



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 01:16 pm BST

PDB ID : 4K7H
Title : Major capsid protein P1 of the Pseudomonas phage phi6
Authors : Boura, E.; Nemecek, D.; Plevka, P.; Steven, C.A.; Hurley, J.H.
Deposited on : 2013-04-17
Resolution : 3.60 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
Xtriage (Phenix)	:	1.13
EDS	:	2.11
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

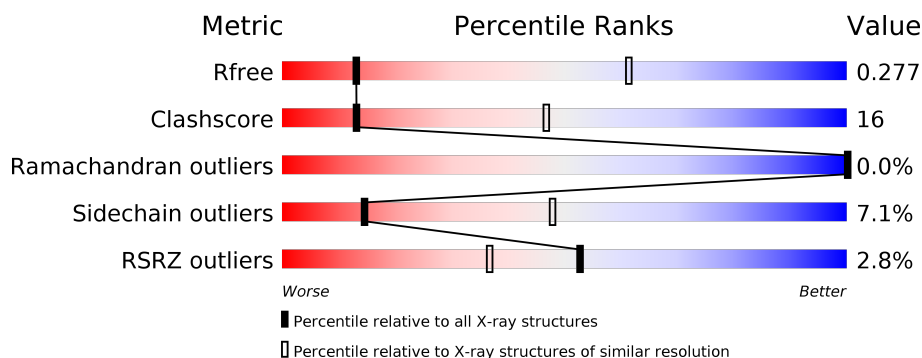
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1257 (3.70-3.50)
Clashscore	141614	1353 (3.70-3.50)
Ramachandran outliers	138981	1307 (3.70-3.50)
Sidechain outliers	138945	1307 (3.70-3.50)
RSRZ outliers	127900	1161 (3.70-3.50)

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	775	
1	B	775	
1	C	775	
1	D	775	
1	E	775	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 29340 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 Major inner protein P1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	760	Total	C	N	O	S	0	0	0
			5868	3709	1032	1105	22			
1	B	760	Total	C	N	O	S	0	0	0
			5868	3709	1032	1105	22			
1	C	760	Total	C	N	O	S	0	0	0
			5868	3709	1032	1105	22			
1	D	760	Total	C	N	O	S	0	0	0
			5868	3709	1032	1105	22			
1	E	760	Total	C	N	O	S	0	0	0
			5868	3709	1032	1105	22			

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	EXPRESSION TAG	UNP P11126
A	770	HIS	-	EXPRESSION TAG	UNP P11126
A	771	HIS	-	EXPRESSION TAG	UNP P11126
A	772	HIS	-	EXPRESSION TAG	UNP P11126
A	773	HIS	-	EXPRESSION TAG	UNP P11126
A	774	HIS	-	EXPRESSION TAG	UNP P11126
A	775	HIS	-	EXPRESSION TAG	UNP P11126
B	1	GLY	-	EXPRESSION TAG	UNP P11126
B	770	HIS	-	EXPRESSION TAG	UNP P11126
B	771	HIS	-	EXPRESSION TAG	UNP P11126
B	772	HIS	-	EXPRESSION TAG	UNP P11126
B	773	HIS	-	EXPRESSION TAG	UNP P11126
B	774	HIS	-	EXPRESSION TAG	UNP P11126
B	775	HIS	-	EXPRESSION TAG	UNP P11126
C	1	GLY	-	EXPRESSION TAG	UNP P11126
C	770	HIS	-	EXPRESSION TAG	UNP P11126
C	771	HIS	-	EXPRESSION TAG	UNP P11126
C	772	HIS	-	EXPRESSION TAG	UNP P11126
C	773	HIS	-	EXPRESSION TAG	UNP P11126

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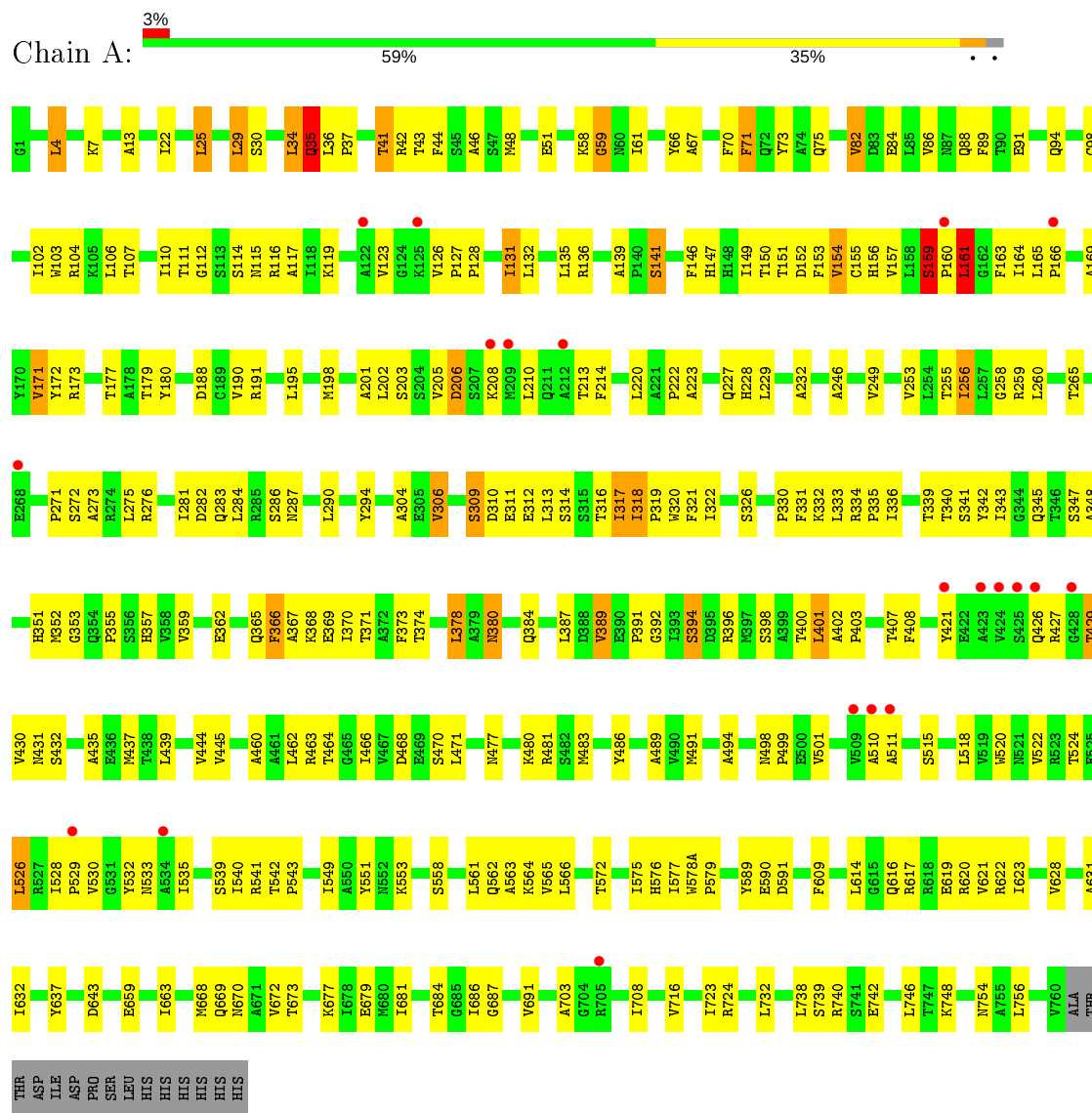
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Chain	Residue	Modelled	Actual	Comment	Reference
C	774	HIS	-	EXPRESSION TAG	UNP P11126
C	775	HIS	-	EXPRESSION TAG	UNP P11126
D	1	GLY	-	EXPRESSION TAG	UNP P11126
D	770	HIS	-	EXPRESSION TAG	UNP P11126
D	771	HIS	-	EXPRESSION TAG	UNP P11126
D	772	HIS	-	EXPRESSION TAG	UNP P11126
D	773	HIS	-	EXPRESSION TAG	UNP P11126
D	774	HIS	-	EXPRESSION TAG	UNP P11126
D	775	HIS	-	EXPRESSION TAG	UNP P11126
E	1	GLY	-	EXPRESSION TAG	UNP P11126
E	770	HIS	-	EXPRESSION TAG	UNP P11126
E	771	HIS	-	EXPRESSION TAG	UNP P11126
E	772	HIS	-	EXPRESSION TAG	UNP P11126
E	773	HIS	-	EXPRESSION TAG	UNP P11126
E	774	HIS	-	EXPRESSION TAG	UNP P11126
E	775	HIS	-	EXPRESSION TAG	UNP P11126

3 Residue-property plots [i](#)

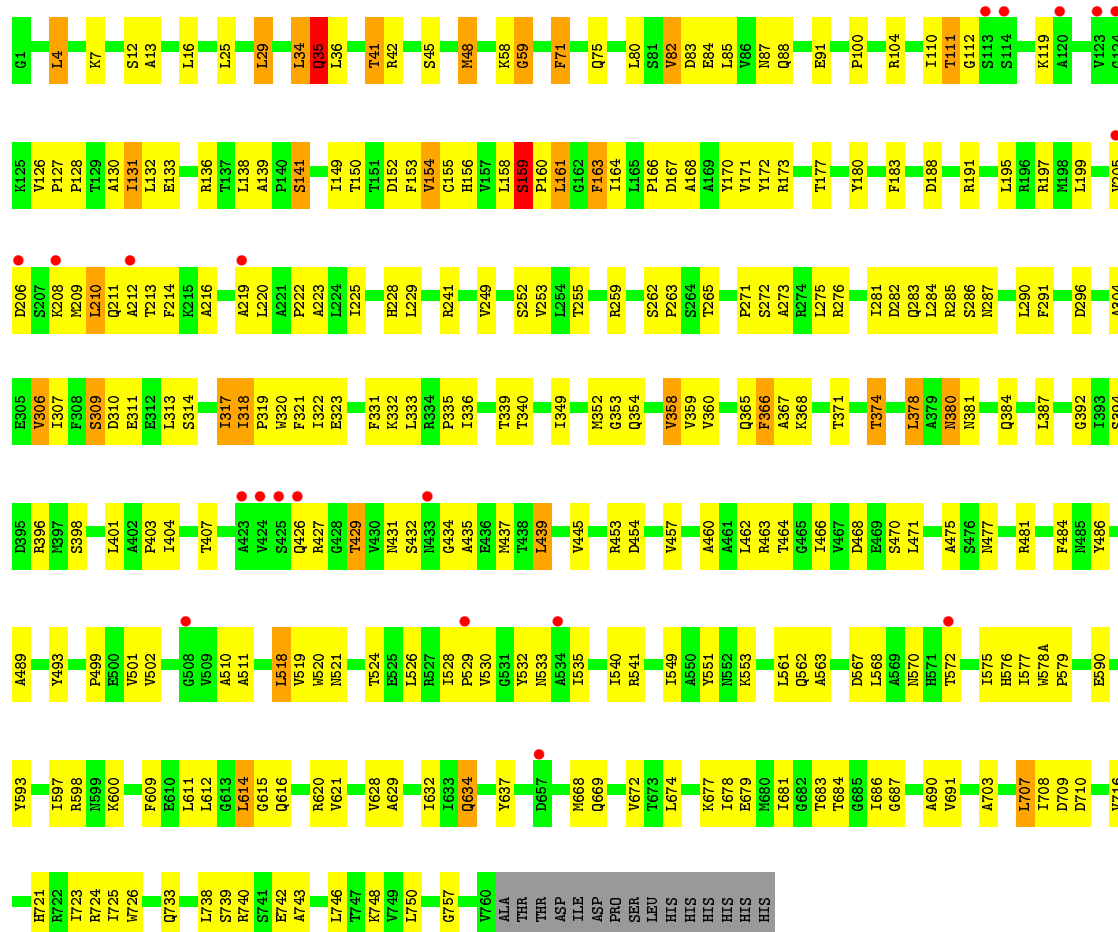
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Major inner protein P1

