11	1:A:195:ASP:HB2	1.45	0.96
1:B:18:ASN:ND2	1:B:18:ASN:N	2.09	0.96
1:A:2:THR:HB	1:A:27:ILE:HG23	1.47	0.96
1:B:54:GLN:NE2	1:B:56:LEU:O	1.97	0.96
1:B:332:LEU:C	1:B:332:LEU:HD23	1.86	0.96
1:A:7:TYR:CB	1:A:52:VAL:HB	1.95	0.96
1:A:7:TYR:HB2	1:A:52:VAL:CB	1.95	0.95
1:B:81:VAL:CG1	1:B:84:ILE:HD11	1.97	0.95
1:B:154:THR:O	1:B:154:THR:HG22	1.66	0.95
1:A:53:TYR:CD1	1:A:78:ASN:HB3	2.02	0.95
1:B:177:ILE:HG22	1:B:178:PHE:N	1.79	0.95
1:A:74:MET:HE1	1:A:96:ILE:HD11	1.46	0.94
1:A:9:ILE:HG21	1:A:31:TYR:CD2	2.03	0.94
1:A:245:VAL:HG13	1:A:254:ILE:HD12	1.47	0.94
1:A:210:VAL:HG13	1:A:212:ALA:H	1.29	0.94
1:B:9:ILE:HG21	1:B:31:TYR:CD2	2.02	0.93
1:A:25:LYS:CB	1:A:25:LYS:NZ	2.32	0.92
1:A:3:LYS:CG	1:A:47:ALA:CB	2.48	0.92
1:B:86:MET:HE1	1:B:332:LEU:HA	1.51	0.92
1:A:3:LYS:CD	1:A:47:ALA:HB2	1.99	0.92
1:B:75:SER:OG	1:B:97:THR:OG1	1.87	0.92
1:A:210:VAL:CG1	1:A:212:ALA:H	1.83	0.91
1:A:53:TYR:HE1	1:A:78:ASN:CB	1.77	0.91
1:B:81:VAL:HG12	1:B:84:ILE:CD1	2.00	0.90
1:A:278:PHE:CE2	1:A:284:ALA:HB2	2.07	0.90
1:B:218:ASN:C	1:B:218:ASN:HD22	1.75	0.90
1:B:133:ASP:OD1	1:B:135:ARG:HG2	1.70	0.90
1:A:306:VAL:CA	1:A:309:MET:HG3	2.02	0.89
1:A:113:ILE:CD1	1:B:116:ALA:HB1	2.03	0.89
1:B:86:MET:HB3	1:B:332:LEU:HG	1.53	0.89
1:B:90:LYS:HB2	1:B:332:LEU:CD1	2.03	0.89
2:B:401:NAI:H5N	3:B:402:OXM:HN2	1.16	0.88
1:A:53:TYR:HE1	1:A:78:ASN:CG	1.75	0.88
1:B:82:ASP:HA	1:B:336:LYS:HG2	1.55	0.88
1:A:7:TYR:CD2	1:A:36:LEU:HD12	2.09	0.88
1:B:218:ASN:ND2	1:B:218:ASN:C	2.26	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:87:ASP:O	1:B:91:GLU:N	2.06	0.88
1:A:113:ILE:HD11	1:B:116:ALA:HB1	1.56	0.87
1:B:82:ASP:HA	1:B:336:LYS:CG	2.04	0.87
1:A:25:LYS:HZ2	1:A:25:LYS:HB3	1.37	0.87
1:B:162:MET:HE3	1:B:174:ALA:HB2	1.56	0.86
1:A:306:VAL:HA	1:A:309:MET:CG	2.03	0.86
1:B:10:ARG:NH2	1:B:306:VAL:HG13	1.90	0.86
1:B:1:MET:HG3	1:B:2:THR:H	1.34	0.86
1:A:7:TYR:CE2	1:A:36:LEU:HD12	2.11	0.85
1:A:9:ILE:CD1	1:A:77:ARG:NH1	2.40	0.85
1:B:21:LYS:C	1:B:21:LYS:HE2	1.96	0.85
1:B:262:TYR:HB3	1:B:265:GLU:HB3	1.59	0.84
1:B:162:MET:HE2	1:B:172:VAL:CG1	2.06	0.84
1:B:57:ASP:N	1:B:57:ASP:OD1	2.10	0.84
1:A:21:LYS:CE	1:A:21:LYS:HA	2.00	0.84
1:A:85:ASP:O	1:A:89:ALA:HB2	1.77	0.84
1:B:35:LEU:HD23	1:B:35:LEU:H	1.39	0.84
1:B:63:LEU:HD12	1:B:63:LEU:H	1.41	0.84
1:B:213:ASN:HD21	2:B:401:NAI:H61A	1.25	0.84
1:A:285:ASP:OD2	1:A:289:ARG:NH1	2.12	0.83
2:A:401:NAI:H42N	3:A:402:OXM:C1	2.09	0.83
1:B:218:ASN:HD21	1:B:220:LYS:H	1.22	0.83
1:A:6:ALA:HB3	1:A:31:TYR:HB3	1.59	0.83
1:B:114:GLN:O	1:B:118:VAL:HG23	1.78	0.83
1:B:48:ASP:O	1:B:73:LYS:HD2	1.78	0.83
1:B:297:HIS:NE2	3:B:402:OXM:O1	2.12	0.82
1:B:54:GLN:HE21	1:B:56:LEU:C	1.83	0.82
1:B:86:MET:CE	1:B:332:LEU:CA	2.56	0.82
1:A:295:THR:HG22	1:A:296:PRO:HD2	1.60	0.82
1:A:149:VAL:HG21	1:A:165:MET:CE	2.10	0.82
1:B:287:ILE:HA	1:B:294:VAL:HG21	1.59	0.82
1:A:25:LYS:HZ2	1:A:25:LYS:CB	1.91	0.81
1:B:210:VAL:HG12	1:B:212:ALA:H	1.45	0.81
1:B:64:GLN:HA	1:B:67:ALA:HB3	1.62	0.81
1:B:63:LEU:H	1:B:63:LEU:CD1	1.93	0.81
1:A:297:HIS:NE2	3:A:402:OXM:O1	2.14	0.81
1:B:21:LYS:HA	1:B:21:LYS:HE2	1.61	0.81
1:A:210:VAL:HG12	1:A:213:ASN:H	1.45	0.81
1:A:74:MET:O	1:A:96:ILE:HA	1.80	0.81
1:B:162:MET:HE2	1:B:172:VAL:HG11	1.63	0.81
1:A:190:VAL:HG11	1:A:195:ASP:CB	2.11	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:162:MET:CE	1:B:172:VAL:CG1	2.60	0.80
1:A:319:LYS:NZ	1:A:324:GLU:OE1	2.14	0.80
1:A:64:GLN:HA	1:A:67:ALA:HB3	1.63	0.80
1:A:2:THR:O	1:A:28:ASP:HB3	1.80	0.80
1:A:3:LYS:CG	1:A:47:ALA:HB2	2.11	0.80
1:B:63:LEU:N	1:B:63:LEU:CD1	2.45	0.79
1:A:7:TYR:CG	1:A:36:LEU:HD12	2.18	0.79
1:A:5:PHE:HE1	1:A:30:ASP:HB3	1.47	0.79
1:A:38:PRO:HG3	1:A:62:THR:OG1	1.82	0.79
1:B:332:LEU:CD2	1:B:332:LEU:C	2.51	0.79
1:A:267:GLY:O	1:A:271:LYS:NZ	2.12	0.79
1:B:213:ASN:ND2	2:B:401:NAI:N6A	2.31	0.79
1:B:110:HIS:O	1:B:114:GLN:HG2	1.82	0.79
1:A:190:VAL:CG1	1:A:195:ASP:HB2	2.12	0.79
1:B:219:ASP:OD2	1:B:247:ARG:NH1	2.16	0.78
1:B:287:ILE:HA	1:B:294:VAL:CG2	2.13	0.78
1:B:319:LYS:HZ2	1:B:324:GLU:HB3	1.48	0.78
1:A:53:TYR:CE1	1:A:78:ASN:CG	2.55	0.78
1:B:218:ASN:ND2	1:B:220:LYS:N	2.32	0.78
1:A:102:TYR:HB2	1:A:305:ALA:HB1	1.66	0.78
1:A:229:VAL:HG22	1:A:230:VAL:N	1.99	0.77
1:B:219:ASP:CG	1:B:247:ARG:HH12	1.87	0.77
1:A:84:ILE:HD11	1:A:86:MET:SD	2.24	0.77
1:A:178:PHE:O	1:A:178:PHE:CD1	2.37	0.77
1:A:74:MET:HE1	1:A:96:ILE:CD1	2.14	0.77
1:B:319:LYS:NZ	1:B:324:GLU:HB3	2.00	0.77
1:B:35:LEU:N	1:B:35:LEU:CD2	2.48	0.77
1:B:277:GLU:O	1:B:279:PRO:HD3	1.85	0.77
1:A:14:GLU:CB	1:A:15:PRO:HD3	2.15	0.76
1:B:29:VAL:O	1:B:30:ASP:OD1	2.02	0.76
1:A:186:LYS:NZ	1:A:186:LYS:HB2	1.97	0.76
1:A:318:LEU:HD23	1:A:318:LEU:O	1.85	0.76
1:B:332:LEU:CD2	1:B:332:LEU:O	2.33	0.76
1:A:10:ARG:HB2	1:A:13:GLU:HG3	1.68	0.76
1:B:307:ARG:HG2	1:B:307:ARG:O	1.85	0.76
1:A:14:GLU:HB2	1:A:15:PRO:HD3	1.68	0.76
1:A:149:VAL:HG11	1:A:165:MET:HE3	1.67	0.76
1:A:6:ALA:HB1	1:A:9:ILE:HD13	1.67	0.76
1:A:9:ILE:HD12	1:A:77:ARG:HH12	1.49	0.76
1:A:149:VAL:HG21	1:A:165:MET:HE3	1.68	0.75
1:B:177:ILE:CG2	1:B:178:PHE:N	2.48	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:HIS:CD2	1:A:157:ILE:H	2.04	0.75
1:A:6:ALA:HB1	1:A:9:ILE:CD1	2.17	0.75
1:B:156:HIS:CD2	2:B:401:NAI:O1N	2.40	0.75
1:B:54:GLN:NE2	1:B:56:LEU:CB	2.50	0.75
1:B:155:GLY:O	1:B:156:HIS:C	2.24	0.75
1:A:210:VAL:CG2	1:A:211:PRO:HD2	2.16	0.75
1:A:273:TRP:CZ3	1:A:279:PRO:HG3	2.21	0.75
1:B:273:TRP:CZ3	1:B:279:PRO:HG3	2.22	0.75
1:A:59:THR:O	1:A:63:LEU:HD13	1.85	0.75
1:A:219:ASP:OD1	1:A:247:ARG:NH1	2.19	0.74
1:B:210:VAL:HG13	1:B:211:PRO:HD2	1.68	0.74
1:B:25:LYS:HE2	1:B:25:LYS:HA	1.69	0.74
1:A:4:VAL:CG1	1:A:317:ASN:HD22	2.01	0.74
1:B:99:VAL:HG12	1:B:99:VAL:O	1.86	0.74
1:A:310:VAL:O	1:A:313:ALA:CB	2.35	0.74
1:A:17:LEU:HD12	1:A:314:PHE:HZ	1.52	0.74
1:B:154:THR:HG21	1:B:183:LEU:CD2	2.17	0.74
1:B:54:GLN:HE21	1:B:56:LEU:CA	2.01	0.74
2:B:401:NAI:H42N	3:B:402:OXM:C1	2.18	0.73
1:A:139:THR:HG22	1:A:139:THR:O	1.87	0.73
1:B:40:THR:O	1:B:42:LYS:N	2.21	0.73
1:A:245:VAL:CG1	1:A:254:ILE:HD12	2.18	0.73
1:A:154:THR:HG22	1:A:154:THR:O	1.90	0.72
1:A:2:THR:O	1:A:28:ASP:CB	2.36	0.72
1:A:317:ASN:O	1:A:320:LEU:N	2.22	0.72
1:B:86:MET:HE2	1:B:332:LEU:CA	2.20	0.72
1:B:10:ARG:HH22	1:B:306:VAL:HG13	1.52	0.72
1:B:319:LYS:HD2	1:B:326:PRO:HA	1.72	0.72
1:B:98:ASN:HD21	1:B:328:SER:HB3	1.54	0.72
1:A:48:ASP:HB3	1:A:321:ILE:HG12	1.71	0.72
1:B:222:ILE:HA	1:B:225:MET:SD	2.29	0.72
1:B:335:ASN:ND2	1:B:337:PHE:OXT	2.22	0.72
1:B:21:LYS:HG2	1:B:29:VAL:HG21	1.70	0.72
1:B:87:ASP:O	1:B:90:LYS:N	2.22	0.72
1:A:3:LYS:O	1:A:48:ASP:N	2.23	0.71
1:B:103:SER:O	1:B:103:SER:OG	2.06	0.71
1:B:21:LYS:O	1:B:21:LYS:HE2	1.89	0.71
1:A:177:ILE:HG22	1:A:178:PHE:N	2.06	0.71
1:A:47:ALA:O	1:A:71:VAL:HG22	1.91	0.71
1:A:88:LYS:HA	1:A:91:GLU:HB2	1.71	0.71
1:B:217:ILE:HA	1:B:221:SER:OG	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:401:NAI:C4N	3:B:402:OXM:C1	2.69	0.71
1:A:6:ALA:HA	1:A:51:VAL:O	1.91	0.71
1:B:151:VAL:HG21	1:B:162:MET:HG2	1.72	0.71
1:A:259:MET:HG2	1:A:294:VAL:HG22	1.73	0.71
1:A:210:VAL:CG1	1:A:212:ALA:N	2.54	0.70
1:A:49:GLY:HA2	1:A:73:LYS:O	1.90	0.70
1:B:218:ASN:HD21	1:B:220:LYS:N	1.88	0.70
1:A:144:VAL:O	1:A:146:ASP:N	2.24	0.70
1:A:273:TRP:CE3	1:A:279:PRO:HG3	2.25	0.70
1:A:136:TRP:O	1:B:301:TYR:CE2	2.44	0.70
1:A:7:TYR:CZ	1:A:36:LEU:HD12	2.26	0.70
1:B:17:LEU:C	1:B:18:ASN:HD22	1.95	0.70
1:A:176:ASP:OD2	2:A:401:NAI:H4B	1.90	0.70
1:A:99:VAL:O	1:A:99:VAL:HG12	1.90	0.70
1:B:162:MET:CE	1:B:172:VAL:HG11	2.20	0.70
1:A:5:PHE:CE1	1:A:30:ASP:HB3	2.26	0.70
1:B:23:ALA:O	1:B:25:LYS:HG2	1.91	0.70
1:A:236:ARG:O	1:A:239:LEU:HG	1.92	0.69
1:A:74:MET:CE	1:A:96:ILE:CD1	2.69	0.69
1:B:278:PHE:CD1	1:B:279:PRO:HD2	2.25	0.69
1:B:177:ILE:HG22	1:B:178:PHE:H	1.57	0.69
1:B:20:TRP:CE2	1:B:24:HIS:CD2	2.81	0.69
1:B:48:ASP:HB3	1:B:321:ILE:CD1	2.23	0.69
1:B:236:ARG:HG2	2:B:401:NAI:O2D	1.92	0.69
1:B:81:VAL:CB	1:B:84:ILE:HD11	2.22	0.69
1:A:270:ASN:HA	1:B:134:LEU:O	1.93	0.69
1:B:154:THR:O	1:B:154:THR:CG2	2.40	0.69
1:B:36:LEU:HD11	1:B:41:ALA:HB2	1.73	0.69
1:B:32:THR:HG23	1:B:33:ASP:N	2.07	0.69
1:B:142:ARG:HH11	1:B:147:GLN:HE21	1.40	0.69
1:A:113:ILE:O	1:A:117:ARG:HG3	1.92	0.69
1:B:14:GLU:HB3	1:B:15:PRO:HD3	1.75	0.69
1:B:35:LEU:HD13	1:B:54:GLN:HG3	1.74	0.69
1:A:43:LEU:C	1:A:45:LYS:H	1.96	0.69
1:B:285:ASP:OD2	1:B:289:ARG:NH1	2.25	0.69
1:B:308:ASN:O	1:B:312:LYS:HB2	1.94	0.68
1:B:14:GLU:HB3	1:B:15:PRO:CD	2.24	0.68
1:B:88:LYS:O	1:B:89:ALA:C	2.32	0.68
1:A:2:THR:CB	1:A:27:ILE:HG23	2.22	0.68
1:A:142:ARG:HH11	1:A:147:GLN:HE21	1.42	0.68
1:B:157:ILE:CD1	2:B:401:NAI:H51N	2.21	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:87:ASP:OD1	1:B:87:ASP:N	2.26	0.68
1:B:262:TYR:O	1:B:265:GLU:HB3	1.93	0.67
1:B:74:MET:O	1:B:96:ILE:CG2	2.38	0.67
1:B:9:ILE:HG21	1:B:31:TYR:CE2	2.28	0.67
1:A:218:ASN:ND2	1:A:220:LYS:H	1.92	0.67
1:A:162:MET:HG2	1:A:172:VAL:HG11	1.75	0.67
1:A:9:ILE:HG21	1:A:31:TYR:CE2	2.30	0.67
1:B:27:ILE:CD1	1:B:318:LEU:HD11	2.24	0.67
1:B:214:VAL:HG13	1:B:238:ARG:HB3	1.77	0.67
1:A:136:TRP:O	1:B:301:TYR:HE2	1.76	0.67
1:B:222:ILE:O	1:B:225:MET:CB	2.37	0.67
1:B:192:SER:O	1:B:195:ASP:HB2	1.95	0.66
1:B:89:ALA:O	1:B:93:GLY:N	2.28	0.66
1:A:229:VAL:CG2	1:A:230:VAL:N	2.57	0.66
1:A:8:ALA:HB2	1:A:35:LEU:HD22	1.76	0.66
1:B:2:THR:CB	1:B:27:ILE:HG23	2.22	0.66
1:A:305:ALA:O	1:A:308:ASN:N	2.29	0.66
1:B:54:GLN:HE21	1:B:56:LEU:CB	2.08	0.66
1:A:123:LYS:HE2	1:A:290:PRO:HA	1.77	0.66
1:B:102:TYR:HD2	1:B:309:MET:HG3	1.61	0.66
1:A:20:TRP:CE3	1:A:20:TRP:C	2.69	0.66
1:A:74:MET:CE	1:A:96:ILE:HD11	2.22	0.66
1:B:98:ASN:C	1:B:98:ASN:HD22	1.98	0.66
1:A:250:ASP:OD1	1:A:289:ARG:NH2	2.28	0.66
1:A:101:VAL:O	1:A:101:VAL:HG12	1.95	0.66
1:A:35:LEU:HD13	1:A:54:GLN:CG	2.25	0.66
1:A:310:VAL:HG12	1:A:311:VAL:N	2.10	0.66
1:A:62:THR:HA	1:A:65:ALA:HB3	1.78	0.65
1:B:142:ARG:NH1	1:B:147:GLN:HE21	1.94	0.65
1:B:241:ASP:O	1:B:244:ALA:N	2.28	0.65
1:B:54:GLN:HG2	1:B:56:LEU:H	1.60	0.65
1:B:64:GLN:HA	1:B:67:ALA:CB	2.25	0.65
1:A:319:LYS:NZ	1:A:324:GLU:CB	2.59	0.65
1:A:7:TYR:O	1:A:52:VAL:HA	1.97	0.65
1:B:317:ASN:O	1:B:320:LEU:HB2	1.96	0.65
1:A:48:ASP:O	1:A:71:VAL:HG13	1.97	0.65
1:B:7:TYR:OH	1:B:43:LEU:HB3	1.97	0.65
1:B:63:LEU:O	1:B:66:LEU:HB3	1.97	0.65
1:B:193:LEU:HG	1:B:197:TYR:CE1	2.32	0.65
1:B:9:ILE:CG2	1:B:9:ILE:O	2.45	0.65
1:A:162:MET:HB2	1:A:163:ARG:NH1	2.12	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:TYR:CG	1:A:36:LEU:CD1	2.80	0.65
1:B:85:ASP:OD2	1:B:88:LYS:CB	2.39	0.65
1:A:210:VAL:HG13	1:A:211:PRO:CD	2.26	0.64
1:A:108:ALA:HB3	1:A:160:VAL:HG11	1.78	0.64
1:A:3:LYS:HB3	1:A:47:ALA:CA	2.18	0.64
1:B:14:GLU:N	1:B:15:PRO:HD2	2.13	0.64
1:B:123:LYS:HD3	1:B:290:PRO:O	1.96	0.64
1:B:39:GLU:OE1	1:B:39:GLU:O	2.15	0.64
1:A:154:THR:CG2	1:A:154:THR:O	2.45	0.64
1:A:102:TYR:HA	1:A:308:ASN:HD22	1.62	0.64
1:A:260:ASP:OD1	1:A:297:HIS:HA	1.96	0.64
1:A:3:LYS:CG	1:A:47:ALA:HB1	2.14	0.64
2:A:401:NAI:H42N	3:A:402:OXM:N1	2.11	0.64
1:A:52:VAL:O	1:A:76:LEU:HD13	1.98	0.64
1:B:142:ARG:NH2	1:B:228:GLY:O	2.30	0.64
1:A:190:VAL:CG1	1:A:195:ASP:CB	2.74	0.64
1:A:205:LEU:N	1:A:205:LEU:HD13	2.12	0.64
1:B:332:LEU:O	1:B:332:LEU:HD22	1.97	0.64
1:B:98:ASN:ND2	1:B:328:SER:HB3	2.13	0.64
1:B:82:ASP:HA	1:B:336:LYS:HG3	1.79	0.64
1:A:229:VAL:CG2	1:A:230:VAL:H	2.11	0.63
1:B:86:MET:HG2	1:B:336:LYS:HD3	1.81	0.63
1:B:23:ALA:O	1:B:25:LYS:N	2.31	0.63
1:A:90:LYS:HD2	1:A:90:LYS:O	1.97	0.63
1:B:102:TYR:CD2	1:B:309:MET:HG3	2.33	0.63
1:B:317:ASN:O	1:B:320:LEU:N	2.30	0.63
1:B:2:THR:HG22	1:B:3:LYS:N	2.12	0.63
1:A:277:GLU:CA	1:A:277:GLU:OE1	2.37	0.63
1:A:9:ILE:CG2	1:A:31:TYR:CD2	2.80	0.63
1:A:149:VAL:HG21	1:A:165:MET:HE1	1.81	0.63
1:B:38:PRO:HA	1:B:65:ALA:CB	2.29	0.63
1:A:2:THR:HB	1:A:27:ILE:CG2	2.26	0.63
1:A:3:LYS:HG2	1:A:47:ALA:HB2	1.66	0.63
1:A:3:LYS:CB	1:A:47:ALA:HA	2.18	0.63
1:B:63:LEU:O	1:B:66:LEU:N	2.32	0.63
1:A:281:LYS:O	1:A:285:ASP:N	2.31	0.63
1:A:113:ILE:HD13	1:B:116:ALA:CB	2.29	0.62
1:A:35:LEU:HD13	1:A:54:GLN:HG3	1.81	0.62
1:B:102:TYR:CD2	1:B:309:MET:CG	2.81	0.62
1:A:108:ALA:CB	1:A:160:VAL:CG1	2.78	0.62
1:A:2:THR:HG21	1:A:321:ILE:HG21	1.79	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:LYS:HD2	1:A:321:ILE:HA	1.81	0.62
1:B:21:LYS:HA	1:B:21:LYS:CE	2.29	0.62
1:A:278:PHE:CD1	1:A:279:PRO:HD2	2.34	0.62
1:B:184:GLU:HA	1:B:189:TYR:HD1	1.63	0.62
1:A:278:PHE:HE2	1:A:284:ALA:HB2	1.65	0.62
1:B:319:LYS:CB	1:B:326:PRO:HB3	2.30	0.62
1:B:319:LYS:CD	1:B:326:PRO:HA	2.29	0.62
1:A:98:ASN:ND2	1:A:100:PRO:HD3	2.15	0.62
1:B:17:LEU:HB3	1:B:18:ASN:ND2	2.14	0.62
1:B:88:LYS:O	1:B:92:LEU:N	2.17	0.62
1:A:4:VAL:CG1	1:A:317:ASN:ND2	2.63	0.61
1:B:13:GLU:OE1	1:B:77:ARG:NH2	2.33	0.61
1:A:283:LEU:O	1:A:287:ILE:HG13	2.01	0.61
1:A:330:VAL:HG12	1:A:330:VAL:O	1.98	0.61
1:A:60:ALA:HB2	1:A:85:ASP:OD2	1.99	0.61
1:A:50:VAL:N	1:A:73:LYS:O	2.32	0.61
1:B:297:HIS:HE2	3:B:402:OXM:C1	2.12	0.61
1:B:159:GLN:O	1:B:162:MET:HB2	2.01	0.61
1:B:25:LYS:CE	1:B:25:LYS:HA	2.30	0.61
1:A:222:ILE:HA	1:A:225:MET:SD	2.41	0.61
1:A:31:TYR:HD1	1:A:31:TYR:H	1.47	0.61
1:B:18:ASN:O	1:B:22:GLU:HB2	2.00	0.61
1:B:218:ASN:O	1:B:222:ILE:HG13	2.01	0.61
1:B:282:ARG:O	1:B:283:LEU:C	2.38	0.61
1:A:21:LYS:HG3	1:A:29:VAL:HB	1.82	0.61
1:A:2:THR:CG2	1:A:321:ILE:HG21	2.31	0.61
1:A:7:TYR:CD1	1:A:36:LEU:HD12	2.34	0.61
1:A:186:LYS:HE2	1:A:188:TYR:CE2	2.36	0.61
1:A:319:LYS:HZ1	1:A:324:GLU:CB	2.14	0.61
1:A:331:ALA:O	1:A:333:ASN:N	2.34	0.61
1:B:327:ASP:O	1:B:328:SER:CB	2.47	0.61
1:B:86:MET:O	1:B:332:LEU:HD12	2.01	0.61
1:A:20:TRP:O	1:A:20:TRP:CE3	2.53	0.60
1:A:113:ILE:CD1	1:B:116:ALA:CB	2.75	0.60
1:B:219:ASP:CG	1:B:247:ARG:NH1	2.53	0.60
1:B:316:ASN:OD1	1:B:327:ASP:N	2.29	0.60
1:A:162:MET:CB	1:A:163:ARG:NH1	2.64	0.60
1:A:49:GLY:CA	1:A:73:LYS:O	2.49	0.60
1:B:54:GLN:HG2	1:B:55:GLN:N	2.14	0.60
1:A:182:GLU:OE1	1:A:183:LEU:CD1	2.50	0.60
1:A:242:THR:O	1:A:246:ILE:HG13	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:25:LYS:HE2	1:B:25:LYS:CA	2.32	0.60
1:B:12:ASP:O	1:B:15:PRO:HG2	2.02	0.60
1:B:98:ASN:C	1:B:98:ASN:ND2	2.54	0.60
1:B:316:ASN:HD21	1:B:327:ASP:C	2.05	0.60
1:A:260:ASP:HA	1:A:295:THR:O	2.01	0.60
1:A:113:ILE:HD13	1:B:116:ALA:HB1	1.83	0.60
1:B:142:ARG:HD2	1:B:147:GLN:HE22	1.67	0.60
1:A:210:VAL:O	1:A:214:VAL:HG23	2.02	0.60
1:A:209:ASP:C	1:A:209:ASP:OD1	2.39	0.60
1:A:197:TYR:O	1:A:225:MET:HA	2.01	0.60
1:A:19:GLU:CA	1:A:22:GLU:OE1	2.39	0.60
1:B:315:ASN:O	1:B:318:LEU:N	2.35	0.60
1:A:192:SER:O	1:A:195:ASP:HB2	2.02	0.59
1:B:21:LYS:HG2	1:B:29:VAL:CG2	2.32	0.59
1:A:261:THR:HG23	1:A:265:GLU:OE1	2.02	0.59
1:A:318:LEU:O	1:A:322:ASN:HB2	2.02	0.59
1:A:96:ILE:HG22	1:A:330:VAL:HG23	1.80	0.59
1:A:319:LYS:HZ1	1:A:324:GLU:HB3	1.65	0.59
1:A:7:TYR:CE1	1:A:36:LEU:HD12	2.37	0.59
1:B:138:PRO:O	1:B:140:ILE:HG22	2.02	0.59
1:B:240:VAL:HG12	1:B:241:ASP:N	2.17	0.59
1:B:97:THR:HG21	1:B:316:ASN:HB3	1.84	0.59
1:A:5:PHE:CZ	1:A:31:TYR:O	2.55	0.59
1:B:90:LYS:HZ2	1:B:93:GLY:HA2	1.67	0.59
1:A:5:PHE:CD1	1:A:30:ASP:O	2.55	0.59
1:A:58:TYR:CD2	1:A:84:ILE:CG2	2.86	0.59
1:A:209:ASP:O	1:A:209:ASP:OD1	2.21	0.59
1:B:39:GLU:C	1:B:39:GLU:OE1	2.41	0.59
1:A:210:VAL:HG12	1:A:212:ALA:N	2.17	0.59
1:B:11:LYS:O	1:B:15:PRO:HD2	2.03	0.59
1:B:18:ASN:O	1:B:22:GLU:CB	2.51	0.59
1:B:20:TRP:HE3	1:B:21:LYS:N	2.01	0.59
1:A:152:VAL:O	1:A:206:HIS:N	2.34	0.58
1:A:142:ARG:NH2	1:A:228:GLY:O	2.35	0.58
1:A:102:TYR:HB2	1:A:305:ALA:CB	2.31	0.58
1:B:207:VAL:HG22	1:B:208:PRO:CD	2.32	0.58
1:B:36:LEU:HD13	1:B:41:ALA:HA	1.84	0.58
1:B:5:PHE:O	1:B:50:VAL:HA	2.03	0.58
1:A:323:GLY:O	1:A:324:GLU:HG3	2.02	0.58
1:B:297:HIS:CD2	3:B:402:OXM:O1	2.55	0.58
1:A:149:VAL:CG2	1:A:165:MET:CE	2.81	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:VAL:CG1	1:A:165:MET:HE3	2.33	0.58
1:B:32:THR:CG2	1:B:33:ASP:N	2.66	0.58
1:B:125:MET:O	1:B:128:LYS:N	2.34	0.58
1:A:154:THR:HG21	1:A:189:TYR:OH	2.04	0.58
1:B:90:LYS:NZ	1:B:93:GLY:HA2	2.18	0.58
1:A:31:TYR:CD1	1:A:31:TYR:N	2.72	0.58
1:B:162:MET:HE1	1:B:172:VAL:CG1	2.34	0.58
1:A:209:ASP:HA	1:A:239:LEU:HD21	1.86	0.58
1:A:297:HIS:CD2	3:A:402:OXM:O1	2.57	0.58
1:A:196:LEU:C	1:A:196:LEU:HD23	2.24	0.58
1:B:135:ARG:HG3	1:B:135:ARG:HH11	1.67	0.58
1:B:54:GLN:NE2	1:B:56:LEU:C	2.50	0.58
1:A:317:ASN:O	1:A:318:LEU:C	2.40	0.57
1:B:285:ASP:O	1:B:289:ARG:HG2	2.03	0.57
1:B:36:LEU:HD12	1:B:37:THR:H	1.63	0.57
1:A:210:VAL:HG13	1:A:211:PRO:N	2.18	0.57