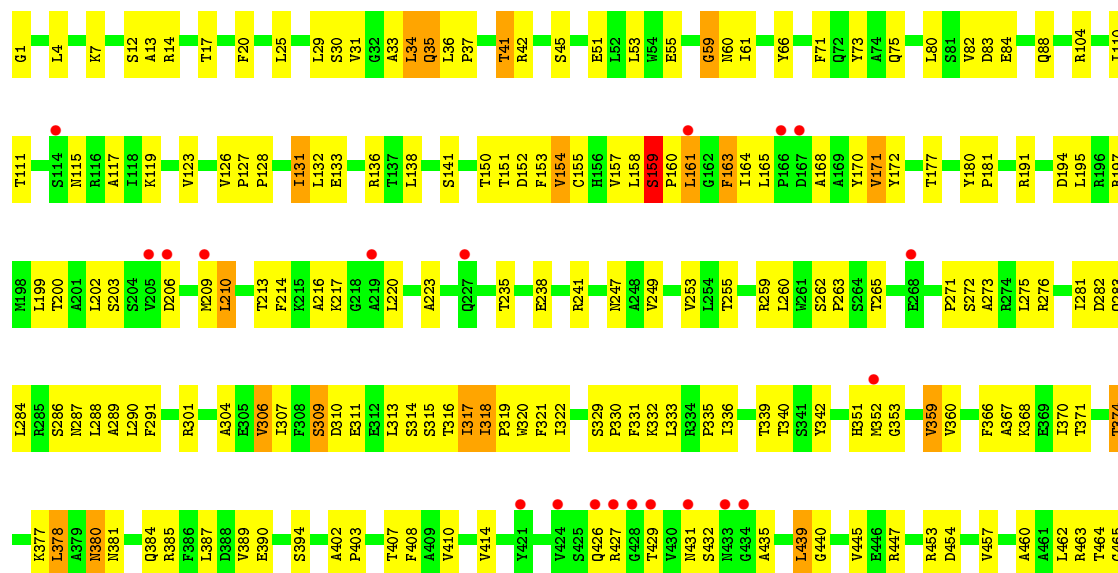


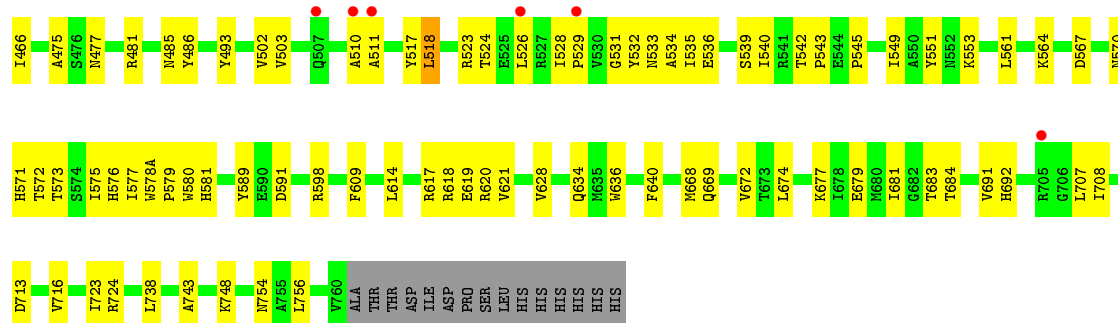
• Molecule 1: Major inner protein P1



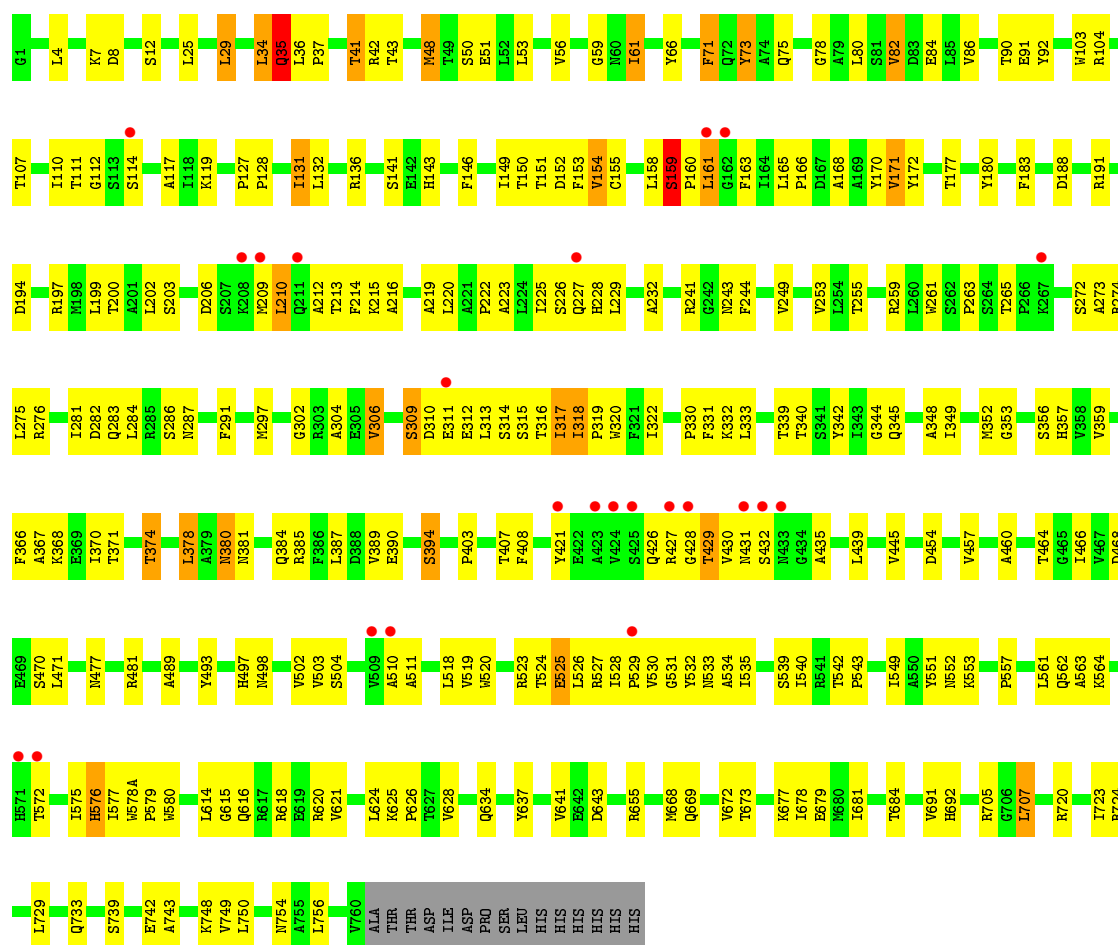


• Molecule 1: Major inner protein P1

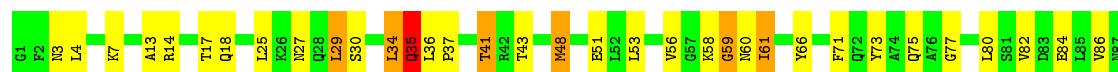




• Molecule 1: Major inner protein P1



• Molecule 1: Major inner protein P1





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	182.59Å 278.85Å 246.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.92 – 3.60 40.92 – 3.60	Depositor EDS
% Data completeness (in resolution range)	91.0 (40.92-3.60) 91.0 (40.92-3.60)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	0.19	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 3.57Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.217 , 0.274 0.222 , 0.277	Depositor DCC
R_{free} test set	3350 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	118.3	Xtrriage
Anisotropy	0.115	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 150.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	29340	wwPDB-VP
Average B, all atoms (Å ²)	178.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.79% 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 ⓘ

5.1 Standard geometry ⓘ

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	0.41	0/5988	0.67	5/8146 (0.1%)
1	B	0.42	0/5988	0.67	5/8146 (0.1%)
1	C	0.40	0/5988	0.66	3/8146 (0.0%)
1	D	0.42	0/5988	0.68	4/8146 (0.0%)
1	E	0.43	0/5988	0.69	6/8146 (0.1%)
All	All	0.42	0/29940	0.68	23/40730 (0.1%)

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	4
1	B	0	5
1	C	0	3
1	D	0	5
1	E	0	4
All	All	0	21

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	161	LEU	CA-CB-CG	6.90	131.16	115.30
1	B	161	LEU	CA-CB-CG	6.81	130.97	115.30
1	E	59	GLY	N-CA-C	-6.64	96.49	113.10
1	B	59	GLY	N-CA-C	-6.42	97.06	113.10
1	D	161	LEU	CA-CB-CG	6.32	129.83	115.30
1	A	161	LEU	CA-CB-CG	6.30	129.78	115.30
1	D	35	GLN	N-CA-C	6.20	127.75	111.00
1	A	401	LEU	CA-CB-CG	6.10	129.32	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	161	LEU	CA-CB-CG	5.90	128.88	115.30
1	D	59	GLY	N-CA-C	-5.78	98.66	113.10
1	C	35	GLN	N-CA-C	5.74	126.51	111.00
1	C	59	GLY	N-CA-C	-5.65	98.98	113.10
1	A	35	GLN	N-CA-C	5.65	126.25	111.00
1	E	35	GLN	N-CA-C	5.64	126.24	111.00
1	B	29	LEU	CA-CB-CG	5.43	127.78	115.30
1	A	29	LEU	CA-CB-CG	5.34	127.59	115.30
1	E	77	GLY	N-CA-C	-5.15	100.24	113.10
1	A	59	GLY	N-CA-C	-5.12	100.29	113.10
1	B	757	GLY	N-CA-C	-5.11	100.32	113.10
1	D	29	LEU	CA-CB-CG	5.11	127.06	115.30
1	E	29	LEU	CA-CB-CG	5.03	126.88	115.30
1	E	260	LEU	CA-CB-CG	5.03	126.88	115.30
1	B	35	GLN	N-CA-C	5.01	124.52	111.00

There are no chirality outliers.

All (21) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	159	SER	Peptide
1	A	318	ILE	Peptide
1	A	34	LEU	Peptide
1	A	35	GLN	Peptide
1	B	111	THR	Peptide
1	B	159	SER	Peptide
1	B	318	ILE	Peptide
1	B	34	LEU	Peptide
1	B	35	GLN	Peptide
1	C	159	SER	Peptide
1	C	318	ILE	Peptide
1	C	34	LEU	Peptide
1	D	159	SER	Peptide
1	D	318	ILE	Peptide
1	D	34	LEU	Peptide
1	D	35	GLN	Peptide
1	D	78	GLY	Peptide
1	E	159	SER	Peptide
1	E	318	ILE	Peptide
1	E	34	LEU	Peptide
1	E	35	GLN	Peptide

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	5868	0	5807	213	0
1	B	5868	0	5807	203	0
1	C	5868	0	5807	188	1
1	D	5868	0	5807	195	2
1	E	5868	0	5807	169	1
All	All	29340	0	29035	949	2

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 16.