1:A:214:VAL:HG12	1:A:214:VAL:O	2.03	0.57
1:B:42:LYS:HB3	1:B:42:LYS:NZ	2.19	0.57
1:A:267:GLY:HA2	1:A:271:LYS:HZ1	1.69	0.57
1:A:300:PHE:C	1:A:300:PHE:CD1	2.78	0.57
1:A:63:LEU:O	1:A:67:ALA:N	2.27	0.57
1:B:278:PHE:CE2	1:B:284:ALA:HB2	2.39	0.57
1:B:86:MET:SD	1:B:336:LYS:HE2	2.45	0.57
1:B:87:ASP:O	1:B:88:LYS:C	2.41	0.57
1:A:201:ASP:OD1	1:A:226:LYS:NZ	2.32	0.57
1:B:173:ILE:HD11	1:B:199:GLN:HG3	1.87	0.57
1:A:96:ILE:O	1:A:330:VAL:HB	2.04	0.57
1:B:77:ARG:HG3	1:B:313:ALA:CB	2.35	0.57
1:A:182:GLU:C	1:A:182:GLU:CD	2.64	0.57
1:A:25:LYS:NZ	1:A:25:LYS:C	2.58	0.57
1:A:311:VAL:C	1:A:313:ALA:N	2.56	0.57
1:B:181:PRO:HA	1:B:184:GLU:OE2	2.05	0.57
1:A:186:LYS:HB2	1:A:186:LYS:HZ3	1.69	0.57
1:A:301:TYR:OH	1:B:138:PRO:HA	2.04	0.57
1:A:20:TRP:CE2	1:A:314:PHE:HB3	2.39	0.57
1:A:213:ASN:ND2	2:A:401:NAI:N6A	2.52	0.56
1:A:315:ASN:O	1:A:318:LEU:N	2.38	0.56
1:B:29:VAL:O	1:B:30:ASP:CG	2.43	0.56
1:B:48:ASP:HB3	1:B:321:ILE:HG12	1.86	0.56
1:A:135:ARG:HG3	1:A:135:ARG:HH11	1.70	0.56
1:B:28:ASP:OD1	1:B:29:VAL:N	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:GLU:OE2	1:B:302:THR:HG21	2.06	0.56
1:A:235:SER:HA	2:A:401:NAI:H1D	1.87	0.56
1:A:58:TYR:CD2	1:A:84:ILE:HG23	2.40	0.56
1:A:270:ASN:HA	1:B:135:ARG:HA	1.87	0.56
1:B:319:LYS:HB3	1:B:326:PRO:HB3	1.88	0.56
1:B:42:LYS:HB3	1:B:42:LYS:HZ2	1.69	0.56
1:A:245:VAL:HG13	1:A:254:ILE:HD13	1.82	0.56
1:A:263:GLU:HG3	1:A:264:ASP:OD1	2.05	0.56
1:A:7:TYR:CD1	1:A:36:LEU:CD1	2.88	0.56
1:B:27:ILE:HD12	1:B:318:LEU:HD11	1.87	0.56
1:B:235:SER:HA	2:B:401:NAI:H1D	1.88	0.56
1:A:108:ALA:HB1	1:A:160:VAL:HG12	1.88	0.56
1:A:81:VAL:O	1:A:84:ILE:HG13	2.05	0.56
1:B:10:ARG:NH2	1:B:306:VAL:CG1	2.65	0.56
1:B:38:PRO:HA	1:B:65:ALA:HB1	1.88	0.56
1:A:64:GLN:HA	1:A:67:ALA:CB	2.36	0.56
2:B:401:NAI:C4N	3:B:402:OXM:N1	2.66	0.56
1:B:125:MET:HE3	1:B:128:LYS:HE3	1.88	0.56
1:B:142:ARG:HH11	1:B:147:GLN:NE2	2.03	0.56
1:A:205:LEU:N	1:A:205:LEU:CD1	2.68	0.56
1:B:173:ILE:CD1	1:B:199:GLN:HG3	2.36	0.56
1:B:297:HIS:NE2	2:B:401:NAI:H42N	2.21	0.56
1:B:35:LEU:CD1	1:B:54:GLN:HG3	2.36	0.56
1:B:86:MET:CG	1:B:336:LYS:HD3	2.36	0.55
1:A:21:LYS:CE	1:A:21:LYS:CA	2.70	0.55
1:A:182:GLU:OE1	1:A:183:LEU:HD13	2.06	0.55
1:A:21:LYS:CG	1:A:29:VAL:HB	2.36	0.55
1:B:157:ILE:HD12	2:B:401:NAI:C5D	2.26	0.55
1:B:259:MET:HG3	1:B:261:THR:O	2.05	0.55
1:A:14:GLU:CB	1:A:15:PRO:CD	2.83	0.55
1:A:210:VAL:CB	1:A:211:PRO:HD2	2.37	0.55
1:A:281:LYS:O	1:A:284:ALA:N	2.40	0.55
1:A:329:PRO:O	1:A:332:LEU:CD2	2.55	0.55
1:B:321:ILE:HG22	1:B:322:ASN:N	2.22	0.55
1:A:17:LEU:HD12	1:A:314:PHE:CZ	2.36	0.55
1:A:319:LYS:HZ2	1:A:324:GLU:HB2	1.71	0.55
1:B:190:VAL:HG13	1:B:195:ASP:HB2	1.88	0.55
1:B:210:VAL:O	1:B:214:VAL:HG23	2.07	0.55
1:A:143:GLU:O	1:A:147:GLN:OE1	2.25	0.55
1:B:58:TYR:CD2	1:B:84:ILE:HG23	2.42	0.55
1:A:311:VAL:C	1:A:313:ALA:H	2.10	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:PRO:O	1:A:65:ALA:HB1	2.07	0.55
1:A:8:ALA:C	1:A:77:ARG:HH22	2.10	0.55
1:B:210:VAL:CG1	1:B:211:PRO:HD2	2.37	0.55
1:B:332:LEU:HD23	1:B:332:LEU:O	1.98	0.55
1:B:334:LYS:N	1:B:334:LYS:HD2	2.21	0.55
1:B:66:LEU:CD2	1:B:94:PHE:HZ	2.08	0.55
1:A:73:LYS:CD	1:A:321:ILE:HA	2.37	0.55
1:B:222:ILE:HD13	1:B:254:ILE:HD11	1.89	0.55
1:B:90:LYS:O	1:B:93:GLY:N	2.40	0.55
1:A:86:MET:O	1:A:89:ALA:HB3	2.07	0.55
1:B:18:ASN:O	1:B:22:GLU:N	2.35	0.55
1:A:145:ARG:HB2	1:A:168:PHE:O	2.07	0.55
1:A:48:ASP:O	1:A:73:LYS:HB2	2.07	0.55
1:A:283:LEU:HD12	1:A:283:LEU:O	2.06	0.54
1:A:4:VAL:HG13	1:A:317:ASN:HD22	1.72	0.54
1:B:194:ASP:O	1:B:198:LYS:HG2	2.07	0.54
1:A:149:VAL:CG2	1:A:165:MET:HE3	2.35	0.54
1:A:20:TRP:CZ3	1:A:29:VAL:HG21	2.42	0.54
1:A:319:LYS:NZ	1:A:324:GLU:HB3	2.22	0.54
1:A:5:PHE:HD2	1:A:7:TYR:CE1	2.26	0.54
1:B:173:ILE:HD11	1:B:199:GLN:NE2	2.22	0.54
1:B:214:VAL:O	1:B:215:HIS:HB2	2.07	0.54
1:B:197:TYR:O	1:B:225:MET:HA	2.07	0.54
1:A:260:ASP:CG	1:A:298:THR:H	2.10	0.54
1:A:96:ILE:CG2	1:A:97:THR:N	2.71	0.54
1:B:90:LYS:HD2	1:B:90:LYS:O	2.08	0.54
1:B:64:GLN:O	1:B:68:ASP:OD1	2.26	0.54
1:A:24:HIS:CE1	1:A:318:LEU:HD12	2.43	0.54
1:A:331:ALA:O	1:A:332:LEU:C	2.46	0.54
1:A:37:THR:OG1	1:A:40:THR:N	2.39	0.54
1:A:59:THR:HB	1:A:61:ASP:OD2	2.07	0.54
1:B:210:VAL:O	1:B:212:ALA:N	2.41	0.54
1:A:54:GLN:HB2	1:A:58:TYR:OH	2.08	0.54
1:B:53:TYR:O	1:B:54:GLN:HB2	2.07	0.54
1:B:1:MET:CG	1:B:2:THR:N	2.53	0.54
1:A:280:ASP:C	1:A:280:ASP:OD1	2.47	0.53
1:B:78:ASN:HA	1:B:102:TYR:HE2	1.73	0.53
1:A:218:ASN:HD21	1:A:220:LYS:HB2	1.73	0.53
1:A:38:PRO:CG	1:A:62:THR:OG1	2.54	0.53
1:A:11:LYS:HG3	1:A:12:ASP:N	2.17	0.53
1:A:19:GLU:HA	1:A:22:GLU:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:10:ARG:HB2	1:B:13:GLU:HG3	1.91	0.53
1:A:264:ASP:OD1	1:A:264:ASP:N	2.42	0.53
1:B:64:GLN:OE1	1:B:68:ASP:HB3	2.08	0.53
1:A:302:THR:HG21	1:B:143:GLU:CG	2.39	0.53
1:A:96:ILE:HG22	1:A:97:THR:N	2.23	0.53
1:B:162:MET:HE2	1:B:172:VAL:HG13	1.88	0.53
1:B:54:GLN:HG2	1:B:56:LEU:N	2.22	0.53
1:B:210:VAL:C	1:B:212:ALA:N	2.61	0.53
1:B:10:ARG:NH1	1:B:53:TYR:HE2	2.06	0.53
1:B:85:ASP:O	1:B:89:ALA:HB2	2.09	0.53
1:A:108:ALA:HB3	1:A:160:VAL:CG1	2.38	0.53
1:A:210:VAL:HG13	1:A:211:PRO:HD2	1.90	0.53
1:A:213:ASN:HD21	2:A:401:NAI:C6A	2.21	0.53
1:A:302:THR:HG21	1:B:143:GLU:HG3	1.90	0.53
1:B:11:LYS:HG3	1:B:11:LYS:O	2.09	0.53
1:B:235:SER:HB2	2:B:401:NAI:C4D	2.38	0.53
1:A:135:ARG:HH11	1:A:135:ARG:CG	2.21	0.52
1:A:229:VAL:O	1:A:255:PHE:HB3	2.08	0.52
1:A:177:ILE:CG2	1:A:178:PHE:N	2.71	0.52
1:A:229:VAL:HG22	1:A:230:VAL:H	1.71	0.52
1:A:38:PRO:N	1:A:62:THR:HG23	2.24	0.52
1:A:6:ALA:HB3	1:A:31:TYR:CB	2.35	0.52
1:B:108:ALA:HB1	1:B:161:PHE:HB2	1.90	0.52
1:B:190:VAL:HG13	1:B:195:ASP:CB	2.39	0.52
1:A:18:ASN:O	1:A:22:GLU:CB	2.58	0.52
1:A:20:TRP:HE3	1:A:21:LYS:N	2.08	0.52
1:A:281:LYS:HD2	1:A:281:LYS:C	2.30	0.52
1:A:47:ALA:O	1:A:71:VAL:CG2	2.58	0.52
1:A:58:TYR:HB2	1:A:84:ILE:HG22	1.91	0.52
1:A:270:ASN:CA	1:B:134:LEU:O	2.57	0.52
1:A:270:ASN:N	1:B:134:LEU:O	2.41	0.52
1:B:17:LEU:HG	1:B:314:PHE:CZ	2.44	0.52
1:B:235:SER:HB2	2:B:401:NAI:H4D	1.92	0.52
1:A:318:LEU:CD2	1:A:318:LEU:O	2.57	0.52
1:A:9:ILE:CG2	1:A:31:TYR:HD2	2.19	0.52
1:B:214:VAL:O	1:B:214:VAL:HG12	2.09	0.52
1:B:266:VAL:CG1	1:B:266:VAL:O	2.58	0.52
1:B:96:ILE:HG22	1:B:97:THR:N	2.25	0.52
1:B:173:ILE:HD11	1:B:199:GLN:HE21	1.74	0.52
1:B:176:ASP:OD1	2:B:401:NAI:H1B	2.09	0.52
1:A:180:ASN:ND2	1:A:183:LEU:HD22	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:9:ILE:CG2	1:B:31:TYR:CD2	2.85	0.52
1:B:5:PHE:HE2	1:B:7:TYR:CZ	2.28	0.52
1:A:210:VAL:CG1	1:A:212:ALA:HB3	2.40	0.52
1:B:318:LEU:O	1:B:322:ASN:HB2	2.10	0.51
2:B:401:NAI:H42N	3:B:402:OXM:O1	2.08	0.51
1:A:20:TRP:O	1:A:20:TRP:CD2	2.63	0.51
1:A:297:HIS:NE2	2:A:401:NAI:C7N	2.73	0.51
1:B:86:MET:HB3	1:B:332:LEU:CG	2.35	0.51
1:A:108:ALA:CB	1:A:160:VAL:HG12	2.40	0.51
1:B:14:GLU:CB	1:B:15:PRO:CD	2.87	0.51
1:B:81:VAL:HG11	1:B:330:VAL:CG1	2.20	0.51
1:B:180:ASN:O	1:B:184:GLU:HB3	2.10	0.51
1:B:242:THR:HG22	1:B:246:ILE:HD12	1.92	0.51
1:B:86:MET:CE	1:B:332:LEU:HG	2.40	0.51
1:A:266:VAL:O	1:A:266:VAL:HG13	2.11	0.51
1:A:7:TYR:N	1:A:51:VAL:O	2.42	0.51
1:B:20:TRP:CE3	1:B:21:LYS:N	2.78	0.51
1:B:261:THR:HG23	1:B:265:GLU:OE1	2.11	0.51
1:A:12:ASP:O	1:A:16:PHE:CE2	2.64	0.51
1:B:142:ARG:HD2	1:B:147:GLN:NE2	2.25	0.51
1:B:314:PHE:O	1:B:315:ASN:O	2.28	0.51
1:B:79:VAL:HG13	1:B:80:GLY:N	2.25	0.51
1:B:125:MET:CE	1:B:128:LYS:CE	2.89	0.51
1:A:269:PHE:HD1	1:B:134:LEU:HD23	1.76	0.51
1:A:17:LEU:HD23	1:A:18:ASN:HD22	1.76	0.51
1:A:153:GLY:HA3	1:A:206:HIS:O	2.11	0.51
1:A:306:VAL:O	1:A:309:MET:HB2	2.11	0.51
1:A:58:TYR:HD2	1:A:84:ILE:HG23	1.74	0.51
1:A:9:ILE:HG22	1:A:9:ILE:O	2.10	0.51
1:B:210:VAL:O	1:B:213:ASN:N	2.44	0.51
1:B:27:ILE:HD11	1:B:318:LEU:HD11	1.93	0.51
1:B:155:GLY:N	2:B:401:NAI:H51A	2.26	0.50
1:B:20:TRP:CE3	1:B:21:LYS:HA	2.47	0.50
1:B:48:ASP:HB3	1:B:321:ILE:CG1	2.41	0.50
1:B:85:ASP:O	1:B:89:ALA:CB	2.59	0.50
1:A:105:ASN:O	1:A:109:GLU:HB2	2.11	0.50
1:A:222:ILE:O	1:A:225:MET:HB2	2.11	0.50
1:A:329:PRO:O	1:A:332:LEU:HD23	2.12	0.50
1:B:21:LYS:HE3	1:B:24:HIS:O	2.10	0.50
1:B:48:ASP:HB3	1:B:321:ILE:HD11	1.93	0.50
1:A:21:LYS:NZ	1:A:21:LYS:O	2.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:LYS:O	1:A:132:ARG:CB	2.59	0.50
1:A:82:ASP:OD1	1:A:82:ASP:C	2.49	0.50
1:B:11:LYS:O	1:B:15:PRO:CD	2.59	0.50
1:A:219:ASP:CG	1:A:247:ARG:NH1	2.65	0.50
1:B:302:THR:HG22	1:B:305:ALA:H	1.76	0.50
1:A:305:ALA:O	1:A:308:ASN:HB2	2.12	0.50
1:B:175:TYR:CD2	1:B:193:LEU:HD13	2.46	0.50
1:A:131:LYS:O	1:A:132:ARG:HB2	2.10	0.50
1:A:278:PHE:HE2	1:A:280:ASP:O	1.94	0.50
1:B:190:VAL:CG1	1:B:195:ASP:HB2	2.41	0.50
1:A:32:THR:CG2	1:A:33:ASP:N	2.75	0.50
1:A:35:LEU:HD13	1:A:54:GLN:HG2	1.94	0.50
1:A:105:ASN:HD22	1:B:145:ARG:NH2	2.08	0.50
1:B:151:VAL:HG21	1:B:162:MET:HE2	1.93	0.50
1:A:11:LYS:NZ	1:A:14:GLU:CD	2.65	0.50
1:A:31:TYR:HD1	1:A:31:TYR:N	2.06	0.50
1:A:319:LYS:NZ	1:A:324:GLU:CD	2.64	0.50
1:B:207:VAL:CG1	1:B:216:MET:HE1	2.42	0.50
1:B:28:ASP:OD1	1:B:30:ASP:OD1	2.29	0.50
1:A:110:HIS:O	1:A:114:GLN:HG2	2.11	0.49
1:A:193:LEU:HG	1:A:197:TYR:CZ	2.47	0.49
1:A:295:THR:HG22	1:A:296:PRO:CD	2.38	0.49
1:B:229:VAL:HG22	1:B:230:VAL:N	2.27	0.49
1:A:305:ALA:O	1:A:306:VAL:C	2.49	0.49
1:B:18:ASN:ND2	1:B:18:ASN:H	2.01	0.49
1:B:118:VAL:HG21	1:B:258:VAL:HG23	1.94	0.49
1:A:11:LYS:O	1:A:14:GLU:HB2	2.12	0.49
1:A:155:GLY:N	2:A:401:NAI:H52A	2.28	0.49
1:A:74:MET:HE2	1:A:96:ILE:CD1	2.42	0.49
1:B:273:TRP:CH2	1:B:279:PRO:HG3	2.47	0.49
1:A:35:LEU:O	1:A:37:THR:HG23	2.13	0.49
1:A:82:ASP:OD1	1:A:82:ASP:O	2.31	0.49
1:A:8:ALA:O	1:A:77:ARG:NH2	2.45	0.49
1:B:90:LYS:O	1:B:91:GLU:C	2.45	0.49
1:B:151:VAL:HG21	1:B:162:MET:CE	2.42	0.49
1:B:286:LEU:O	1:B:287:ILE:C	2.51	0.49
1:A:190:VAL:CG1	1:A:191:ASP:N	2.75	0.49
1:A:99:VAL:O	1:A:99:VAL:CG1	2.58	0.49
1:A:269:PHE:CD1	1:B:134:LEU:HD23	2.46	0.49
1:B:154:THR:HG21	1:B:183:LEU:HD23	1.90	0.49
1:A:135:ARG:NH2	1:B:272:ASP:HB2	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:308:ASN:O	1:B:312:LYS:N	2.45	0.49
1:B:9:ILE:HG23	1:B:9:ILE:O	2.13	0.49
1:A:198:LYS:HB2	1:A:198:LYS:HE3	1.61	0.49
1:B:327:ASP:O	1:B:328:SER:HB2	2.11	0.49
1:B:310:VAL:O	1:B:313:ALA:HB3	2.13	0.49
1:B:319:LYS:HB2	1:B:326:PRO:HB3	1.93	0.49
1:B:125:MET:CE	1:B:128:LYS:HE3	2.43	0.49
1:B:36:LEU:HD13	1:B:41:ALA:CA	2.43	0.48
1:A:237:GLY:H	1:A:261:THR:HG21	1.78	0.48
1:B:257:PHE:CZ	1:B:259:MET:CE	2.96	0.48
1:A:283:LEU:C	1:A:283:LEU:HD12	2.33	0.48
1:A:318:LEU:HD23	1:A:318:LEU:C	2.34	0.48
1:B:2:THR:HG22	1:B:3:LYS:H	1.78	0.48
1:A:210:VAL:HG13	1:A:212:ALA:N	2.11	0.48
1:A:18:ASN:O	1:A:22:GLU:HB3	2.13	0.48
1:A:235:SER:CA	2:A:401:NAI:H1D	2.44	0.48
1:A:39:GLU:O	1:A:42:LYS:HG2	2.13	0.48
1:B:32:THR:HG22	1:B:34:LYS:O	2.13	0.48
1:A:142:ARG:HH11	1:A:147:GLN:NE2	2.11	0.48
1:A:278:PHE:CE2	1:A:280:ASP:O	2.66	0.48
1:A:328:SER:O	1:A:332:LEU:HD21	2.13	0.48
1:B:143:GLU:O	1:B:147:GLN:OE1	2.31	0.48
1:B:74:MET:O	1:B:96:ILE:HA	2.13	0.48
1:A:135:ARG:NH1	1:A:135:ARG:CG	2.77	0.48
1:A:24:HIS:CE1	1:A:318:LEU:CD1	2.97	0.48
1:B:173:ILE:HD11	1:B:199:GLN:CG	2.43	0.48
1:B:257:PHE:CZ	1:B:259:MET:HE3	2.49	0.48
1:A:20:TRP:HZ3	1:A:29:VAL:HG21	1.77	0.48
1:A:217:ILE:HB	1:A:240:VAL:HG13	1.95	0.48
1:A:2:THR:HG22	1:A:321:ILE:HD13	1.96	0.48
1:A:334:LYS:HA	1:A:334:LYS:HD3	1.63	0.48
1:A:5:PHE:HA	1:A:30:ASP:O	2.13	0.48
1:A:109:GLU:OE1	1:B:143:GLU:HB3	2.14	0.48
1:A:59:THR:C	1:A:61:ASP:N	2.64	0.48
1:B:207:VAL:HG22	1:B:208:PRO:HD2	1.94	0.48
1:A:2:THR:CG2	1:A:321:ILE:HD13	2.44	0.47
1:A:149:VAL:CG2	1:A:165:MET:HE1	2.42	0.47
1:A:209:ASP:HB2	1:A:236:ARG:CB	2.43	0.47
1:A:97:THR:CA	1:A:330:VAL:HG23	2.45	0.47
1:B:5:PHE:HA	1:B:30:ASP:O	2.14	0.47
1:B:120:ARG:O	1:B:121:GLN:HB2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:TRP:NE1	1:B:270:ASN:ND2	2.62	0.47
1:A:132:ARG:NH1	1:B:288:ASP:OD1	2.44	0.47
1:B:45:LYS:HA	1:B:69:ALA:HB1	1.96	0.47
1:B:75:SER:OG	1:B:97:THR:CB	2.62	0.47
1:B:124:ARG:O	1:B:128:LYS:HG3	2.15	0.47
1:A:129:MET:SD	1:B:296:PRO:HG3	2.55	0.47
1:B:316:ASN:HD21	1:B:327:ASP:CB	2.27	0.47
1:B:36:LEU:C	1:B:36:LEU:HD12	2.32	0.47
1:B:2:THR:CG2	1:B:3:LYS:N	2.76	0.47
1:B:207:VAL:CG1	1:B:216:MET:CE	2.92	0.47
1:B:241:ASP:O	1:B:242:THR:C	2.53	0.47
1:B:10:ARG:HH21	1:B:306:VAL:CG1	2.27	0.47
1:A:105:ASN:ND2	1:B:145:ARG:NH2	2.63	0.47
1:B:6:ALA:N	1:B:30:ASP:O	2.44	0.47
1:B:7:TYR:HB2	1:B:52:VAL:HB	1.97	0.47
1:B:88:LYS:O	1:B:92:LEU:HD12	2.15	0.47
1:A:151:VAL:HG23	1:A:173:ILE:O	2.15	0.47
1:B:125:MET:HE3	1:B:128:LYS:CE	2.44	0.47
1:B:125:MET:O	1:B:128:LYS:HB2	2.15	0.47
1:B:90:LYS:HD2	1:B:90:LYS:HA	1.26	0.47
1:A:19:GLU:CA	1:A:22:GLU:HB3	2.44	0.47
1:A:157:ILE:CD1	2:A:401:NAI:H51N	2.21	0.47
1:A:232:VAL:HG22	1:A:258:VAL:HB	1.96	0.47
1:B:251:SER:OG	1:B:252:GLY:N	2.47	0.47
1:A:235:SER:HA	2:A:401:NAI:H2N	1.96	0.47
1:B:154:THR:HG23	1:B:159:GLN:CG	2.45	0.47
1:B:86:MET:HE2	1:B:332:LEU:HG	1.95	0.47
1:B:32:THR:CG2	1:B:34:LYS:O	2.62	0.47
1:B:43:LEU:O	1:B:43:LEU:HD12	2.14	0.47
1:B:43:LEU:C	1:B:45:LYS:H	2.17	0.47
1:B:88:LYS:C	1:B:92:LEU:HD12	2.35	0.47
1:B:1:MET:CG	1:B:2:THR:H	2.16	0.47
1:B:86:MET:CE	1:B:332:LEU:CB	2.93	0.47
1:B:86:MET:O	1:B:89:ALA:HB3	2.15	0.47
1:A:142:ARG:NH1	1:A:147:GLN:HE21	2.11	0.46
1:A:267:GLY:O	1:A:271:LYS:HD3	2.16	0.46
1:B:149:VAL:HG22	1:B:202:VAL:HB	1.97	0.46
1:B:9:ILE:CG2	1:B:31:TYR:HD2	2.27	0.46
1:B:319:LYS:HD3	1:B:325:LYS:C	2.36	0.46
1:B:37:THR:HB	1:B:38:PRO:HD2	1.97	0.46
1:B:38:PRO:HG3	1:B:62:THR:HA	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:THR:O	1:A:63:LEU:CD1	2.60	0.46
1:A:64:GLN:O	1:A:65:ALA:C	2.53	0.46
1:A:113:ILE:HD13	1:B:116:ALA:HB3	1.97	0.46
1:A:136:TRP:HE1	1:B:270:ASN:ND2	2.13	0.46
1:B:7:TYR:HE1	1:B:40:THR:HG22	1.79	0.46
1:B:42:LYS:NZ	1:B:42:LYS:CB	2.78	0.46
1:B:86:MET:O	1:B:332:LEU:CD1	2.63	0.46
1:A:103:SER:HA	1:A:104:PRO:HD2	1.85	0.46
1:A:107:ILE:HG23	1:A:299:ALA:HB1	1.97	0.46
1:B:129:MET:O	1:B:132:ARG:HD2	2.15	0.46
1:B:20:TRP:HE3	1:B:21:LYS:CA	2.29	0.46
1:B:222:ILE:HD13	1:B:222:ILE:HG23	1.69	0.46
1:B:231:ILE:O	1:B:257:PHE:HA	2.16	0.46
1:A:155:GLY:O	1:A:156:HIS:C	2.51	0.46
1:A:193:LEU:HG	1:A:197:TYR:CE1	2.50	0.46
1:A:228:GLY:CA	1:A:255:PHE:HB2	2.45	0.46
1:A:102:TYR:CE2	1:A:309:MET:SD	3.08	0.46
1:A:90:LYS:C	1:A:92:LEU:N	2.67	0.46
1:A:6:ALA:HB1	1:A:9:ILE:HD11	1.93	0.46
1:B:135:ARG:CG	1:B:135:ARG:HH11	2.29	0.46
1:B:17:LEU:HD21	1:B:29:VAL:HG11	1.98	0.46
1:A:270:ASN:O	1:A:270:ASN:CG	2.50	0.46
1:B:90:LYS:CB	1:B:332:LEU:CD1	2.86	0.46
1:B:40:THR:C	1:B:42:LYS:N	2.66	0.46
1:A:71:VAL:HG12	1:A:73:LYS:H	1.79	0.46
1:B:218:ASN:HD22	1:B:220:LYS:H	1.52	0.46
1:A:59:THR:O	1:A:61:ASP:N	2.49	0.46
1:A:62:THR:HA	1:A:65:ALA:CB	2.46	0.46
1:B:5:PHE:HB2	1:B:47:ALA:CB	2.46	0.46
1:B:96:ILE:HG22	1:B:97:THR:H	1.80	0.46
1:A:185:LYS:HA	1:A:185:LYS:HD2	1.28	0.46
1:B:102:TYR:HD2	1:B:309:MET:CG	2.22	0.46
1:A:132:ARG:NH2	1:B:284:ALA:HB1	2.30	0.46
1:A:143:GLU:OE1	1:A:145:ARG:HD2	2.16	0.45
1:A:182:GLU:OE1	1:A:183:LEU:HD12	2.15	0.45
1:A:123:LYS:HE2	1:A:289:ARG:O	2.16	0.45
1:B:164:ILE:O	1:B:168:PHE:HD2	1.98	0.45
1:A:162:MET:HB3	1:A:163:ARG:NH1	2.31	0.45
1:B:179:LYS:O	1:B:180:ASN:C	2.54	0.45
1:B:207:VAL:CG2	2:B:401:NAI:C4A	2.94	0.45
1:B:314:PHE:O	1:B:315:ASN:C	2.55	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:GLU:O	1:A:279:PRO:HD3	2.16	0.45
1:A:156:HIS:CD2	2:A:401:NAI:O2N	2.69	0.45
1:B:40:THR:C	1:B:42:LYS:H	2.19	0.45
1:A:128:LYS:HB3	1:A:133:ASP:HB3	1.98	0.45
1:A:139:THR:CG2	1:A:139:THR:O	2.52	0.45
1:A:152:VAL:HB	1:A:205:LEU:HD12	1.98	0.45
1:A:97:THR:OG1	1:A:320:LEU:HD21	2.17	0.45
1:A:37:THR:O	1:A:38:PRO:C	2.55	0.45
1:B:257:PHE:HZ	1:B:259:MET:CE	2.29	0.45
1:A:38:PRO:HG3	1:A:62:THR:HG1	1.77	0.45
1:A:61:ASP:OD1	1:A:62:THR:N	2.49	0.45
1:A:20:TRP:CD2	1:A:20:TRP:C	2.89	0.45
1:A:210:VAL:HG12	1:A:213:ASN:N	2.23	0.45
1:A:31:TYR:HB2	1:A:32:THR:H	1.61	0.45
1:A:49:GLY:HA3	1:A:317:ASN:HD21	1.82	0.45
1:A:74:MET:CE	1:A:96:ILE:HD13	2.47	0.45
1:A:60:ALA:HB1	1:A:88:LYS:HG3	1.98	0.45
1:A:180:ASN:HA	1:A:181:PRO:HD2	1.69	0.45
1:A:237:GLY:N	1:A:261:THR:HG21	2.32	0.45
1:A:318:LEU:CD2	1:A:318:LEU:C	2.85	0.45
1:B:282:ARG:HG3	1:B:283:LEU:H	1.81	0.45
1:A:278:PHE:CD2	1:A:284:ALA:HB2	2.50	0.45
1:B:17:LEU:HB3	1:B:18:ASN:HD21	1.80	0.45
1:B:210:VAL:C	1:B:212:ALA:H	2.19	0.45
1:B:255:PHE:O	1:B:291:ASN:ND2	2.47	0.45
1:B:64:GLN:C	1:B:66:LEU:N	2.68	0.45
1:B:85:ASP:O	1:B:89:ALA:N	2.44	0.45