All (949) 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:C:51:GLU:H	1:C:564:LYS:HE3	1.32	0.92
1:D:367:ALA:HB1	1:D:368:LYS:HA	1.51	0.91
1:A:51:GLU:H	1:A:564:LYS:HE3	1.36	0.90
1:E:318:ILE:HG22	1:E:320:TRP:HB3	1.54	0.89
1:E:367:ALA:HB1	1:E:368:LYS:HA	1.55	0.86
1:C:367:ALA:HB1	1:C:368:LYS:HA	1.55	0.85
1:B:259:ARG:HH22	1:B:306:VAL:HG21	1.41	0.85
1:B:367:ALA:HB1	1:B:368:LYS:HA	1.57	0.84
1:A:620:ARG:NH2	1:C:84:GLU:OE2	2.11	0.83
1:B:679:GLU:HG3	1:B:724:ARG:HG2	1.61	0.82
1:D:620:ARG:NH2	1:E:84:GLU:OE2	2.13	0.82
1:D:51:GLU:H	1:D:564:LYS:HE3	1.45	0.81
1:C:259:ARG:HH22	1:C:306:VAL:HG21	1.46	0.81
1:D:259:ARG:HH22	1:D:306:VAL:HG21	1.43	0.80
1:A:367:ALA:HB1	1:A:368:LYS:HA	1.64	0.78
1:A:319:PRO:O	1:A:322:ILE:N	2.17	0.77
1:A:679:GLU:HG3	1:A:724:ARG:HG2	1.66	0.77
1:B:387:LEU:H	1:B:572:THR:HG22	1.51	0.76
1:D:225:ILE:HA	1:D:228:HIS:HB3	1.65	0.76
1:B:445:VAL:HG11	1:B:634:GLN:HG2	1.67	0.75
1:E:259:ARG:HH22	1:E:306:VAL:HG21	1.50	0.75
1:E:374:THR:HB	1:E:621:VAL:HG12	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:210:LEU:HD11	1:D:228:HIS:HE1	1.49	0.75
1:A:691:VAL:HG13	1:A:723:ILE:HG12	1.68	0.75
1:A:318:ILE:HG21	1:A:320:TRP:HE3	1.50	0.74
1:D:317:ILE:HG13	1:D:318:ILE:HG23	1.70	0.74
1:C:620:ARG:NH2	1:D:84:GLU:OE2	2.20	0.74
1:B:317:ILE:HG13	1:B:318:ILE:HG23	1.71	0.73
1:D:430:VAL:HG22	1:D:529:PRO:HB3	1.71	0.72
1:A:42:ARG:HG2	1:A:335:PRO:HA	1.71	0.72
1:C:75:GLN:HG2	1:C:177:THR:HG23	1.72	0.72
1:B:210:LEU:HD11	1:B:228:HIS:HE1	1.53	0.72
1:D:309:SER:HB3	1:D:313:LEU:HB2	1.72	0.72
1:C:157:VAL:HB	1:C:210:LEU:HD12	1.72	0.71
1:E:445:VAL:HG11	1:E:634:GLN:HG2	1.72	0.71
1:A:317:ILE:HG13	1:A:318:ILE:HG23	1.72	0.71
1:A:368:LYS:HE3	1:A:565:VAL:HG12	1.74	0.70
1:C:535:ILE:HA	1:C:540:ILE:HD13	1.74	0.70
1:E:317:ILE:HG13	1:E:318:ILE:HG23	1.74	0.69
1:D:75:GLN:HG2	1:D:177:THR:HG23	1.73	0.69
1:B:172:TYR:HA	1:B:578(A):TRP:HB3	1.74	0.69
1:B:309:SER:HB3	1:B:313:LEU:HB2	1.74	0.69
1:C:313:LEU:O	1:C:317:ILE:N	2.19	0.69
1:A:378:LEU:HD21	1:A:384:GLN:HB3	1.73	0.69
1:C:390:GLU:OE1	1:C:618:ARG:NH1	2.26	0.69
1:A:367:ALA:HA	1:A:401:LEU:HD11	1.75	0.69
1:B:577:ILE:HG23	1:B:578(A):TRP:CE3	2.27	0.68
1:E:310:ASP:OD1	1:E:314:SER:N	2.26	0.68
1:A:259:ARG:HH22	1:A:306:VAL:HG21	1.58	0.68
1:E:318:ILE:HB	1:E:321:PHE:H	1.58	0.68
1:B:318:ILE:HG12	1:B:320:TRP:HE3	1.58	0.67
1:B:572:THR:OG1	1:B:577:ILE:HD11	1.94	0.67
1:C:83:ASP:OD1	1:C:191:ARG:NH1	2.27	0.67
1:E:225:ILE:HA	1:E:228:HIS:HB3	1.75	0.67
1:D:691:VAL:HG13	1:D:723:ILE:HG12	1.74	0.67
1:B:271:PRO:O	1:B:276:ARG:NH1	2.27	0.67
1:B:197:ARG:NH2	1:B:241:ARG:O	2.27	0.67
1:D:36:LEU:O	1:D:503:VAL:N	2.22	0.67
1:E:80:LEU:HG	1:E:84:GLU:HG2	1.77	0.67
1:E:318:ILE:HG21	1:E:320:TRP:HE3	1.60	0.67
1:E:535:ILE:HA	1:E:540:ILE:HD13	1.76	0.67
1:B:84:GLU:OE2	1:E:620:ARG:NH2	2.28	0.67
1:E:282:ASP:OD2	1:E:283:GLN:N	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:58:LYS:HD2	1:E:166:PRO:HB2	1.76	0.67
1:C:197:ARG:NH2	1:C:241:ARG:O	2.29	0.66
1:C:577:ILE:HG23	1:C:578(A):TRP:CE3	2.30	0.66
1:E:145:LEU:HD21	1:E:172:TYR:HE1	1.61	0.66
1:B:691:VAL:HG13	1:B:723:ILE:HG12	1.75	0.66
1:E:343:ILE:HD13	1:E:362:GLU:HG2	1.77	0.66
1:A:562:GLN:NE2	1:A:563:ALA:O	2.29	0.66
1:D:319:PRO:O	1:D:322:ILE:N	2.24	0.66
1:D:426:GLN:CB	1:D:427:ARG:HA	2.25	0.65
1:B:530:VAL:HG21	1:B:551:TYR:CE1	2.31	0.65
1:D:720:ARG:HD2	1:D:724:ARG:HH21	1.59	0.65
1:A:89:PHE:HE2	1:A:149:ILE:HG21	1.61	0.65
1:C:317:ILE:HG13	1:C:318:ILE:HG23	1.77	0.65
1:D:367:ALA:CB	1:D:368:LYS:HA	2.25	0.65
1:A:152:ASP:HA	1:A:155:CYS:HB2	1.78	0.65
1:C:206:ASP:HA	1:C:209:MET:HG2	1.76	0.65
1:E:426:GLN:CB	1:E:427:ARG:HA	2.27	0.65
1:A:577:ILE:HG23	1:A:578(A):TRP:CE3	2.32	0.64
1:B:42:ARG:HG2	1:B:335:PRO:HA	1.78	0.64
1:B:562:GLN:NE2	1:B:563:ALA:O	2.31	0.64
1:C:367:ALA:CB	1:C:368:LYS:HA	2.27	0.64
1:D:7:LYS:HE3	1:D:529:PRO:O	1.96	0.64
1:C:523:ARG:HG2	1:C:539:SER:HB3	1.77	0.64
1:E:318:ILE:CG2	1:E:320:TRP:HB3	2.26	0.64
1:D:445:VAL:HG11	1:D:634:GLN:HG2	1.79	0.64
1:A:272:SER:HB3	1:A:275:LEU:HG	1.80	0.64
1:E:197:ARG:HA	1:E:200:THR:HG22	1.80	0.64
1:D:523:ARG:HG2	1:D:539:SER:HB3	1.79	0.63
1:B:426:GLN:CB	1:B:427:ARG:HA	2.28	0.63
1:B:387:LEU:H	1:B:572:THR:CG2	2.12	0.63
1:D:180:TYR:HE1	1:D:489:ALA:HA	1.63	0.63
1:B:91:GLU:OE1	1:E:620:ARG:NH1	2.32	0.63
1:D:42:ARG:HB3	1:D:333:LEU:HD11	1.79	0.63
1:B:354:GLN:HG2	1:B:529:PRO:HD3	1.81	0.63
1:B:7:LYS:HE3	1:B:529:PRO:O	1.98	0.63
1:E:61:ILE:HD11	1:E:153:PHE:HA	1.79	0.63
1:A:310:ASP:OD1	1:A:314:SER:N	2.31	0.63
1:B:319:PRO:O	1:B:322:ILE:N	2.28	0.62
1:A:347:SER:HB3	1:A:355:PRO:HB3	1.80	0.62
1:C:36:LEU:HG	1:C:37:PRO:HD2	1.80	0.62
1:E:180:TYR:HE1	1:E:489:ALA:HA	1.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:7:LYS:NZ	1:D:435:ALA:H	1.96	0.62
1:A:380:ASN:N	1:A:380:ASN:OD1	2.30	0.62
1:E:577:ILE:HG23	1:E:578(A):TRP:CE3	2.34	0.62
1:E:367:ALA:CB	1:E:368:LYS:HA	2.28	0.62
1:E:36:LEU:HG	1:E:37:PRO:HD2	1.81	0.62
1:D:429:THR:HB	1:D:431:ASN:H	1.65	0.62
1:D:210:LEU:HD21	1:D:228:HIS:CE1	2.35	0.62
1:C:309:SER:HB3	1:C:313:LEU:HB2	1.82	0.61
1:D:274:ARG:HH22	1:D:312:GLU:HG3	1.64	0.61
1:A:36:LEU:HG	1:A:37:PRO:HD2	1.80	0.61
1:C:168:ALA:HB1	1:C:170:TYR:HE2	1.64	0.61
1:C:319:PRO:O	1:C:322:ILE:N	2.29	0.61
1:A:172:TYR:HA	1:A:578(A):TRP:HB3	1.83	0.61
1:B:401:LEU:HA	1:B:404:ILE:HD12	1.83	0.61
1:D:387:LEU:HB2	1:D:572:THR:HG21	1.82	0.61
1:A:287:ASN:HB3	1:A:290:LEU:HD22	1.83	0.61
1:C:374:THR:HB	1:C:621:VAL:HG12	1.83	0.61
1:A:468:ASP:OD2	1:A:470:SER:OG	2.17	0.61
1:A:462:LEU:HD11	1:A:486:TYR:CD2	2.35	0.61
1:E:572:THR:OG1	1:E:577:ILE:HD11	2.01	0.61
1:B:318:ILE:HD13	1:B:321:PHE:H	1.65	0.61
1:C:426:GLN:CB	1:C:427:ARG:HA	2.29	0.61
1:C:691:VAL:HG13	1:C:723:ILE:HG12	1.83	0.61
1:B:273:ALA:HA	1:B:276:ARG:HB2	1.82	0.61
1:C:378:LEU:HD21	1:C:384:GLN:HB3	1.82	0.61
1:A:533:ASN:ND2	1:A:551:TYR:OH	2.33	0.61
1:C:249:VAL:O	1:C:253:VAL:HG12	2.01	0.61
1:C:7:LYS:NZ	1:C:435:ALA:H	1.98	0.61
1:E:477:ASN:O	1:E:481:ARG:HG2	2.00	0.61
1:B:332:LYS:HD2	1:B:333:LEU:H	1.66	0.60
1:A:112:GLY:HA2	1:C:115:ASN:HD22	1.65	0.60
1:D:281:ILE:HA	1:D:284:LEU:HB2	1.83	0.60
1:E:110:ILE:HD12	1:E:111:THR:HG23	1.83	0.60
1:E:408:PHE:HE2	1:E:681:ILE:HD11	1.66	0.60
1:C:387:LEU:HD11	1:C:577:ILE:HG21	1.82	0.60
1:B:127:PRO:HG2	1:B:130:ALA:HB2	1.84	0.60
1:B:374:THR:HB	1:B:621:VAL:HG12	1.82	0.60
1:B:367:ALA:CB	1:B:368:LYS:HA	2.30	0.60
1:C:477:ASN:O	1:C:481:ARG:HG2	2.02	0.60
1:E:75:GLN:HG2	1:E:177:THR:HG23	1.83	0.60
1:B:674:LEU:HD23	1:B:750:LEU:HD13	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:426:GLN:CB	1:A:427:ARG:HA	2.32	0.60
1:B:396:ARG:NH1	1:B:612:LEU:O	2.34	0.60
1:E:210:LEU:HD11	1:E:228:HIS:HE1	1.66	0.60
1:E:319:PRO:O	1:E:322:ILE:N	2.33	0.59
1:B:249:VAL:O	1:B:253:VAL:HG12	2.03	0.59
1:A:139:ALA:O	1:A:141:SER:N	2.35	0.59