1:A:300:PHE:CG	1:A:301:TYR:N	2.84	0.44
1:B:154:THR:HG23	1:B:159:GLN:HG2	1.98	0.44
1:B:20:TRP:CE3	1:B:21:LYS:CA	3.00	0.44
1:A:245:VAL:O	1:A:246:ILE:C	2.53	0.44
1:B:143:GLU:OE1	1:B:145:ARG:HD2	2.18	0.44
1:B:287:ILE:HA	1:B:294:VAL:HG23	1.97	0.44
1:B:90:LYS:C	1:B:93:GLY:H	2.21	0.44
1:B:21:LYS:CE	1:B:24:HIS:O	2.65	0.44
1:B:302:THR:CG2	1:B:304:HIS:H	2.30	0.44
1:B:77:ARG:O	1:B:309:MET:HG2	2.17	0.44
1:A:9:ILE:HD12	1:A:77:ARG:CZ	2.43	0.44
1:A:15:PRO:O	1:A:18:ASN:HB2	2.17	0.44
1:A:168:PHE:CE2	1:B:109:GLU:HG2	2.53	0.44
1:A:207:VAL:HA	1:A:208:PRO:HD3	1.89	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:ASN:HA	1:B:181:PRO:HD3	1.80	0.44
1:B:78:ASN:N	1:B:78:ASN:OD1	2.51	0.44
1:A:7:TYR:CD2	1:A:36:LEU:CD1	2.94	0.44
1:B:47:ALA:O	1:B:71:VAL:HG21	2.17	0.44
1:A:128:LYS:HE3	1:A:135:ARG:O	2.18	0.44
1:A:190:VAL:HG12	1:A:192:SER:H	1.82	0.44
1:A:302:THR:CG2	1:B:143:GLU:HG3	2.47	0.44
1:A:89:ALA:O	1:A:94:PHE:HB2	2.18	0.44
1:B:319:LYS:CE	1:B:325:LYS:O	2.66	0.44
1:B:297:HIS:HE2	2:B:401:NAI:H42N	1.82	0.44
1:A:144:VAL:C	1:A:146:ASP:H	2.21	0.44
1:A:238:ARG:HG2	1:A:238:ARG:H	1.40	0.44
1:A:168:PHE:HE2	1:B:109:GLU:HG2	1.83	0.44
1:B:184:GLU:HA	1:B:189:TYR:CD1	2.49	0.44
1:A:113:ILE:HD11	1:B:116:ALA:CB	2.38	0.44
1:A:282:ARG:HD3	1:A:282:ARG:HH11	1.43	0.44
1:A:37:THR:OG1	1:A:40:THR:OG1	1.69	0.44
1:B:268:VAL:HG11	1:B:283:LEU:HD23	1.98	0.44
1:B:10:ARG:HH11	1:B:53:TYR:HE2	1.65	0.44
1:A:140:ILE:HG13	1:B:301:TYR:CE1	2.53	0.43
1:B:125:MET:HE1	1:B:128:LYS:CE	2.48	0.43
1:B:134:LEU:HD12	1:B:134:LEU:N	2.33	0.43
1:B:270:ASN:O	1:B:271:LYS:HD3	2.18	0.43
1:B:278:PHE:CD2	1:B:284:ALA:HB2	2.52	0.43
1:B:37:THR:O	1:B:38:PRO:C	2.55	0.43
1:B:64:GLN:CA	1:B:67:ALA:HB3	2.42	0.43
1:B:193:LEU:HA	1:B:193:LEU:HD12	1.71	0.43
1:B:260:ASP:CG	1:B:298:THR:H	2.17	0.43
1:B:5:PHE:CE2	1:B:7:TYR:CZ	3.06	0.43
1:A:20:TRP:O	1:A:24:HIS:HB2	2.18	0.43
1:A:237:GLY:H	1:A:261:THR:CG2	2.31	0.43
1:A:2:THR:CG2	1:A:27:ILE:HG23	2.48	0.43
1:A:96:ILE:CB	1:A:330:VAL:HG21	2.42	0.43
1:A:38:PRO:N	1:A:62:THR:CG2	2.81	0.43
1:A:64:GLN:O	1:A:68:ASP:OD1	2.37	0.43
1:A:144:VAL:C	1:A:146:ASP:N	2.72	0.43
1:A:316:ASN:ND2	1:A:327:ASP:O	2.52	0.43
1:B:9:ILE:HG21	1:B:31:TYR:HD2	1.68	0.43
1:A:105:ASN:ND2	1:B:145:ARG:CZ	2.81	0.43
1:B:158:GLY:O	1:B:162:MET:HG3	2.19	0.43
1:B:317:ASN:O	1:B:320:LEU:CB	2.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:235:SER:HB2	2:B:401:NAI:H1D	2.00	0.43
1:A:159:GLN:O	1:A:163:ARG:HD2	2.18	0.43
1:A:163:ARG:O	1:A:166:GLU:HB2	2.18	0.43
1:B:207:VAL:HG11	1:B:216:MET:HE1	2.01	0.43
1:B:21:LYS:O	1:B:23:ALA:N	2.51	0.43
1:B:36:LEU:CD1	1:B:41:ALA:HB2	2.43	0.43
1:B:9:ILE:HG22	1:B:9:ILE:O	2.16	0.43
1:A:156:HIS:N	1:A:156:HIS:CD2	2.86	0.43
1:A:177:ILE:HA	1:A:177:ILE:HD12	1.63	0.43
1:B:177:ILE:HD13	2:B:401:NAI:C2A	2.49	0.43
1:B:173:ILE:CD1	1:B:199:GLN:CG	2.97	0.43
1:B:53:TYR:O	1:B:54:GLN:CB	2.67	0.43
1:A:237:GLY:N	1:A:261:THR:CG2	2.82	0.43
1:B:262:TYR:O	1:B:265:GLU:CB	2.64	0.43
1:B:328:SER:N	1:B:329:PRO:CD	2.82	0.43
1:A:190:VAL:HG12	1:A:192:SER:N	2.33	0.43
1:B:240:VAL:HG12	1:B:241:ASP:H	1.84	0.43
1:B:261:THR:HG22	1:B:262:TYR:N	2.34	0.43
1:A:184:GLU:HB3	1:A:189:TYR:CD2	2.54	0.42
1:B:122:ASP:O	1:B:125:MET:N	2.52	0.42
1:B:210:VAL:HB	1:B:213:ASN:HD22	1.84	0.42
1:B:65:ALA:O	1:B:68:ASP:OD1	2.37	0.42
1:A:267:GLY:HA2	1:A:271:LYS:NZ	2.34	0.42
1:A:155:GLY:N	2:A:401:NAI:C5B	2.83	0.42
1:B:173:ILE:O	1:B:173:ILE:HG22	2.14	0.42
1:B:32:THR:HG23	1:B:34:LYS:H	1.83	0.42
1:B:61:ASP:O	1:B:63:LEU:N	2.53	0.42
1:A:315:ASN:O	1:A:317:ASN:N	2.52	0.42
1:A:331:ALA:H	1:A:332:LEU:HG	1.84	0.42
1:B:48:ASP:O	1:B:71:VAL:HG13	2.18	0.42
1:B:302:THR:HG23	1:B:304:HIS:H	1.83	0.42
1:B:10:ARG:HH12	1:B:309:MET:HE1	1.85	0.42
1:B:234:CYS:O	2:B:401:NAI:N7N	2.52	0.42
1:A:270:ASN:HA	1:B:134:LEU:C	2.39	0.42
1:A:58:TYR:CD2	1:A:84:ILE:HG22	2.54	0.42
1:B:135:ARG:NH1	1:B:135:ARG:CG	2.81	0.42
1:B:180:ASN:OD1	1:B:180:ASN:C	2.58	0.42
1:B:241:ASP:OD2	1:B:244:ALA:HB2	2.20	0.42
1:A:287:ILE:HD13	1:A:287:ILE:HG21	1.74	0.42
1:A:37:THR:C	1:A:39:GLU:N	2.72	0.42
1:B:183:LEU:HD13	1:B:183:LEU:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:401:NAI:C5N	3:B:402:OXM:HN2	1.92	0.42
1:A:4:VAL:HG13	1:A:317:ASN:ND2	2.33	0.42
1:A:208:PRO:HG2	2:A:401:NAI:H8A	2.01	0.42
1:B:316:ASN:HD21	1:B:327:ASP:CA	2.32	0.42
1:A:20:TRP:CE3	1:A:21:LYS:HA	2.55	0.42
1:A:32:THR:HG23	1:A:33:ASP:H	1.84	0.42
1:A:55:GLN:O	1:A:55:GLN:HG2	2.20	0.42
1:B:20:TRP:CZ3	1:B:29:VAL:HG21	2.55	0.42
1:B:235:SER:HA	2:B:401:NAI:H2N	2.01	0.42
1:B:61:ASP:O	1:B:62:THR:C	2.57	0.42
1:A:103:SER:HB2	1:B:145:ARG:HH12	1.85	0.42
1:A:210:VAL:CG1	1:A:211:PRO:HD2	2.49	0.42
1:A:317:ASN:O	1:A:319:LYS:N	2.53	0.42
1:A:7:TYR:CD2	1:A:36:LEU:HA	2.54	0.42
1:A:97:THR:HG23	1:A:329:PRO:HA	2.01	0.42
1:A:43:LEU:C	1:A:45:LYS:N	2.68	0.42
1:A:85:ASP:O	1:A:89:ALA:CB	2.57	0.42
1:B:154:THR:H	2:B:401:NAI:H4B	1.84	0.42
1:B:293:LEU:HD12	1:B:293:LEU:HA	1.91	0.42
1:B:40:THR:O	1:B:43:LEU:N	2.50	0.42
1:A:217:ILE:CG2	1:A:240:VAL:HG12	2.50	0.41
1:A:88:LYS:O	1:A:92:LEU:HB2	2.19	0.41
1:B:197:TYR:N	1:B:197:TYR:CD1	2.87	0.41
1:B:213:ASN:O	1:B:215:HIS:N	2.52	0.41
1:A:66:LEU:HD23	1:A:94:PHE:CZ	2.55	0.41
1:B:282:ARG:HG3	1:B:283:LEU:N	2.36	0.41
1:B:61:ASP:C	1:B:63:LEU:N	2.73	0.41
1:B:77:ARG:HG3	1:B:313:ALA:HB2	2.02	0.41
1:A:56:LEU:HD12	1:A:56:LEU:HA	1.56	0.41
1:A:71:VAL:HG12	1:A:73:LYS:N	2.35	0.41
1:A:7:TYR:O	1:A:8:ALA:HB3	2.20	0.41
1:B:319:LYS:HD3	1:B:325:LYS:O	2.20	0.41
1:A:144:VAL:HG23	1:A:144:VAL:H	1.68	0.41
1:A:209:ASP:HB2	1:A:236:ARG:HB3	2.02	0.41
1:A:268:VAL:HG11	1:A:283:LEU:HD23	2.03	0.41
1:A:306:VAL:HG21	1:B:140:ILE:CD1	2.51	0.41
1:B:151:VAL:CG2	1:B:162:MET:HE2	2.51	0.41
1:B:5:PHE:CD2	1:B:7:TYR:CE2	3.09	0.41
1:A:260:ASP:OD2	1:A:298:THR:N	2.33	0.41
1:A:300:PHE:CD1	1:A:301:TYR:N	2.88	0.41
1:A:39:GLU:HG3	1:A:40:THR:N	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:ASP:O	1:B:244:ALA:C	2.59	0.41
1:A:182:GLU:OE1	1:A:183:LEU:N	2.53	0.41
1:A:183:LEU:HA	1:A:183:LEU:HD12	1.78	0.41
1:A:263:GLU:C	1:A:265:GLU:H	2.23	0.41
1:A:267:GLY:C	1:A:271:LYS:HZ2	2.10	0.41
1:A:281:LYS:HE3	1:A:281:LYS:HB3	1.63	0.41
1:A:308:ASN:O	1:A:309:MET:C	2.59	0.41
1:A:7:TYR:CE1	1:A:36:LEU:CD1	3.02	0.41
1:A:38:PRO:HA	1:A:62:THR:CG2	2.19	0.41
1:A:5:PHE:O	1:A:50:VAL:CG1	2.48	0.41
1:B:262:TYR:CE2	1:B:283:LEU:HB2	2.55	0.41
1:A:20:TRP:C	1:A:20:TRP:HE3	2.20	0.41
1:B:242:THR:O	1:B:246:ILE:HD12	2.21	0.41
1:A:182:GLU:OE1	1:A:182:GLU:C	2.59	0.41
1:A:266:VAL:O	1:A:266:VAL:CG1	2.68	0.41
1:B:319:LYS:HD3	1:B:326:PRO:CA	2.50	0.41
1:A:96:ILE:HG21	1:A:330:VAL:HG21	1.82	0.41
1:A:98:ASN:OD1	1:A:332:LEU:HD13	2.20	0.41
1:B:10:ARG:NH2	1:B:13:GLU:HG2	2.36	0.41
1:B:178:PHE:O	1:B:180:ASN:N	2.53	0.41
1:B:32:THR:HG23	1:B:34:LYS:N	2.36	0.41
1:B:183:LEU:CD1	1:B:183:LEU:N	2.84	0.41
1:B:262:TYR:HB3	1:B:265:GLU:CB	2.40	0.41
1:B:335:ASN:O	1:B:335:ASN:ND2	2.54	0.41
1:A:49:GLY:HA3	1:A:73:LYS:HB3	2.03	0.41
1:B:177:ILE:HA	1:B:177:ILE:HD12	1.69	0.41
1:B:282:ARG:O	1:B:285:ASP:N	2.54	0.41
1:A:209:ASP:OD2	1:A:238:ARG:HG3	2.21	0.40
1:A:260:ASP:OD2	1:A:295:THR:HB	2.21	0.40
1:B:214:VAL:O	1:B:215:HIS:CB	2.68	0.40
1:B:273:TRP:CZ3	1:B:279:PRO:CG	2.98	0.40
1:B:261:THR:OG1	1:B:297:HIS:CE1	2.74	0.40
1:B:7:TYR:HE1	1:B:40:THR:CG2	2.34	0.40
1:A:11:LYS:HE3	1:A:11:LYS:O	2.21	0.40
1:A:262:TYR:CE2	1:A:283:LEU:HB2	2.56	0.40
1:B:6:ALA:O	1:B:31:TYR:HA	2.21	0.40
1:A:24:HIS:ND1	1:A:318:LEU:HD12	2.37	0.40
1:A:25:LYS:O	1:A:25:LYS:NZ	2.54	0.40
1:A:71:VAL:CG1	1:A:73:LYS:H	2.33	0.40
1:B:17:LEU:HD21	1:B:29:VAL:CG1	2.52	0.40
1:B:307:ARG:O	1:B:311:VAL:HB	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:86:MET:HE2	1:B:332:LEU:CG	2.52	0.40
1:B:90:LYS:C	1:B:92:LEU:N	2.70	0.40
1:A:178:PHE:O	1:A:180:ASN:N	2.55	0.40
1:A:217:ILE:HA	1:A:221:SER:OG	2.21	0.40
1:A:52:VAL:HG22	1:A:58:TYR:OH	2.21	0.40
1:B:261:THR:CG2	1:B:265:GLU:OE1	2.69	0.40
1:B:331:ALA:O	1:B:333:ASN:N	2.55	0.40
1:B:233:ASN:ND2	1:B:240:VAL:HG23	2.36	0.40
1:B:262:TYR:O	1:B:265:GLU:CG	2.70	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 X-ray entries followed by that with respect to entries of similar resolution.