1:B:4:LEU:HB2	1:B:12:SER:OG	2.03	0.59
1:A:13:ALA:HA	1:A:463:ARG:HA	1.85	0.59
1:B:210:LEU:HD21	1:B:228:HIS:CE1	2.37	0.59
1:A:34:LEU:HD22	1:A:35:GLN:NE2	2.17	0.59
1:A:572:THR:OG1	1:A:577:ILE:HD11	2.03	0.59
1:A:91:GLU:OE1	1:B:620:ARG:NH1	2.35	0.59
1:C:282:ASP:OD2	1:C:283:GLN:N	2.35	0.59
1:D:577:ILE:HG23	1:D:578(A):TRP:CE3	2.37	0.59
1:E:249:VAL:O	1:E:253:VAL:HG12	2.03	0.59
1:A:104:ARG:NH1	1:A:223:ALA:O	2.36	0.59
1:A:530:VAL:HG21	1:A:551:TYR:CE1	2.37	0.59
1:C:464:THR:OG1	1:C:466:ILE:HG12	2.01	0.59
1:A:112:GLY:HA2	1:C:115:ASN:ND2	2.18	0.59
1:A:75:GLN:HG2	1:A:177:THR:HG23	1.84	0.59
1:A:367:ALA:CB	1:A:368:LYS:HA	2.33	0.59
1:E:7:LYS:HE3	1:E:529:PRO:O	2.02	0.58
1:D:255:THR:OG1	1:D:304:ALA:HB1	2.04	0.58
1:C:7:LYS:HE3	1:C:529:PRO:O	2.03	0.58
1:A:271:PRO:O	1:A:276:ARG:NH1	2.37	0.58
1:C:540:ILE:HG21	1:C:551:TYR:CE2	2.38	0.58
1:A:408:PHE:HE2	1:A:681:ILE:HD11	1.68	0.58
1:D:314:SER:HA	1:D:317:ILE:C	2.24	0.58
1:D:378:LEU:HD21	1:D:384:GLN:HB3	1.86	0.58
1:A:282:ASP:OD2	1:A:283:GLN:N	2.37	0.58
1:D:318:ILE:CG2	1:D:320:TRP:HB3	2.33	0.58
1:D:533:ASN:HB2	1:D:540:ILE:HG12	1.86	0.58
1:E:309:SER:HB3	1:E:313:LEU:HB2	1.85	0.58
1:C:80:LEU:HG	1:C:84:GLU:HG2	1.85	0.57
1:D:249:VAL:O	1:D:253:VAL:HG12	2.04	0.57
1:D:36:LEU:HG	1:D:37:PRO:HD2	1.86	0.57
1:A:498:ASN:HB2	1:A:520:TRP:HD1	1.68	0.57
1:B:629:ALA:HA	1:B:632:ILE:HD12	1.86	0.57
1:D:7:LYS:HZ2	1:D:435:ALA:H	1.52	0.57
1:B:733:GLN:HE21	1:B:743:ALA:HB3	1.69	0.57
1:C:620:ARG:NH1	1:D:91:GLU:OE1	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:172:TYR:HA	1:E:578(A):TRP:HB3	1.85	0.57
1:A:318:ILE:HD13	1:A:321:PHE:HB2	1.86	0.57
1:A:522:VAL:O	1:A:539:SER:HA	2.04	0.57
1:D:183:PHE:CD1	1:D:297:MET:HB2	2.39	0.57
1:D:107:THR:OG1	1:D:226:SER:OG	2.22	0.57
1:C:310:ASP:OD1	1:C:314:SER:N	2.36	0.57
1:C:380:ASN:N	1:C:380:ASN:OD1	2.37	0.57
1:D:535:ILE:HA	1:D:540:ILE:HD13	1.86	0.57
1:D:172:TYR:HA	1:D:578(A):TRP:HB3	1.85	0.57
1:E:206:ASP:HA	1:E:209:MET:HG2	1.87	0.57
1:A:131:ILE:HD11	1:A:151:THR:OG1	2.05	0.57
1:B:156:HIS:CE1	1:B:208:LYS:HG2	2.40	0.57
1:D:342:TYR:CG	1:D:561:LEU:HD22	2.39	0.57
1:A:313:LEU:O	1:A:317:ILE:N	2.34	0.56
1:C:462:LEU:HD11	1:C:486:TYR:CD2	2.40	0.56
1:A:256:ILE:HG22	1:A:259:ARG:HH21	1.70	0.56
1:A:7:LYS:NZ	1:A:435:ALA:H	2.02	0.56
1:B:313:LEU:O	1:B:317:ILE:N	2.29	0.56
1:E:48:MET:HB2	1:E:561:LEU:HD11	1.87	0.56
1:B:339:THR:HG23	1:B:340:THR:HG23	1.87	0.56
1:B:530:VAL:HG21	1:B:551:TYR:HE1	1.71	0.56
1:A:104:ARG:NH2	1:A:114:SER:O	2.36	0.56
1:B:310:ASP:HB3	1:B:311:GLU:HA	1.86	0.56
1:E:460:ALA:O	1:E:464:THR:HG22	2.06	0.56
1:C:281:ILE:HA	1:C:284:LEU:HB2	1.88	0.56
1:D:282:ASP:OD2	1:D:283:GLN:N	2.39	0.56
1:E:318:ILE:HD13	1:E:321:PHE:HB2	1.87	0.56
1:B:209:MET:O	1:B:213:THR:N	2.36	0.56
1:D:206:ASP:HA	1:D:209:MET:HG2	1.88	0.56
1:D:692:HIS:CD2	1:E:302:GLY:HA3	2.41	0.56
1:D:210:LEU:HD21	1:D:228:HIS:NE2	2.21	0.56
1:D:468:ASP:OD2	1:D:470:SER:OG	2.24	0.56
1:E:408:PHE:CE2	1:E:681:ILE:HD11	2.41	0.56
1:B:318:ILE:HB	1:B:320:TRP:N	2.21	0.56
1:A:102:ILE:O	1:A:106:LEU:HG	2.05	0.55
1:C:155:CYS:O	1:C:159:SER:OG	2.24	0.55
1:A:255:THR:OG1	1:A:304:ALA:HB1	2.06	0.55
1:B:365:GLN:HB3	1:B:562:GLN:HA	1.89	0.55
1:B:502:VAL:HB	1:B:519:VAL:HG22	1.87	0.55
1:D:61:ILE:HD12	1:D:203:SER:HB3	1.87	0.55
1:C:61:ILE:HD11	1:C:153:PHE:HA	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:168:ALA:HB1	1:C:170:TYR:CE2	2.42	0.55
1:E:464:THR:OG1	1:E:466:ILE:HG12	2.05	0.55
1:C:523:ARG:HA	1:C:539:SER:HA	1.89	0.55
1:A:309:SER:HB3	1:A:313:LEU:HB2	1.89	0.55
1:E:468:ASP:OD2	1:E:470:SER:OG	2.23	0.55
1:C:154:VAL:O	1:C:158:LEU:HB2	2.07	0.55
1:E:104:ARG:NH1	1:E:223:ALA:HA	2.22	0.55
1:A:318:ILE:HG22	1:A:320:TRP:HB3	1.87	0.54
1:C:31:VAL:HG12	1:C:33:ALA:H	1.71	0.54
1:E:154:VAL:O	1:E:158:LEU:HB2	2.07	0.54
1:A:510:ALA:N	1:A:511:ALA:HA	2.21	0.54
1:A:345:GLN:NE2	1:A:549:ILE:O	2.34	0.54
1:E:313:LEU:O	1:E:317:ILE:N	2.31	0.54
1:A:351:HIS:CD2	1:A:352:MET:HG3	2.43	0.54
1:C:45:SER:HB2	1:C:180:TYR:HE2	1.71	0.54
1:C:197:ARG:HA	1:C:200:THR:HG22	1.89	0.54
1:D:273:ALA:HA	1:D:276:ARG:HB2	1.90	0.54
1:A:44:PHE:CE1	1:A:333:LEU:HB2	2.42	0.54
1:A:367:ALA:HB1	1:A:368:LYS:CA	2.37	0.54
1:B:282:ASP:OD2	1:B:283:GLN:N	2.40	0.54
1:A:374:THR:HB	1:A:621:VAL:HG12	1.90	0.54
1:B:668:MET:O	1:B:672:VAL:HG13	2.08	0.54
1:B:80:LEU:HG	1:B:84:GLU:HG2	1.89	0.54
1:C:510:ALA:N	1:C:511:ALA:HA	2.23	0.54
1:D:80:LEU:HG	1:D:84:GLU:HG2	1.89	0.54
1:E:310:ASP:HB3	1:E:311:GLU:HA	1.90	0.54
1:B:510:ALA:N	1:B:511:ALA:HA	2.24	0.53
1:C:481:ARG:O	1:C:485:ASN:ND2	2.41	0.53
1:D:510:ALA:N	1:D:511:ALA:HA	2.24	0.53
1:A:147:HIS:O	1:A:151:THR:OG1	2.15	0.53
1:A:460:ALA:O	1:A:464:THR:HG22	2.08	0.53
1:D:502:VAL:HB	1:D:519:VAL:HG22	1.90	0.53
1:D:578(A):TRP:HB2	1:D:579:PRO:HD2	1.90	0.53
1:E:230:ALA:O	1:E:234:THR:OG1	2.23	0.53
1:E:342:TYR:CG	1:E:561:LEU:HD22	2.42	0.53
1:E:197:ARG:NH2	1:E:241:ARG:O	2.42	0.53
1:E:209:MET:O	1:E:213:THR:N	2.40	0.53
1:A:703:ALA:HA	1:A:708:ILE:HG13	1.91	0.53
1:B:477:ASN:O	1:B:481:ARG:HG2	2.09	0.53
1:D:165:LEU:HD13	1:E:227:GLN:HG2	1.88	0.53
1:B:392:GLY:O	1:B:396:ARG:HB2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:332:LYS:HD2	1:D:333:LEU:H	1.73	0.53
1:D:460:ALA:O	1:D:464:THR:HG22	2.08	0.53
1:A:670:ASN:O	1:A:673:THR:OG1	2.23	0.53
1:C:351:HIS:CD2	1:C:352:MET:HG3	2.44	0.53
1:D:7:LYS:HA	1:D:531:GLY:HA2	1.90	0.53
1:A:206:ASP:N	1:A:206:ASP:OD1	2.40	0.53
1:A:520:TRP:O	1:A:541:ARG:HA	2.08	0.53
1:C:367:ALA:HB1	1:C:368:LYS:CA	2.34	0.53
1:D:733:GLN:HE21	1:D:743:ALA:HB3	1.73	0.53
1:E:14:ARG:O	1:E:17:THR:OG1	2.25	0.53
1:E:160:PRO:O	1:E:161:LEU:HB3	2.07	0.53
1:A:35:GLN:OE1	1:A:35:GLN:N	2.42	0.53
1:C:111:THR:HG21	1:C:123:VAL:HG11	1.91	0.53
1:C:531:GLY:O	1:C:533:ASN:ND2	2.42	0.53
1:E:145:LEU:HD21	1:E:172:TYR:CE1	2.43	0.53
1:A:131:ILE:HD12	1:A:135:LEU:HD12	1.91	0.53
1:E:429:THR:HB	1:E:431:ASN:H	1.74	0.53
1:B:352:MET:HB2	1:B:353:GLY:HA2	1.91	0.53
1:C:104:ARG:NH1	1:C:223:ALA:HA	2.23	0.53
1:C:668:MET:O	1:C:672:VAL:HG13	2.09	0.53
1:B:462:LEU:HD11	1:B:486:TYR:CD2	2.44	0.52
1:C:61:ILE:HD12	1:C:203:SER:HB3	1.90	0.52
1:C:209:MET:O	1:C:213:THR:N	2.40	0.52
1:C:1:GLY:H1	1:C:440:GLY:HA2	1.74	0.52
1:A:533:ASN:HB2	1:A:540:ILE:HG12	1.91	0.52
1:C:119:LYS:HE2	1:C:220:LEU:HA	1.92	0.52
1:C:255:THR:OG1	1:C:304:ALA:HB1	2.09	0.52
1:D:339:THR:HG23	1:D:340:THR:HG23	1.91	0.52
1:D:171:VAL:HB	1:D:575:ILE:HG21	1.92	0.52
1:D:679:GLU:HG3	1:D:724:ARG:HG2	1.90	0.52
1:E:210:LEU:HD11	1:E:228:HIS:CE1	2.43	0.52
1:C:445:VAL:HG11	1:C:634:GLN:HG2	1.92	0.52
1:D:310:ASP:OD1	1:D:314:SER:N	2.42	0.52
1:B:126:VAL:N	1:B:163:PHE:O	2.42	0.52
1:D:56:VAL:HG22	1:D:170:TYR:HB2	1.90	0.52
1:D:374:THR:HB	1:D:621:VAL:HG12	1.92	0.52
1:C:35:GLN:N	1:C:35:GLN:OE1	2.43	0.52
1:C:359:VAL:HG21	1:C:414:VAL:HG12	1.92	0.52
1:D:309:SER:HB3	1:D:313:LEU:CB	2.39	0.52