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	335/337 (99%)	263 (78%)	59 (18%)	13 (4%)	3 6
1	B	335/337 (99%)	271 (81%)	44 (13%)	20 (6%)	1 2
All	All	670/674 (99%)	534 (80%)	103 (15%)	33 (5%)	2 4

All (33) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	134	LEU
1	A	179	LYS
1	A	332	LEU
1	B	24	HIS
1	B	41	ALA
1	B	60	ALA
1	B	179	LYS
1	B	214	VAL
1	B	215	HIS

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Mol	Chain	Res	Type
1	B	315	ASN
1	A	25	LYS
1	A	139	THR
1	A	145	ARG
1	A	215	HIS
1	A	310	VAL
1	A	331	ALA
1	B	156	HIS
1	B	197	TYR
1	B	225	MET
1	B	238	ARG
1	B	316	ASN
1	B	328	SER
1	B	332	LEU
1	A	44	ALA
1	A	103	SER
1	B	132	ARG
1	A	309	MET
1	B	62	THR
1	B	103	SER
1	B	334	LYS
1	A	181	PRO
1	B	177	ILE
1	B	211	PRO

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 X-ray entries followed by that with respect to entries of similar resolution.

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	286/286 (100%)	211 (74%)	75 (26%)	0	1
1	B	286/286 (100%)	217 (76%)	69 (24%)	0	2
All	All	572/572 (100%)	428 (75%)	144 (25%)	0	1

All (144) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	VAL
1	A	11	LYS
1	A	12	ASP
1	A	17	LEU
1	A	20	TRP
1	A	21	LYS
1	A	25	LYS
1	A	27	ILE
1	A	30	ASP
1	A	31	TYR
1	A	33	ASP
1	A	36	LEU
1	A	39	GLU
1	A	40	THR
1	A	48	ASP
1	A	51	VAL
1	A	52	VAL
1	A	54	GLN
1	A	59	THR
1	A	72	THR
1	A	82	ASP
1	A	87	ASP
1	A	88	LYS
1	A	91	GLU
1	A	92	LEU
1	A	94	PHE
1	A	97	THR
1	A	98	ASN
1	A	102	TYR
1	A	109	GLU
1	A	132	ARG
1	A	134	LEU
1	A	138	PRO
1	A	142	ARG
1	A	145	ARG
1	A	156	HIS
1	A	163	ARG
1	A	173	ILE
1	A	176	ASP
1	A	177	ILE
1	A	179	LYS
1	A	182	GLU
1	A	183	LEU

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Mol	Chain	Res	Type
1	A	185	LYS
1	A	186	LYS
1	A	196	LEU
1	A	198	LYS
1	A	205	LEU
1	A	217	ILE
1	A	219	ASP
1	A	225	MET
1	A	238	ARG
1	A	240	VAL
1	A	246	ILE
1	A	259	MET
1	A	264	ASP
1	A	271	LYS
1	A	276	LYS
1	A	277	GLU
1	A	281	LYS
1	A	282	ARG
1	A	283	LEU
1	A	289	ARG
1	A	293	LEU
1	A	295	THR
1	A	297	HIS
1	A	298	THR
1	A	303	THR
1	A	307	ARG
1	A	319	LYS
1	A	320	LEU
1	A	325	LYS
1	A	328	SER
1	A	332	LEU
1	A	335	ASN
1	B	3	LYS
1	B	9	ILE
1	B	11	LYS
1	B	17	LEU
1	B	18	ASN
1	B	21	LYS
1	B	27	ILE
1	B	32	THR
1	B	35	LEU
1	B	36	LEU

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Mol	Chain	Res	Type
1	B	39	GLU
1	B	40	THR
1	B	42	LYS
1	B	43	LEU
1	B	48	ASP
1	B	56	LEU
1	B	57	ASP
1	B	61	ASP
1	B	63	LEU
1	B	64	GLN
1	B	74	MET
1	B	81	VAL
1	B	82	ASP
1	B	84	ILE
1	B	90	LYS
1	B	91	GLU
1	B	94	PHE
1	B	95	GLN
1	B	96	ILE
1	B	97	THR
1	B	98	ASN
1	B	101	VAL
1	B	102	TYR
1	B	126	ASP
1	B	145	ARG
1	B	147	GLN
1	B	151	VAL
1	B	156	HIS
1	B	163	ARG
1	B	177	ILE
1	B	179	LYS
1	B	182	GLU
1	B	183	LEU
1	B	184	GLU
1	B	185	LYS
1	B	190	VAL
1	B	198	LYS
1	B	205	LEU
1	B	218	ASN
1	B	219	ASP
1	B	222	ILE
1	B	225	MET

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Mol	Chain	Res	Type
1	B	258	VAL
1	B	266	VAL
1	B	271	LYS
1	B	277	GLU
1	B	281	LYS
1	B	288	ASP
1	B	289	ARG
1	B	293	LEU
1	B	298	THR
1	B	302	THR
1	B	307	ARG
1	B	320	LEU
1	B	322	ASN
1	B	327	ASP
1	B	333	ASN
1	B	334	LYS
1	B	336	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	55	GLN
1	A	105	ASN
1	A	147	GLN
1	A	156	HIS
1	A	199	GLN
1	A	213	ASN
1	A	218	ASN
1	A	270	ASN
1	A	308	ASN
1	A	317	ASN
1	B	18	ASN
1	B	24	HIS
1	B	54	GLN
1	B	55	GLN
1	B	98	ASN
1	B	110	HIS
1	B	147	GLN
1	B	156	HIS
1	B	199	GLN
1	B	213	ASN

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Mol	Chain	Res	Type
1	B	218	ASN
1	B	270	ASN
1	B	333	ASN
1	B	335	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	OXM	A	402	-	2,5,5	0.99	0	2,6,6	2.94	2 (100%)
3	OXM	B	402	2	2,5,5	0.92	0	2,6,6	2.08	1 (50%)
2	NAI	B	401	3	42,48,48	2.24	14 (33%)	47,73,73	2.34	15 (31%)
2	NAI	A	401	1	42,48,48	2.20	14 (33%)	47,73,73	2.57	19 (40%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	OXM	A	402	-	-	0/0/4/4	-
3	OXM	B	402	2	-	0/0/4/4	-
2	NAI	B	401	3	-	14/25/72/72	0/5/5/5
2	NAI	A	401	1	1/1/13/16	10/25/72/72	0/5/5/5

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	NAI	O4D-C4D	5.53	1.57	1.45
2	A	401	NAI	C2B-C1B	-5.17	1.45	1.53
2	B	401	NAI	C2A-N3A	5.06	1.40	1.32
2	A	401	NAI	O2B-C2B	-4.85	1.31	1.43
2	B	401	NAI	C4N-C3N	-4.79	1.40	1.49
2	A	401	NAI	C2A-N3A	4.47	1.39	1.32
2	A	401	NAI	C7N-C3N	4.39	1.58	1.48
2	A	401	NAI	C4N-C3N	-4.34	1.41	1.49
2	B	401	NAI	C7N-C3N	4.32	1.58	1.48
2	B	401	NAI	O4B-C4B	4.27	1.54	1.45
2	B	401	NAI	O3B-C3B	3.49	1.51	1.43
2	A	401	NAI	C1D-N1N	3.28	1.55	1.46
2	A	401	NAI	C4A-N3A	3.24	1.40	1.35
2	B	401	NAI	O2B-C2B	-3.16	1.35	1.43
2	B	401	NAI	O2D-C2D	-3.06	1.35	1.43
2	A	401	NAI	O4B-C4B	2.94	1.51	1.45
2	B	401	NAI	C4A-N3A	2.80	1.39	1.35
2	A	401	NAI	C6N-C5N	2.66	1.38	1.33
2	A	401	NAI	O4D-C4D	2.65	1.50	1.45
2	B	401	NAI	C1D-N1N	2.59	1.53	1.46
2	A	401	NAI	O2D-C2D	-2.45	1.37	1.43
2	A	401	NAI	C4N-C5N	-2.32	1.42	1.48
2	B	401	NAI	C4N-C5N	-2.25	1.43	1.48
2	B	401	NAI	O4B-C1B	-2.21	1.38	1.41
2	B	401	NAI	C6N-C5N	2.20	1.37	1.33
2	A	401	NAI	C3D-C4D	2.14	1.58	1.53
2	A	401	NAI	O4D-C1D	2.14	1.47	1.42
2	B	401	NAI	O3D-C3D	-2.13	1.38	1.43

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	NAI	C3N-C2N-N1N	-6.96	113.16	123.10
2	B	401	NAI	C3N-C2N-N1N	-6.49	113.83	123.10
2	A	401	NAI	O4B-C1B-C2B	5.66	115.19	106.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	NAI	C2A-N1A-C6A	5.10	127.48	118.75
2	A	401	NAI	O2B-C2B-C3B	5.07	128.22	111.82
2	A	401	NAI	C1D-N1N-C2N	-4.92	112.91	121.11
2	B	401	NAI	C2A-N1A-C6A	4.81	126.99	118.75
2	B	401	NAI	C1D-N1N-C2N	-4.34	113.89	121.11
2	B	401	NAI	C2D-C3D-C4D	4.05	110.51	102.64
2	A	401	NAI	C5A-C6A-N6A	4.02	126.47	120.35
2	A	401	NAI	N3A-C2A-N1A	-3.95	122.50	128.68
2	A	401	NAI	O2B-C2B-C1B	3.90	125.26	110.85
2	A	401	NAI	C2D-C3D-C4D	3.80	110.03	102.64
2	B	401	NAI	C5A-C6A-N6A	3.78	126.10	120.35
2	A	401	NAI	C5A-C6A-N1A	-3.77	111.81	120.35
2	B	401	NAI	C5A-C6A-N1A	-3.71	111.95	120.35
2	B	401	NAI	C2D-C1D-N1N	3.71	122.59	113.30
2	B	401	NAI	N3A-C2A-N1A	-3.70	122.89	128.68
3	A	402	OXM	C2-C1-N1	3.51	121.70	115.85
2	B	401	NAI	C2B-C3B-C4B	3.27	108.99	102.64
2	B	401	NAI	O4D-C1D-N1N	3.21	114.34	108.06
2	A	401	NAI	C2D-C1D-N1N	3.10	121.08	113.30
2	B	401	NAI	O3D-C3D-C2D	2.99	121.49	111.82
2	B	401	NAI	O2B-C2B-C3B	2.90	121.19	111.82
2	B	401	NAI	O2D-C2D-C3D	2.88	121.13	111.82
2	A	401	NAI	O3D-C3D-C4D	-2.67	103.34	111.05
2	B	401	NAI	O4D-C4D-C3D	-2.64	99.88	105.11
2	A	401	NAI	PN-O5D-C5D	2.64	137.16	121.68
2	A	401	NAI	O3B-C3B-C2B	2.61	120.27	111.82
2	A	401	NAI	C2B-C3B-C4B	2.60	107.69	102.64
3	B	402	OXM	O1-C1-N1	-2.39	119.19	122.58
3	A	402	OXM	O1-C1-N1	-2.22	119.42	122.58
2	A	401	NAI	O4D-C4D-C3D	-2.12	100.92	105.11
2	B	401	NAI	O2D-C2D-C1D	2.12	117.10	110.02
2	A	401	NAI	O7N-C7N-C3N	-2.09	116.96	120.90
2	A	401	NAI	O2D-C2D-C1D	2.07	116.93	110.02
2	A	401	NAI	O3D-C3D-C2D	2.05	118.45	111.82

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	401	NAI	C1B

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	NAI	C5B-O5B-PA-O1A
2	B	401	NAI	C5B-O5B-PA-O2A
2	B	401	NAI	O4B-C4B-C5B-O5B
2	B	401	NAI	C5D-O5D-PN-O3
2	B	401	NAI	C5D-O5D-PN-O1N
2	B	401	NAI	O4D-C4D-C5D-O5D
2	A	401	NAI	C5B-O5B-PA-O3
2	A	401	NAI	C4B-C5B-O5B-PA
2	B	401	NAI	C3B-C4B-C5B-O5B
2	B	401	NAI	C3D-C4D-C5D-O5D
2	A	401	NAI	C3D-C4D-C5D-O5D
2	A	401	NAI	O4D-C4D-C5D-O5D
2	B	401	NAI	C2D-C1D-N1N-C2N
2	B	401	NAI	C2D-C1D-N1N-C6N
2	A	401	NAI	O4D-C1D-N1N-C2N
2	A	401	NAI	O4B-C4B-C5B-O5B
2	A	401	NAI	C5B-O5B-PA-O1A
2	B	401	NAI	O4D-C1D-N1N-C6N
2	A	401	NAI	C2D-C1D-N1N-C2N
2	A	401	NAI	O4D-C1D-N1N-C6N
2	B	401	NAI	O4D-C1D-N1N-C2N
2	A	401	NAI	C3B-C4B-C5B-O5B
2	B	401	NAI	C5B-O5B-PA-O3
2	B	401	NAI	PN-O3-PA-O2A

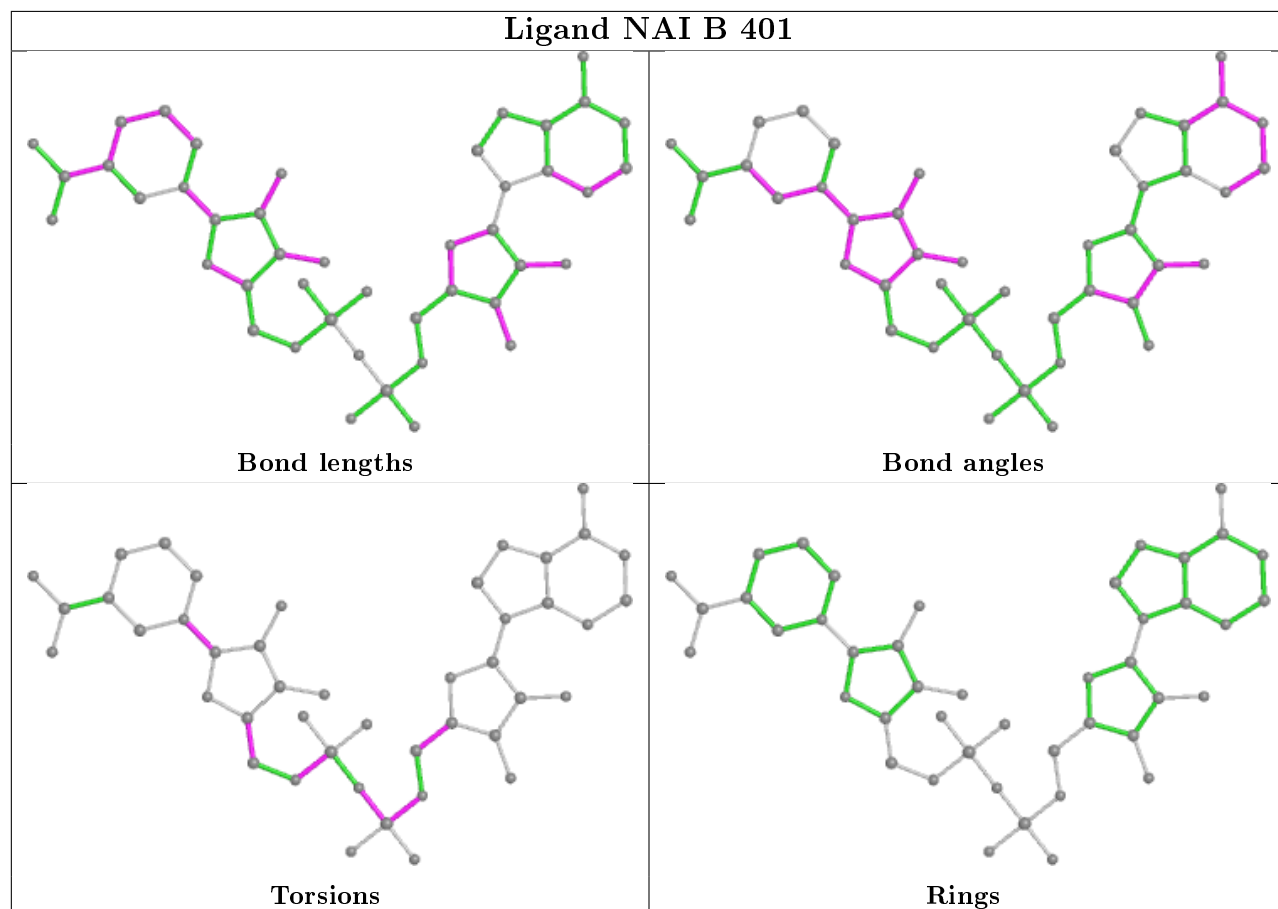
There are no ring outliers.