1:B:156:HIS:HE1	1:B:208:LYS:HG2	1.75	0.52
1:E:210:LEU:HD21	1:E:228:HIS:NE2	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:521:ASN:OD1	1:B:541:ARG:HG2	2.08	0.52
1:B:58:LYS:HD2	1:B:166:PRO:HB2	1.92	0.52
1:B:669:GLN:O	1:B:672:VAL:HG22	2.10	0.52
1:D:209:MET:O	1:D:213:THR:N	2.42	0.52
1:C:679:GLU:HG3	1:C:724:ARG:HG2	1.90	0.52
1:D:73:TYR:HE1	1:D:143:HIS:HB3	1.75	0.51
1:E:58:LYS:CD	1:E:166:PRO:HB2	2.39	0.51
1:C:4:LEU:HB2	1:C:12:SER:OG	2.11	0.51
1:D:275:LEU:HB3	1:D:315:SER:HB3	1.92	0.51
1:D:531:GLY:O	1:D:533:ASN:ND2	2.43	0.51
1:E:182:ASN:OD1	1:E:183:PHE:N	2.43	0.51
1:E:35:GLN:N	1:E:35:GLN:OE1	2.43	0.51
1:E:502:VAL:HB	1:E:519:VAL:HG22	1.92	0.51
1:C:493:TYR:HD2	1:C:549:ILE:HD13	1.75	0.51
1:B:139:ALA:O	1:B:141:SER:N	2.43	0.51
1:C:669:GLN:O	1:C:672:VAL:HG22	2.10	0.51
1:E:576:HIS:C	1:E:577:ILE:HG12	2.30	0.51
1:A:249:VAL:O	1:A:253:VAL:HG12	2.11	0.51
1:A:339:THR:HG23	1:A:340:THR:HG23	1.93	0.51
1:B:318:ILE:CG2	1:B:320:TRP:HB3	2.41	0.51
1:B:84:GLU:O	1:B:88:GLN:HG3	2.10	0.51
1:C:589:TYR:OH	1:C:591:ASP:OD1	2.27	0.51
1:D:66:TYR:CE2	1:D:149:ILE:HB	2.46	0.51
1:A:213:THR:HG23	1:A:214:PHE:CD1	2.46	0.51
1:A:398:SER:O	1:A:401:LEU:HB3	2.10	0.51
1:A:464:THR:OG1	1:A:466:ILE:HG12	2.11	0.51
1:D:53:LEU:HB3	1:D:171:VAL:HG21	1.93	0.51
1:A:322:ILE:O	1:A:326:SER:N	2.44	0.51
1:A:408:PHE:CE2	1:A:681:ILE:HD11	2.46	0.51
1:B:521:ASN:HA	1:B:540:ILE:O	2.10	0.51
1:A:391:PRO:HA	1:A:394:SER:OG	2.11	0.51
1:B:686:ILE:O	1:B:690:ALA:N	2.41	0.51
1:C:310:ASP:HB3	1:C:311:GLU:HA	1.92	0.51
1:C:34:LEU:HD22	1:C:35:GLN:NE2	2.25	0.51
1:C:708:ILE:HD12	1:C:708:ILE:H	1.76	0.51
1:C:692:HIS:CD2	1:D:302:GLY:HA3	2.45	0.51
1:A:400:THR:OG1	1:A:686:ILE:HD13	2.11	0.51
1:C:165:LEU:HD13	1:D:227:GLN:HG2	1.92	0.51
1:C:460:ALA:O	1:C:464:THR:HG22	2.11	0.51
1:C:342:TYR:CG	1:C:561:LEU:HD22	2.46	0.51
1:A:318:ILE:CG2	1:A:320:TRP:HB3	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:LYS:HE3	1:A:529:PRO:O	2.10	0.51
1:C:273:ALA:HA	1:C:276:ARG:HB2	1.93	0.51
1:C:572:THR:OG1	1:C:577:ILE:HD11	2.11	0.51
1:B:210:LEU:HD11	1:B:228:HIS:CE1	2.40	0.50
1:B:42:ARG:O	1:B:287:ASN:HA	2.11	0.50
1:C:126:VAL:N	1:C:163:PHE:O	2.44	0.50
1:A:540:ILE:HG21	1:A:551:TYR:CE2	2.46	0.50
1:A:84:GLU:OE2	1:B:620:ARG:NH2	2.44	0.50
1:C:683:THR:HG22	1:C:724:ARG:NH1	2.27	0.50
1:B:367:ALA:HA	1:B:401:LEU:HD11	1.93	0.50
1:D:345:GLN:HE22	1:D:552:ASN:HB2	1.77	0.50
1:B:309:SER:HB3	1:B:313:LEU:CB	2.40	0.50
1:A:330:PRO:HG2	1:A:331:PHE:CD2	2.47	0.50
1:A:332:LYS:HD2	1:A:333:LEU:H	1.75	0.50
1:A:352:MET:HB2	1:A:353:GLY:HA2	1.93	0.50
1:B:291:PHE:CZ	1:B:518:LEU:HD13	2.47	0.50
1:B:460:ALA:O	1:B:464:THR:HG22	2.11	0.50
1:B:340:THR:HG21	1:B:493:TYR:HA	1.92	0.50
1:E:721:HIS:O	1:E:725:ILE:HG13	2.11	0.50
1:B:173:ARG:HB3	1:B:578(A):TRP:CE2	2.47	0.50
1:E:41:THR:HG22	1:E:286:SER:OG	2.11	0.50
1:A:22:ILE:HB	1:A:515:SER:HB3	1.94	0.50
1:A:528:ILE:HG12	1:A:535:ILE:HG23	1.92	0.50
1:B:429:THR:HB	1:B:431:ASN:H	1.75	0.50
1:B:360:VAL:HB	1:B:439:LEU:HB3	1.93	0.50
1:C:578(A):TRP:HB2	1:C:579:PRO:HD2	1.93	0.50
1:E:640:PHE:CD2	1:E:674:LEU:HD13	2.47	0.50
1:B:318:ILE:HB	1:B:320:TRP:H	1.75	0.50
1:A:43:THR:O	1:A:333:LEU:HD12	2.12	0.50
1:D:197:ARG:NH2	1:D:241:ARG:O	2.44	0.50
1:E:367:ALA:HB1	1:E:368:LYS:CA	2.35	0.50
1:A:336:ILE:O	1:A:339:THR:HG22	2.11	0.49
1:A:43:THR:HA	1:A:287:ASN:ND2	2.27	0.49
1:A:498:ASN:HB2	1:A:520:TRP:CD1	2.47	0.49
1:B:213:THR:HG23	1:B:214:PHE:CD1	2.47	0.49
1:B:255:THR:OG1	1:B:304:ALA:HB1	2.12	0.49
1:B:180:TYR:HE1	1:B:489:ALA:HA	1.78	0.49
1:D:41:THR:HG22	1:D:286:SER:OG	2.13	0.49
1:B:168:ALA:HB1	1:B:170:TYR:CE2	2.47	0.49
1:E:213:THR:HG23	1:E:214:PHE:CD1	2.47	0.49
1:A:256:ILE:HG22	1:A:259:ARG:NH2	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:GLY:O	1:A:396:ARG:HB2	2.12	0.49
1:B:403:PRO:O	1:B:407:THR:HG22	2.12	0.49
1:C:13:ALA:HA	1:C:463:ARG:HA	1.94	0.49
1:C:42:ARG:O	1:C:287:ASN:HA	2.13	0.49
1:D:119:LYS:HG2	1:D:220:LEU:HA	1.94	0.49
1:C:318:ILE:CG2	1:C:320:TRP:HB3	2.43	0.49
1:C:260:LEU:HD23	1:C:271:PRO:HG3	1.94	0.49
1:C:272:SER:HB3	1:C:275:LEU:HG	1.94	0.49
1:C:309:SER:HB3	1:C:313:LEU:CB	2.42	0.49
1:E:259:ARG:NH2	1:E:306:VAL:HG21	2.22	0.49
1:E:691:VAL:HG13	1:E:723:ILE:HG12	1.93	0.49
1:A:116:ARG:NH2	1:B:112:GLY:HA3	2.27	0.49
1:B:154:VAL:O	1:B:158:LEU:HB2	2.12	0.49
1:C:7:LYS:HE3	1:C:529:PRO:C	2.32	0.49
1:D:4:LEU:HB2	1:D:12:SER:OG	2.13	0.49
1:D:530:VAL:HG21	1:D:551:TYR:CE1	2.48	0.49
1:E:454:ASP:O	1:E:457:VAL:HG12	2.13	0.49
1:E:659:GLU:O	1:E:663:ILE:HG13	2.13	0.49
1:A:348:ALA:N	1:A:357:HIS:O	2.36	0.49
1:A:739:SER:HB3	1:A:742:GLU:CD	2.33	0.49
1:B:259:ARG:O	1:B:265:THR:HG22	2.13	0.49
1:C:318:ILE:HD13	1:C:321:PHE:HB2	1.94	0.49
1:E:255:THR:OG1	1:E:304:ALA:HB1	2.13	0.49
1:A:357:HIS:HB2	1:A:421:TYR:CD2	2.48	0.49
1:A:444:VAL:HG11	1:A:486:TYR:CD1	2.47	0.49
1:B:41:THR:HG22	1:B:286:SER:OG	2.13	0.49
1:C:453:ARG:NH2	1:C:475:ALA:HA	2.28	0.49
1:D:348:ALA:HB3	1:D:357:HIS:H	1.78	0.49
1:D:678:ILE:HD13	1:D:729:LEU:HD21	1.94	0.49
1:E:587:PHE:HB2	1:E:623:ILE:HD13	1.94	0.49
1:B:609:PHE:HB2	1:B:614:LEU:HD12	1.95	0.49
1:A:131:ILE:HG13	1:A:132:LEU:N	2.27	0.48
1:A:115:ASN:HB2	1:B:110:ILE:O	2.13	0.48
1:C:540:ILE:HG21	1:C:551:TYR:HE2	1.77	0.48
1:E:210:LEU:HD21	1:E:228:HIS:CE1	2.48	0.48
1:E:668:MET:O	1:E:672:VAL:HG13	2.13	0.48
1:C:339:THR:HG23	1:C:340:THR:HG23	1.94	0.48
1:D:92:TYR:CE1	1:D:146:PHE:HB3	2.48	0.48
1:A:318:ILE:HG21	1:A:320:TRP:CE3	2.40	0.48
1:D:464:THR:OG1	1:D:466:ILE:HG12	2.12	0.48
1:D:8:ASP:O	1:D:12:SER:HB3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:390:GLU:OE1	1:E:618:ARG:NH1	2.45	0.48
1:A:190:VAL:HB	1:A:246:ALA:HB1	1.95	0.48
1:C:150:THR:O	1:C:153:PHE:HB3	2.13	0.48
1:C:41:THR:H	1:C:286:SER:HG	1.60	0.48
1:D:754:ASN:O	1:D:756:LEU:HD12	2.13	0.48
1:A:160:PRO:O	1:A:161:LEU:HB3	2.14	0.48
1:A:578(A):TRP:HB2	1:A:579:PRO:HD2	1.95	0.48
1:B:738:LEU:HD13	1:B:743:ALA:HB2	1.94	0.48
1:C:454:ASP:O	1:C:457:VAL:HG12	2.14	0.48
1:D:197:ARG:HA	1:D:200:THR:HG22	1.94	0.48
1:D:313:LEU:O	1:D:317:ILE:N	2.30	0.48
1:D:317:ILE:HA	1:D:318:ILE:HA	1.63	0.48
1:E:30:SER:HB3	1:E:517:TYR:CE2	2.48	0.48
1:A:205:VAL:HG23	1:A:206:ASP:OD1	2.14	0.48
1:B:228:HIS:ND1	1:B:229:LEU:HD23	2.29	0.48
1:E:352:MET:HB2	1:E:353:GLY:HA2	1.95	0.48
1:E:373:PHE:HA	1:E:389:VAL:HA	1.95	0.48
1:C:127:PRO:HA	1:C:128:PRO:HD3	1.76	0.48
1:C:216:ALA:HA	1:C:217:LYS:HA	1.53	0.48
1:E:378:LEU:HD21	1:E:384:GLN:HB3	1.96	0.48
1:E:53:LEU:HG	1:E:566:LEU:HD11	1.95	0.48
1:B:578(A):TRP:HB2	1:B:579:PRO:HD2	1.96	0.48
1:C:738:LEU:HD13	1:C:743:ALA:HB2	1.96	0.48
1:D:314:SER:HA	1:D:317:ILE:O	2.13	0.48
1:A:373:PHE:HA	1:A:389:VAL:HA	1.95	0.48
1:A:491:MET:HA	1:A:494:ALA:HB3	1.96	0.48
1:B:398:SER:HA	1:B:401:LEU:HB3	1.96	0.48
1:B:464:THR:OG1	1:B:466:ILE:HG12	2.12	0.48
1:B:528:ILE:HG12	1:B:535:ILE:HG23	1.96	0.48