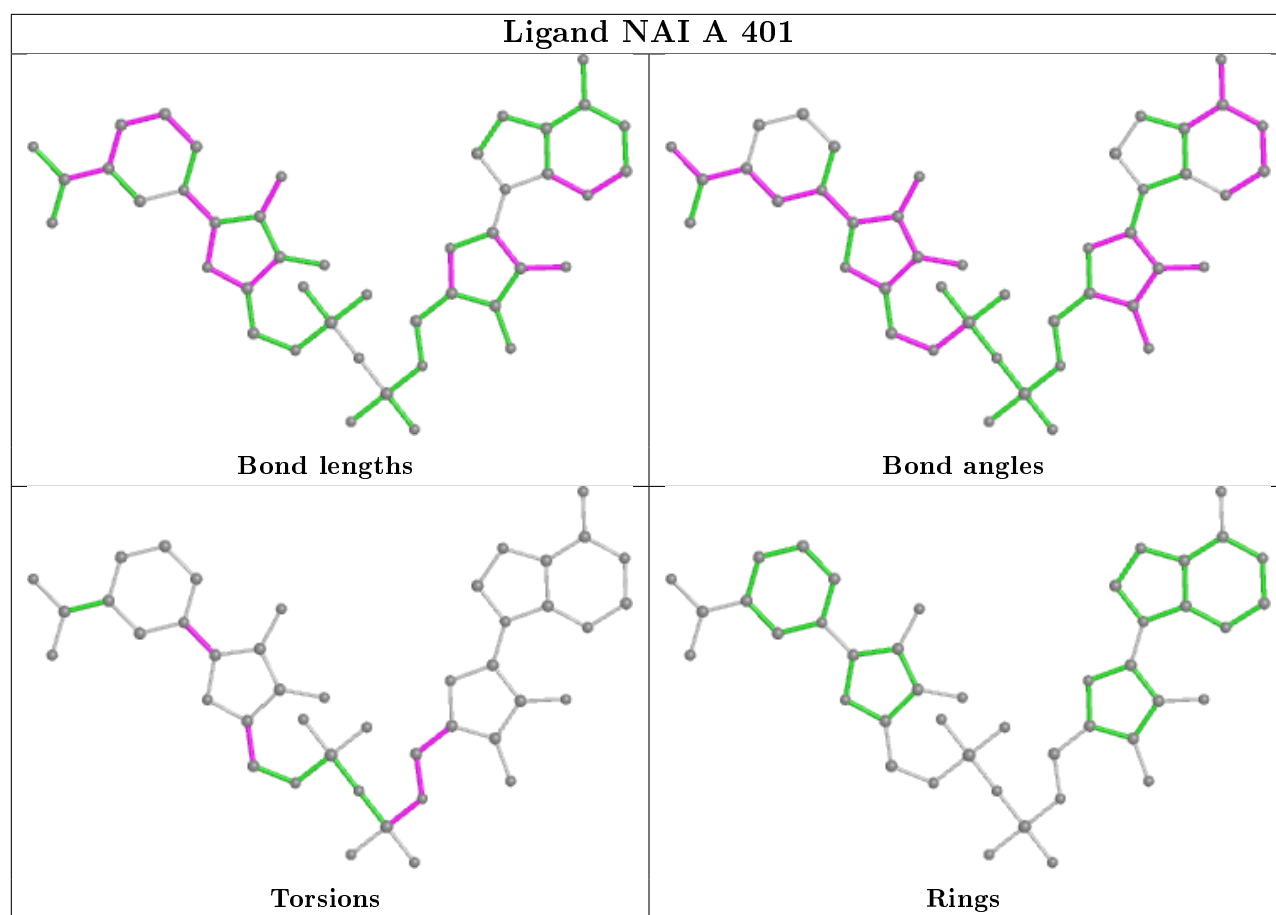
4 monomers are involved in 48 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	OXM	4	0
3	B	402	OXM	11	0
2	B	401	NAI	28	0
2	A	401	NAI	15	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	337/337 (100%)	0.14	34 (10%) 7 5	2, 25, 89, 100	0
1	B	337/337 (100%)	-0.26	8 (2%) 59 60	2, 20, 70, 94	0
All	All	674/674 (100%)	-0.06	42 (6%) 20 19	2, 22, 84, 100	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	333	ASN	6.4
1	B	336	LYS	6.0
1	A	7	TYR	5.7
1	A	8	ALA	4.2
1	B	333	ASN	4.1
1	A	37	THR	3.7
1	A	320	LEU	3.6
1	A	31	TYR	3.6
1	A	332	LEU	3.6
1	A	27	ILE	3.2
1	A	21	LYS	3.1
1	A	70	GLY	3.1
1	A	41	ALA	3.0
1	A	30	ASP	3.0
1	A	67	ALA	3.0
1	B	69	ALA	3.0
1	A	87	ASP	2.9
1	A	81	VAL	2.9
1	B	64	GLN	2.8
1	A	6	ALA	2.8
1	A	60	ALA	2.8
1	B	73	LYS	2.7
1	A	65	ALA	2.7
1	A	59	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	96	ILE	2.7
1	A	93	GLY	2.6
1	A	62	THR	2.6
1	A	92	LEU	2.5
1	A	331	ALA	2.5
1	B	1	MET	2.5
1	A	102	TYR	2.4
1	A	44	ALA	2.3
1	A	36	LEU	2.2
1	A	66	LEU	2.2
1	A	329	PRO	2.2
1	A	69	ALA	2.2
1	B	67	ALA	2.2
1	A	38	PRO	2.1
1	A	68	ASP	2.1
1	A	89	ALA	2.0
1	A	94	PHE	2.0
1	B	178	PHE	2.0

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

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

6.3 Carbohydrates [i](#)

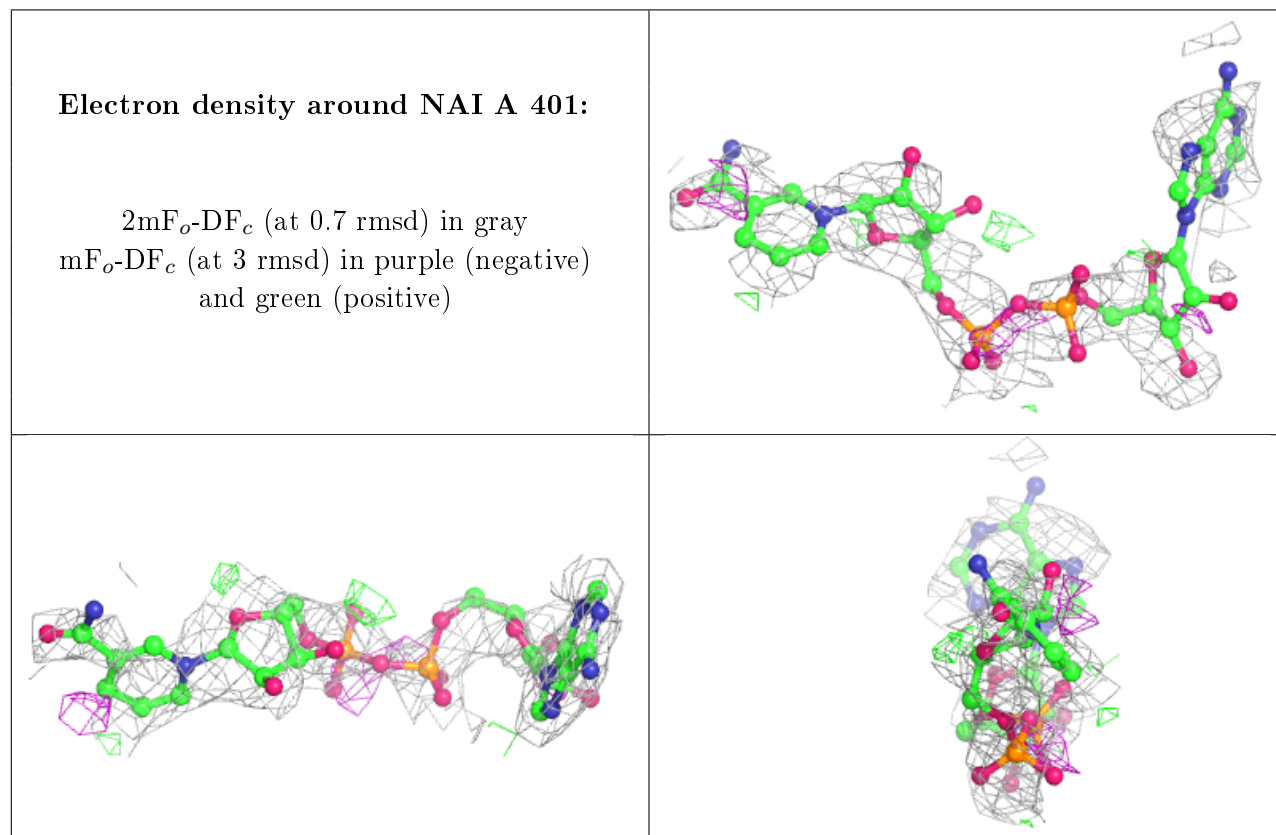
There are no carbohydrates in this entry.

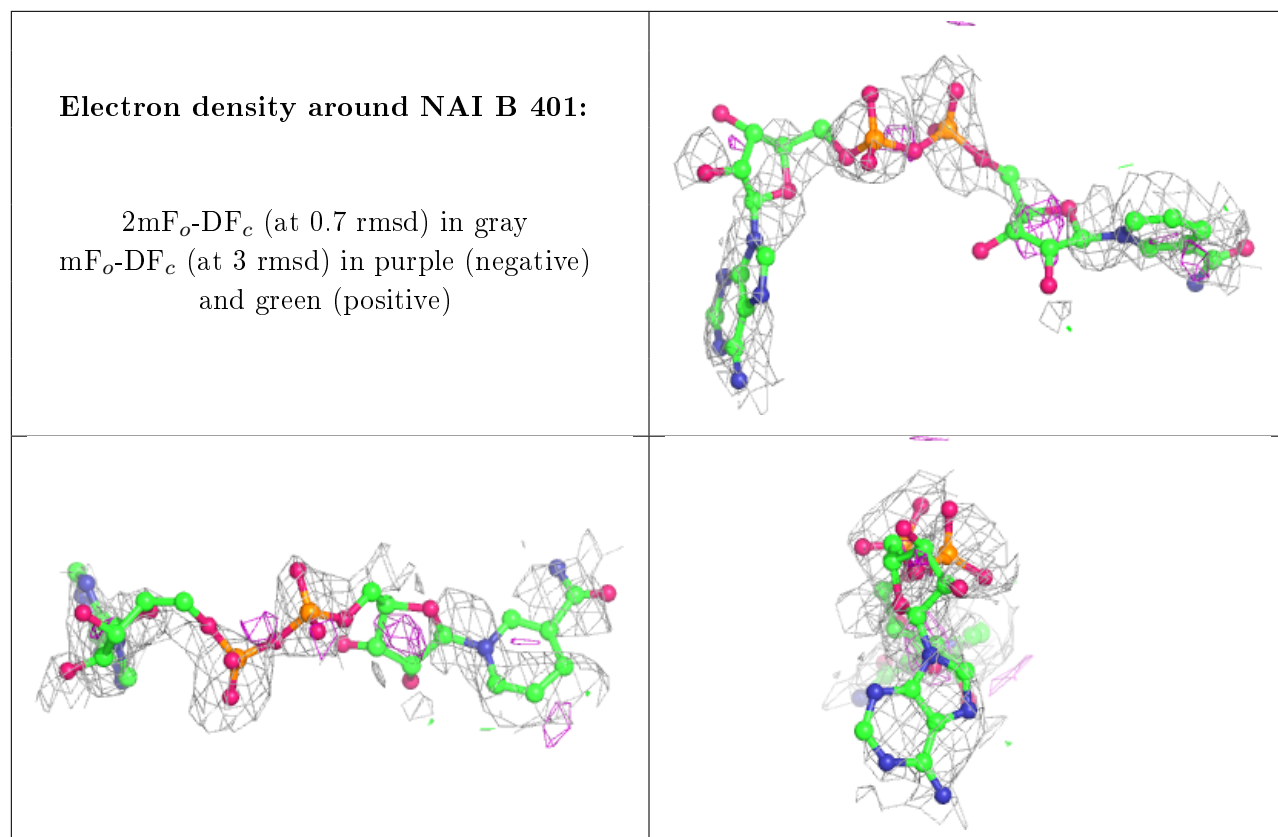
6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	OXM	B	402	6/6	0.10	0.66	92,94,94,95	0
3	OXM	A	402	6/6	0.67	0.49	80,81,82,83	0
2	NAI	A	401	44/44	0.77	0.33	55,73,75,76	0
2	NAI	B	401	44/44	0.79	0.32	58,70,78,79	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers [i](#)

There are no such residues in this entry.