1:C:533:ASN:HB2	1:C:540:ILE:HD11	1.95	0.48
1:D:352:MET:HB2	1:D:353:GLY:HA2	1.96	0.48
1:D:669:GLN:O	1:D:672:VAL:HG22	2.14	0.48
1:B:209:MET:HA	1:B:212:ALA:HB3	1.95	0.48
1:B:598:ARG:HG3	1:B:710:ASP:OD1	2.14	0.48
1:D:36:LEU:HD22	1:D:261:TRP:O	2.14	0.48
1:D:739:SER:O	1:D:742:GLU:HG2	2.14	0.48
1:E:578(A):TRP:HB2	1:E:579:PRO:HD2	1.95	0.48
1:E:669:GLN:O	1:E:672:VAL:HG22	2.14	0.48
1:A:146:PHE:HA	1:A:149:ILE:HG22	1.96	0.47
1:A:310:ASP:HB3	1:A:311:GLU:HA	1.95	0.47
1:C:110:ILE:HD12	1:C:111:THR:N	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:387:LEU:H	1:C:572:THR:HG22	1.78	0.47
1:E:131:ILE:HD11	1:E:151:THR:HA	1.96	0.47
1:B:119:LYS:O	1:B:219:ALA:HB1	2.13	0.47
1:B:380:ASN:OD1	1:B:380:ASN:N	2.47	0.47
1:B:576:HIS:C	1:B:577:ILE:HG12	2.35	0.47
1:D:150:THR:O	1:D:153:PHE:HB3	2.14	0.47
1:D:168:ALA:HB1	1:D:170:TYR:HE2	1.79	0.47
1:E:51:GLU:H	1:E:564:LYS:HE3	1.79	0.47
1:A:67:ALA:HA	1:A:195:LEU:HD23	1.96	0.47
1:A:84:GLU:O	1:A:88:GLN:HG3	2.14	0.47
1:B:206:ASP:O	1:B:210:LEU:HB2	2.14	0.47
1:B:281:ILE:HA	1:B:284:LEU:HB2	1.95	0.47
1:D:272:SER:HB3	1:D:275:LEU:HG	1.96	0.47
1:B:520:TRP:O	1:B:541:ARG:HA	2.14	0.47
1:C:104:ARG:HH12	1:C:223:ALA:HA	1.78	0.47
1:D:342:TYR:CD2	1:D:561:LEU:HD22	2.49	0.47
1:D:34:LEU:HD13	1:D:35:GLN:OE1	2.15	0.47
1:D:370:ILE:O	1:D:394:SER:HB3	2.14	0.47
1:A:41:THR:HG22	1:A:286:SER:OG	2.14	0.47
1:C:528:ILE:HG12	1:C:535:ILE:HG23	1.97	0.47
1:D:209:MET:HA	1:D:212:ALA:HB3	1.95	0.47
1:D:50:SER:HA	1:D:564:LYS:HE3	1.97	0.47
1:D:637:TYR:CZ	1:D:742:GLU:HB2	2.49	0.47
1:A:528:ILE:HG21	1:A:535:ILE:HG21	1.96	0.47
1:B:336:ILE:O	1:B:339:THR:HG22	2.14	0.47
1:D:117:ALA:HB1	1:D:222:PRO:HD2	1.96	0.47
1:A:103:TRP:O	1:A:107:THR:OG1	2.32	0.47
1:B:259:ARG:NH2	1:B:306:VAL:HG21	2.21	0.47
1:C:111:THR:HG21	1:C:123:VAL:CG1	2.44	0.47
1:C:528:ILE:HG21	1:C:535:ILE:HG21	1.96	0.47
1:E:66:TYR:CE2	1:E:149:ILE:HB	2.48	0.47
1:E:317:ILE:HA	1:E:318:ILE:HA	1.52	0.47
1:A:259:ARG:O	1:A:265:THR:HG22	2.14	0.47
1:D:673:THR:O	1:D:677:LYS:HG2	2.15	0.47
1:A:150:THR:O	1:A:153:PHE:HB3	2.15	0.47
1:A:430:VAL:HG22	1:A:529:PRO:HB3	1.96	0.47
1:C:131:ILE:HD11	1:C:151:THR:OG1	2.15	0.47
1:C:53:LEU:HB3	1:C:171:VAL:HG21	1.97	0.47
1:D:104:ARG:NH2	1:D:114:SER:O	2.25	0.47
1:E:126:VAL:N	1:E:163:PHE:O	2.45	0.47
1:E:53:LEU:HB3	1:E:171:VAL:HG21	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:681:ILE:HD13	1:A:732:LEU:HD11	1.97	0.47
1:B:119:LYS:HG2	1:B:220:LEU:HA	1.96	0.47
1:C:567:ASP:OD1	1:C:570:ASN:HB2	2.15	0.47
1:D:168:ALA:HB1	1:D:170:TYR:CE2	2.50	0.47
1:D:477:ASN:O	1:D:481:ARG:HG2	2.14	0.47
1:A:314:SER:HA	1:A:318:ILE:N	2.30	0.47
1:A:480:LYS:HA	1:A:483:MET:HE1	1.97	0.47
1:A:387:LEU:HB2	1:A:572:THR:HG21	1.96	0.47
1:B:149:ILE:HD11	1:B:199:LEU:HD22	1.97	0.47
1:B:637:TYR:CZ	1:B:742:GLU:HB2	2.50	0.47
1:D:274:ARG:NH2	1:D:312:GLU:HG3	2.30	0.47
1:E:673:THR:O	1:E:677:LYS:HG2	2.15	0.47
1:A:317:ILE:HA	1:A:318:ILE:HA	1.51	0.46
1:A:180:TYR:HE1	1:A:489:ALA:HA	1.80	0.46
1:B:225:ILE:HA	1:B:228:HIS:HB3	1.97	0.46
1:C:377:LYS:HA	1:C:385:ARG:HD3	1.97	0.46
1:D:534:ALA:H	1:D:540:ILE:CD1	2.28	0.46
1:E:349:ILE:HD11	1:E:353:GLY:O	2.15	0.46
1:B:4:LEU:N	1:B:437:MET:O	2.46	0.46
1:B:721:HIS:O	1:B:725:ILE:HG13	2.16	0.46
1:C:117:ALA:HB2	1:C:223:ALA:HB2	1.96	0.46
1:C:51:GLU:N	1:C:564:LYS:HE3	2.14	0.46
1:E:654:SER:O	1:E:660:LYS:HD2	2.15	0.46
1:A:477:ASN:O	1:A:481:ARG:HG2	2.15	0.46
1:B:16:LEU:HD23	1:B:16:LEU:HA	1.74	0.46
1:D:380:ASN:N	1:D:380:ASN:OD1	2.46	0.46
1:B:131:ILE:HG13	1:B:132:LEU:N	2.30	0.46
1:B:739:SER:HB3	1:B:742:GLU:CD	2.35	0.46
1:D:103:TRP:O	1:D:107:THR:OG1	2.34	0.46
1:E:59:GLY:HA2	1:E:152:ASP:O	2.15	0.46
1:A:156:HIS:CE1	1:A:208:LYS:HG2	2.51	0.46
1:A:229:LEU:HA	1:A:232:ALA:HB3	1.98	0.46
1:A:281:ILE:HA	1:A:284:LEU:HB2	1.96	0.46
1:A:668:MET:O	1:A:672:VAL:HG13	2.16	0.46
1:B:195:LEU:O	1:B:199:LEU:HG	2.15	0.46
1:B:454:ASP:O	1:B:457:VAL:HG12	2.14	0.46
1:D:160:PRO:O	1:D:161:LEU:HB3	2.15	0.46
1:D:367:ALA:HB1	1:D:368:LYS:CA	2.35	0.46
1:D:562:GLN:NE2	1:D:563:ALA:O	2.49	0.46
1:D:51:GLU:N	1:D:564:LYS:HE3	2.22	0.46
1:D:86:VAL:O	1:D:90:THR:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:528:ILE:HG21	1:B:535:ILE:HG21	1.98	0.46
1:E:387:LEU:H	1:E:572:THR:HG22	1.81	0.46
1:E:641:VAL:HA	1:E:749:VAL:HG21	1.97	0.46
1:B:48:MET:HB2	1:B:561:LEU:HD11	1.98	0.46
1:E:510:ALA:N	1:E:511:ALA:HA	2.31	0.46
1:A:58:LYS:HD2	1:A:166:PRO:HB2	1.98	0.46
1:C:262:SER:HA	1:C:263:PRO:HD2	1.83	0.46
1:C:336:ILE:O	1:C:339:THR:HG22	2.16	0.46
1:D:641:VAL:HA	1:D:749:VAL:HG21	1.98	0.46
1:C:332:LYS:HD2	1:C:333:LEU:H	1.81	0.46
1:D:408:PHE:HE2	1:D:681:ILE:HD11	1.80	0.46
1:E:400:THR:O	1:E:403:PRO:HD2	2.16	0.46
1:B:637:TYR:HD1	1:B:746:LEU:HD13	1.81	0.46
1:C:609:PHE:CD2	1:C:617:ARG:HB2	2.51	0.46
1:D:112:GLY:HA2	1:E:115:ASN:HD22	1.81	0.46
1:D:61:ILE:HD11	1:D:153:PHE:HA	1.97	0.46
1:D:34:LEU:HD22	1:D:35:GLN:CD	2.36	0.46
1:B:111:THR:HA	1:B:112:GLY:HA2	1.78	0.45
1:B:468:ASP:OD2	1:B:470:SER:OG	2.34	0.45
1:B:739:SER:HB3	1:B:742:GLU:HG2	1.98	0.45
1:D:104:ARG:HA	1:D:104:ARG:HD2	1.76	0.45
1:E:528:ILE:HG12	1:E:535:ILE:HG23	1.98	0.45
1:B:35:GLN:N	1:B:35:GLN:OE1	2.49	0.45
1:C:171:VAL:HB	1:C:575:ILE:HG21	1.97	0.45
1:D:229:LEU:HA	1:D:232:ALA:HB3	1.99	0.45
1:D:733:GLN:HE21	1:D:743:ALA:CB	2.28	0.45
1:A:165:LEU:O	1:A:165:LEU:HD12	2.15	0.45
1:A:637:TYR:CD1	1:A:746:LEU:HD13	2.52	0.45
1:B:160:PRO:HG2	1:B:163:PHE:CE2	2.51	0.45
1:B:7:LYS:NZ	1:B:435:ALA:H	2.14	0.45
1:B:82:VAL:HA	1:B:85:LEU:HB3	1.98	0.45
1:C:352:MET:HB2	1:C:353:GLY:HA2	1.97	0.45
1:D:625:LYS:HA	1:D:626:PRO:HD3	1.86	0.45
1:E:104:ARG:HD2	1:E:104:ARG:HA	1.74	0.45
1:E:13:ALA:HA	1:E:463:ARG:HA	1.98	0.45
1:A:111:THR:HG21	1:A:123:VAL:CG1	2.46	0.45
1:A:48:MET:HB2	1:A:561:LEU:HD11	1.98	0.45
1:E:216:ALA:O	1:E:220:LEU:HD11	2.16	0.45
1:E:383:ASN:O	1:E:385:ARG:HG2	2.16	0.45
1:E:462:LEU:HD11	1:E:486:TYR:CD2	2.51	0.45
1:C:387:LEU:H	1:C:572:THR:CG2	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:403:PRO:O	1:C:407:THR:HG22	2.16	0.45
1:D:165:LEU:O	1:D:165:LEU:HD12	2.17	0.45
1:D:149:ILE:HD11	1:D:199:LEU:CD2	2.46	0.45
1:E:318:ILE:HA	1:E:319:PRO:HD2	1.76	0.45
1:E:407:THR:HG23	1:E:408:PHE:CD2	2.51	0.45
1:B:71:PHE:CE2	1:B:331:PHE:HE2	2.35	0.45
1:E:651:ARG:O	1:E:660:LYS:HE3	2.16	0.45
1:A:309:SER:HB3	1:A:313:LEU:HD13	1.98	0.45
1:A:341:SER:HB3	1:A:558:SER:HB2	1.98	0.45
1:A:407:THR:OG1	1:A:677:LYS:HD2	2.16	0.45
1:B:272:SER:HB3	1:B:275:LEU:HG	1.99	0.45
1:B:733:GLN:HE21	1:B:743:ALA:CB	2.30	0.45
1:D:119:LYS:O	1:D:219:ALA:HB1	2.17	0.45
1:D:498:ASN:HB2	1:D:520:TRP:HD1	1.81	0.45
1:E:340:THR:HG21	1:E:493:TYR:HA	1.98	0.45
1:E:169:ALA:O	1:E:575:ILE:HG23	2.17	0.45
1:A:258:GLY:HA3	1:A:294:TYR:CE1	2.52	0.45
1:A:669:GLN:O	1:A:672:VAL:HG22	2.16	0.45
1:B:205:VAL:O	1:B:209:MET:HG2	2.16	0.45
1:B:307:ILE:HG13	1:B:309:SER:H	1.82	0.45
1:C:576:HIS:C	1:C:577:ILE:HG12	2.37	0.45
1:E:56:VAL:HG22	1:E:170:TYR:HB2	1.99	0.45
1:E:34:LEU:HD22	1:E:35:GLN:NE2	2.32	0.45
1:E:431:ASN:O	1:E:432:SER:HB2	2.17	0.45
1:B:431:ASN:O	1:B:432:SER:HB2	2.17	0.45
1:A:119:LYS:HE2	1:A:220:LEU:HA	1.99	0.45
1:A:387:LEU:H	1:A:572:THR:HG22	1.82	0.45
1:A:609:PHE:CE2	1:A:617:ARG:HB2	2.52	0.45
1:B:150:THR:O	1:B:153:PHE:HB3	2.17	0.45
1:B:590:GLU:O	1:B:740:ARG:NH2	2.43	0.45
1:C:131:ILE:HG13	1:C:132:LEU:N	2.32	0.45
1:D:171:VAL:HG12	1:D:576:HIS:O	2.17	0.45
1:D:750:LEU:HA	1:D:750:LEU:HD12	1.79	0.45
1:E:208:LYS:HG2	1:E:211:GLN:HE21	1.82	0.45
1:A:659:GLU:O	1:A:663:ILE:HG13	2.17	0.44
1:B:7:LYS:HE2	1:B:434:GLY:HA3	1.99	0.44
1:B:396:ARG:HG2	1:B:612:LEU:HD22	1.99	0.44
1:D:542:THR:HA	1:D:543:PRO:HD3	1.73	0.44
1:D:668:MET:O	1:D:672:VAL:HG13	2.17	0.44
1:E:228:HIS:ND1	1:E:229:LEU:HD23	2.32	0.44
1:B:159:SER:HB3	1:B:164:ILE:HD11	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:275:LEU:HB3	1:C:315:SER:HB3	1.99	0.44
1:D:191:ARG:O	1:D:194:ASP:HB2	2.17	0.44
1:E:357:HIS:HB2	1:E:421:TYR:HD2	1.82	0.44
1:E:637:TYR:CE1	1:E:641:VAL:HG21	2.52	0.44
1:A:609:PHE:CD1	1:A:616:GLN:O	2.70	0.44
1:E:216:ALA:HA	1:E:217:LYS:HA	1.72	0.44
1:E:84:GLU:O	1:E:88:GLN:HG3	2.16	0.44
1:A:284:LEU:HG	1:A:290:LEU:HD21	2.00	0.44
1:B:100:PRO:O	1:B:104:ARG:HB2	2.18	0.44
1:B:378:LEU:HD11	1:B:384:GLN:HB3	1.99	0.44
1:C:210:LEU:HA	1:C:213:THR:HG22	1.98	0.44
1:C:387:LEU:HB2	1:C:572:THR:HG21	1.98	0.44
1:A:310:ASP:HA	1:A:312:GLU:N	2.33	0.44
1:B:160:PRO:O	1:B:161:LEU:HB3	2.16	0.44
1:C:36:LEU:O	1:C:503:VAL:N	2.43	0.44
1:D:42:ARG:O	1:D:287:ASN:HA	2.18	0.44
1:E:401:LEU:HA	1:E:404:ILE:HD12	1.98	0.44
1:E:542:THR:HA	1:E:543:PRO:HD3	1.77	0.44
1:E:59:GLY:CA	1:E:152:ASP:HB2	2.47	0.44
1:A:378:LEU:HD22	1:A:576:HIS:CE1	2.53	0.44
1:C:360:VAL:HB	1:C:439:LEU:HB3	1.99	0.44
1:C:84:GLU:O	1:C:88:GLN:HG3	2.17	0.44
1:A:104:ARG:HD2	1:A:104:ARG:HA	1.79	0.44
1:A:530:VAL:HG21	1:A:551:TYR:HE1	1.79	0.44
1:B:387:LEU:HG	1:B:572:THR:HG21	1.99	0.44
1:B:597:ILE:HA	1:B:597:ILE:HD13	1.85	0.44
1:B:707:LEU:HD13	1:B:709:ASP:CG	2.38	0.44
1:D:110:ILE:HD12	1:D:111:THR:N	2.33	0.44
1:A:708:ILE:HD12	1:A:708:ILE:H	1.83	0.44
1:B:366:PHE:HE1	1:B:632:ILE:HG21	1.82	0.44
1:D:66:TYR:OH	1:D:152:ASP:OD2	2.36	0.44
1:D:356:SER:HB2	1:D:421:TYR:CD2	2.53	0.44
1:A:365:GLN:HB3	1:A:562:GLN:HA	1.99	0.44
1:A:387:LEU:H	1:A:572:THR:CG2	2.31	0.44
1:B:206:ASP:HA	1:B:209:MET:HG2	2.00	0.44
1:B:593:TYR:HB2	1:B:726:TRP:CE2	2.53	0.44
1:C:164:ILE:HG13	1:C:164:ILE:H	1.67	0.44
1:C:314:SER:HA	1:C:317:ILE:C	2.38	0.44
1:C:408:PHE:HD1	1:C:636:TRP:CE2	2.36	0.44
1:D:132:LEU:O	1:D:136:ARG:HG3	2.17	0.44
1:B:317:ILE:HA	1:B:318:ILE:HA	1.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:34:LEU:HD22	1:C:35:GLN:CD	2.37	0.43
1:D:349:ILE:HD11	1:D:353:GLY:O	2.18	0.43
1:A:260:LEU:HB3	1:A:271:PRO:HG3	1.99	0.43
1:A:445:VAL:HB	1:A:631:ALA:HB1	2.00	0.43
1:A:66:TYR:O	1:A:70:PHE:HD1	2.01	0.43
1:B:156:HIS:O	1:B:211:GLN:NE2	2.51	0.43
1:B:349:ILE:HD11	1:B:353:GLY:O	2.18	0.43
1:B:637:TYR:CE1	1:B:742:GLU:HB2	2.52	0.43
1:C:37:PRO:HA	1:C:502:VAL:HA	2.00	0.43
1:D:403:PRO:O	1:D:407:THR:HG22	2.18	0.43
1:D:431:ASN:O	1:D:432:SER:HB2	2.17	0.43
1:D:525:GLU:OE2	1:D:527:ARG:N	2.51	0.43
1:E:339:THR:HG23	1:E:340:THR:HG23	2.00	0.43
1:E:354:GLN:HG2	1:E:529:PRO:HD3	1.99	0.43
1:B:284:LEU:HG	1:B:290:LEU:HD21	2.00	0.43
1:D:154:VAL:O	1:D:158:LEU:HB2	2.18	0.43
1:D:344:GLY:CA	1:D:557:PRO:HG3	2.48	0.43
1:A:71:PHE:HE1	1:A:188:ASP:HB3	1.84	0.43
1:B:318:ILE:HB	1:B:320:TRP:HB3	2.00	0.43
1:B:358:VAL:HG13	1:B:437:MET:HB2	1.99	0.43
1:B:678:ILE:HA	1:B:681:ILE:HD12	2.01	0.43
1:C:259:ARG:NH2	1:C:306:VAL:HG21	2.24	0.43
1:B:216:ALA:O	1:B:220:LEU:HD11	2.18	0.43
1:B:314:SER:HA	1:B:317:ILE:C	2.39	0.43
1:B:493:TYR:HD2	1:B:549:ILE:HD13	1.84	0.43
1:D:387:LEU:HG	1:D:577:ILE:HG13	2.01	0.43
1:E:150:THR:O	1:E:153:PHE:HB3	2.18	0.43
1:E:533:ASN:N	1:E:533:ASN:OD1	2.49	0.43
1:A:154:VAL:HA	1:A:157:VAL:HG22	2.00	0.43
1:A:30:SER:HB2	1:A:543:PRO:HB3	2.01	0.43
1:A:342:TYR:CD1	1:A:343:ILE:HG12	2.53	0.43
1:A:402:ALA:HB3	1:A:403:PRO:HD3	2.00	0.43
1:A:754:ASN:O	1:A:756:LEU:HD12	2.19	0.43
1:C:42:ARG:HG2	1:C:335:PRO:HA	2.00	0.43
1:D:43:THR:O	1:D:333:LEU:HD12	2.18	0.43
1:D:528:ILE:O	1:D:528:ILE:HD12	2.19	0.43
1:E:387:LEU:H	1:E:572:THR:CG2	2.31	0.43
1:A:71:PHE:CE1	1:A:188:ASP:HB3	2.54	0.43
1:C:410:VAL:O	1:C:414:VAL:HG22	2.19	0.43
1:C:640:PHE:CE2	1:C:674:LEU:HD13	2.54	0.43
1:D:578(A):TRP:CD1	1:D:579:PRO:N	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:111:THR:HA	1:E:112:GLY:HA2	1.75	0.43
1:E:119:LYS:HG2	1:E:220:LEU:HA	2.00	0.43
1:A:46:ALA:HB3	1:A:179:THR:HA	2.01	0.43
1:A:4:LEU:N	1:A:437:MET:O	2.43	0.43
1:A:576:HIS:C	1:A:577:ILE:HG12	2.39	0.43
1:C:104:ARG:HD2	1:C:104:ARG:HA	1.74	0.43
1:C:133:GLU:HA	1:C:136:ARG:CZ	2.48	0.43
1:E:127:PRO:HA	1:E:128:PRO:HD3	1.89	0.43
1:E:43:THR:O	1:E:333:LEU:HD12	2.18	0.43
1:E:34:LEU:HD23	1:E:34:LEU:HA	1.79	0.43
1:A:326:SER:O	1:A:332:LYS:HD3	2.19	0.43
1:A:542:THR:HA	1:A:543:PRO:HD3	1.89	0.43
1:B:155:CYS:O	1:B:159:SER:OG	2.36	0.43
1:D:153:PHE:CD1	1:D:202:LEU:HD12	2.53	0.43
1:D:330:PRO:HG2	1:D:331:PHE:CD2	2.52	0.43
1:D:454:ASP:O	1:D:457:VAL:HG12	2.19	0.43
1:A:348:ALA:HB3	1:A:357:HIS:H	1.83	0.43
1:B:164:ILE:HD12	1:B:164:ILE:O	2.19	0.43
1:C:288:LEU:HD22	1:C:336:ILE:HD11	2.00	0.43
1:C:291:PHE:CE2	1:C:518:LEU:HD13	2.54	0.43
1:D:291:PHE:CE2	1:D:518:LEU:HD13	2.53	0.43
1:D:615:GLY:HA2	1:D:616:GLN:O	2.19	0.43
1:E:309:SER:HB3	1:E:313:LEU:CB	2.49	0.43
1:E:526:LEU:O	1:E:535:ILE:HD11	2.19	0.43
1:A:25:LEU:H	1:A:25:LEU:HG	1.60	0.42
1:A:273:ALA:HA	1:A:276:ARG:HB2	2.01	0.42
1:A:94:GLN:HA	1:A:98:CYS:SG	2.59	0.42
1:B:133:GLU:HA	1:B:136:ARG:CZ	2.49	0.42
1:B:499:PRO:O	1:B:501:VAL:HG22	2.18	0.42
1:C:160:PRO:O	1:C:161:LEU:HB3	2.19	0.42
1:C:408:PHE:HE2	1:C:681:ILE:HD11	1.84	0.42
1:E:170:TYR:HD1	1:E:576:HIS:HB2	1.83	0.42
1:A:343:ILE:HD13	1:A:362:GLU:HG2	2.00	0.42
1:A:366:PHE:HE1	1:A:632:ILE:HG21	1.84	0.42
1:B:567:ASP:OD1	1:B:570:ASN:HB2	2.19	0.42
1:B:703:ALA:HA	1:B:708:ILE:HG13	2.01	0.42
1:C:598:ARG:NH1	1:C:713:ASP:OD1	2.52	0.42
1:D:104:ARG:HH12	1:D:223:ALA:HA	1.83	0.42
1:D:243:ASN:HB3	1:D:244:PHE:H	1.60	0.42
1:D:35:GLN:OE1	1:D:35:GLN:N	2.50	0.42
1:E:34:LEU:HD22	1:E:35:GLN:CD	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198:MET:O	1:A:201:ALA:HB3	2.19	0.42
1:A:89:PHE:CE2	1:A:149:ILE:HD13	2.55	0.42
1:B:59:GLY:CA	1:B:152:ASP:HB2	2.49	0.42
1:B:609:PHE:CD1	1:B:616:GLN:O	2.72	0.42
1:D:318:ILE:HG21	1:D:320:TRP:CE3	2.54	0.42
1:D:370:ILE:HA	1:D:370:ILE:HD13	1.80	0.42
1:D:523:ARG:HA	1:D:539:SER:HA	2.01	0.42
1:D:385:ARG:HG3	1:D:580:TRP:NE1	2.34	0.42
1:E:314:SER:HA	1:E:317:ILE:C	2.40	0.42
1:A:46:ALA:HA	1:A:330:PRO:O	2.20	0.42
1:B:252:SER:O	1:B:255:THR:HB	2.19	0.42
1:B:262:SER:HA	1:B:263:PRO:HD2	1.85	0.42
1:B:481:ARG:O	1:B:484:PHE:HB3	2.19	0.42
1:C:307:ILE:HG13	1:C:309:SER:H	1.84	0.42
1:D:216:ALA:O	1:D:220:LEU:HD11	2.20	0.42
1:D:310:ASP:HB3	1:D:311:GLU:HA	2.02	0.42
1:E:498:ASN:N	1:E:499:PRO:HD3	2.35	0.42
1:E:707:LEU:HA	1:E:707:LEU:HD23	1.69	0.42
1:A:164:ILE:HD12	1:A:164:ILE:O	2.20	0.42
1:B:281:ILE:O	1:B:285:ARG:HG2	2.19	0.42
1:B:318:ILE:HG21	1:B:320:TRP:HB3	2.02	0.42
1:B:13:ALA:HA	1:B:463:ARG:HA	2.02	0.42
1:D:155:CYS:O	1:D:159:SER:OG	2.38	0.42
1:E:578(A):TRP:CD1	1:E:579:PRO:N	2.87	0.42
1:A:111:THR:HA	1:A:112:GLY:HA2	1.93	0.42
1:A:159:SER:HB3	1:A:164:ILE:HD11	2.01	0.42
1:A:318:ILE:HA	1:A:319:PRO:HD2	1.93	0.42
1:B:110:ILE:HD12	1:B:111:THR:N	2.34	0.42
1:B:45:SER:HB2	1:B:180:TYR:HE2	1.83	0.42
1:C:247:ASN:OD1	1:C:301:ARG:NH2	2.52	0.42
1:D:572:THR:OG1	1:D:577:ILE:HD11	2.20	0.42
1:E:727:ALA:O	1:E:731:VAL:HG12	2.18	0.42
1:A:173:ARG:HD2	1:A:566:LEU:HD22	2.02	0.42
1:C:253:VAL:HG21	1:C:321:PHE:CD2	2.55	0.42
1:C:571:HIS:O	1:C:573:THR:N	2.53	0.42
1:A:110:ILE:HD12	1:A:111:THR:N	2.35	0.42
1:B:104:ARG:NH1	1:B:223:ALA:O	2.50	0.42
1:D:212:ALA:HA	1:D:215:LYS:HD3	2.01	0.42
1:E:428:GLY:HA3	1:E:429:THR:HG23	2.00	0.42
1:E:3:ASN:OD1	1:E:438:THR:HB	2.19	0.42
1:A:132:LEU:O	1:A:136:ARG:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:528:ILE:HD12	1:A:528:ILE:O	2.20	0.42
1:A:687:GLY:O	1:A:691:VAL:HG23	2.19	0.42
1:B:83:ASP:OD1	1:B:191:ARG:NH1	2.53	0.42
1:C:317:ILE:HA	1:C:318:ILE:HA	1.48	0.42
1:C:370:ILE:HD13	1:C:370:ILE:HA	1.72	0.42
1:C:42:ARG:HD2	1:C:283:GLN:CD	2.40	0.42
1:C:534:ALA:HB1	1:C:536:GLU:HB2	2.02	0.42
1:D:191:ARG:HA	1:D:191:ARG:HD2	1.84	0.42
1:C:754:ASN:O	1:C:756:LEU:HD12	2.20	0.42
1:D:48:MET:HG3	1:D:561:LEU:HD11	2.02	0.42
1:B:320:TRP:CD1	1:B:323:GLU:HB3	2.54	0.41
1:B:34:LEU:HD22	1:B:35:GLN:NE2	2.35	0.41
1:C:447:ARG:HA	1:C:447:ARG:HD2	1.76	0.41
1:D:131:ILE:HG13	1:D:132:LEU:N	2.34	0.41
1:E:209:MET:HA	1:E:212:ALA:HB3	2.02	0.41
1:E:269:LEU:HD12	1:E:269:LEU:HA	1.92	0.41
1:B:738:LEU:HA	1:B:738:LEU:HD23	1.81	0.41
1:C:7:LYS:HZ2	1:C:435:ALA:H	1.64	0.41
1:C:575:ILE:HG22	1:C:576:HIS:O	2.21	0.41
1:D:165:LEU:HA	1:D:166:PRO:HD3	1.96	0.41
1:D:213:THR:HG23	1:D:214:PHE:CD1	2.55	0.41
1:D:528:ILE:HG12	1:D:535:ILE:HG23	2.03	0.41
1:D:576:HIS:C	1:D:577:ILE:HG12	2.40	0.41
1:E:138:LEU:HA	1:E:138:LEU:HD23	1.78	0.41
1:E:330:PRO:HG2	1:E:331:PHE:CD2	2.55	0.41
1:A:153:PHE:CD1	1:A:202:LEU:HD12	2.56	0.41
1:A:526:LEU:O	1:A:535:ILE:HD11	2.21	0.41
1:B:138:LEU:HA	1:B:138:LEU:HD23	1.83	0.41
1:B:75:GLN:HG2	1:B:177:THR:HG23	2.02	0.41
1:B:387:LEU:HD12	1:B:568:LEU:HD11	2.03	0.41
1:B:600:LYS:HE3	1:B:600:LYS:HB3	1.91	0.41
1:C:55:GLU:HA	1:C:170:TYR:O	2.21	0.41
1:D:408:PHE:CE2	1:D:681:ILE:HD11	2.55	0.41
1:E:380:ASN:N	1:E:380:ASN:OD1	2.45	0.41
1:B:687:GLY:O	1:B:690:ALA:HB3	2.20	0.41
1:B:206:ASP:HA	1:B:209:MET:CG	2.50	0.41
1:C:165:LEU:O	1:C:165:LEU:HD12	2.21	0.41
1:C:153:PHE:CD1	1:C:202:LEU:HD12	2.56	0.41
1:C:172:TYR:HA	1:C:578(A):TRP:HB3	2.02	0.41
1:D:344:GLY:HA3	1:D:557:PRO:HG3	2.03	0.41
1:E:319:PRO:O	1:E:322:ILE:HB	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:429:THR:HB	1:A:431:ASN:H	1.85	0.41
1:A:61:ILE:HD12	1:A:203:SER:HB3	2.02	0.41
1:A:82:VAL:HG12	1:A:188:ASP:CG	2.41	0.41
1:C:181:PRO:HG2	1:C:289:ALA:HB1	2.01	0.41
1:C:309:SER:HB3	1:C:313:LEU:HD22	2.03	0.41
1:C:407:THR:OG1	1:C:677:LYS:HD2	2.21	0.41
1:C:14:ARG:HG2	1:C:465:GLY:HA3	2.01	0.41
1:D:241:ARG:HB2	1:D:243:ASN:OD1	2.19	0.41
1:D:34:LEU:HD23	1:D:34:LEU:HA	1.60	0.41
1:D:7:LYS:NZ	1:D:435:ALA:N	2.65	0.41
1:E:131:ILE:HG13	1:E:132:LEU:N	2.35	0.41
1:E:170:TYR:CD1	1:E:576:HIS:HB2	2.55	0.41
1:E:59:GLY:N	1:E:152:ASP:HB2	2.35	0.41
1:A:169:ALA:O	1:A:575:ILE:HG23	2.21	0.41
1:A:117:ALA:HA	1:A:222:PRO:HG2	2.02	0.41
1:A:590:GLU:O	1:A:740:ARG:NH2	2.54	0.41
1:B:314:SER:HA	1:B:317:ILE:O	2.20	0.41
1:C:138:LEU:HA	1:C:138:LEU:HD23	1.88	0.41
1:C:191:ARG:O	1:C:194:ASP:HB2	2.21	0.41
1:C:259:ARG:O	1:C:265:THR:HG22	2.20	0.41
1:C:528:ILE:H	1:C:528:ILE:HG13	1.68	0.41
1:C:542:THR:HA	1:C:543:PRO:HD3	1.86	0.41
1:D:82:VAL:HG12	1:D:188:ASP:CG	2.41	0.41
1:D:493:TYR:HD2	1:D:549:ILE:HD13	1.84	0.41
1:E:18:GLN:N	1:E:544:GLU:OE2	2.32	0.41
1:B:87:ASN:ND2	1:E:618:ARG:NH2	2.69	0.41
1:E:733:GLN:HE21	1:E:743:ALA:HB3	1.86	0.41
1:A:191:ARG:HA	1:A:191:ARG:HD2	1.82	0.41
1:A:227:GLN:HG2	1:B:167:ASP:HB2	2.01	0.41
1:A:228:HIS:ND1	1:A:229:LEU:HD23	2.36	0.41
1:A:619:GLU:CD	1:A:619:GLU:H	2.24	0.41
1:B:453:ARG:NH2	1:B:475:ALA:HA	2.36	0.41
1:B:611:LEU:HD23	1:B:611:LEU:HA	1.92	0.41
1:B:683:THR:HG22	1:B:724:ARG:NH1	2.36	0.41
1:C:213:THR:HG23	1:C:214:PHE:CD1	2.56	0.41
1:C:329:SER:HA	1:C:330:PRO:HD2	1.76	0.41
1:C:431:ASN:O	1:C:432:SER:HB2	2.20	0.41
1:C:534:ALA:CB	1:C:536:GLU:HB2	2.50	0.41
1:D:127:PRO:HA	1:D:128:PRO:HD3	1.85	0.41
1:A:369:GLU:O	1:A:370:ILE:HD13	2.21	0.41
1:A:7:LYS:HZ2	1:A:435:ALA:H	1.66	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:127:PRO:HA	1:B:128:PRO:HD3	1.91	0.41
1:B:183:PHE:HB3	1:B:296:ASP:OD2	2.21	0.41
1:B:210:LEU:HD21	1:B:228:HIS:NE2	2.35	0.41
1:B:222:PRO:O	1:B:225:ILE:HG13	2.21	0.41
1:B:575:ILE:HG22	1:B:576:HIS:O	2.20	0.41
1:B:615:GLY:HA2	1:B:616:GLN:O	2.20	0.41
1:C:66:TYR:OH	1:C:152:ASP:OD2	2.38	0.41
1:C:340:THR:HG21	1:C:493:TYR:HA	2.03	0.41
1:E:540:ILE:HG21	1:E:551:TYR:CE2	2.56	0.41
1:E:609:PHE:CE1	1:E:610:GLU:HG2	2.56	0.41
1:E:733:GLN:HE21	1:E:743:ALA:CB	2.34	0.41
1:A:127:PRO:HA	1:A:128:PRO:HD3	1.67	0.41
1:B:707:LEU:HD23	1:B:707:LEU:HA	1.75	0.41
1:C:41:THR:HG22	1:C:286:SER:OG	2.21	0.41
1:C:619:GLU:CD	1:C:619:GLU:H	2.23	0.41
1:D:210:LEU:O	1:D:213:THR:HG22	2.21	0.41
1:D:259:ARG:O	1:D:265:THR:HG22	2.21	0.41
1:D:637:TYR:CE1	1:D:742:GLU:HB2	2.55	0.41
1:A:34:LEU:HD22	1:A:35:GLN:CD	2.41	0.41
1:A:499:PRO:O	1:A:501:VAL:HG22	2.21	0.41
1:A:589:TYR:CE2	1:A:591:ASP:HB2	2.56	0.41
1:C:330:PRO:HG2	1:C:331:PHE:CD2	2.56	0.41
1:C:33:ALA:O	1:C:34:LEU:HD23	2.21	0.41
1:C:545:PRO:O	1:C:549:ILE:HG13	2.21	0.41
1:E:207:SER:O	1:E:210:LEU:HB3	2.21	0.41
1:A:111:THR:HG21	1:A:123:VAL:HG13	2.03	0.40
1:A:171:VAL:HG12	1:A:576:HIS:O	2.21	0.40
1:B:378:LEU:HG	1:B:378:LEU:H	1.60	0.40
1:B:637:TYR:CD1	1:B:746:LEU:HD13	2.56	0.40
1:B:82:VAL:HG12	1:B:188:ASP:CG	2.41	0.40
1:A:738:LEU:HA	1:A:738:LEU:HD23	1.83	0.40
1:B:677:LYS:O	1:B:681:ILE:HG13	2.21	0.40
1:C:17:THR:O	1:C:20:PHE:HB3	2.22	0.40
1:C:580:TRP:CE3	1:C:581:HIS:HA	2.56	0.40
1:D:228:HIS:CE1	1:D:229:LEU:HD23	2.55	0.40
1:D:428:GLY:HA3	1:D:429:THR:HG23	2.04	0.40
1:E:254:LEU:HA	1:E:254:LEU:HD23	1.88	0.40
1:E:447:ARG:HD2	1:E:447:ARG:HA	1.79	0.40
1:E:580:TRP:CE3	1:E:581:HIS:HA	2.56	0.40
1:E:7:LYS:HD3	1:E:434:GLY:HA3	2.02	0.40
1:A:314:SER:HA	1:A:317:ILE:C	2.42	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:ARG:HB3	1:A:334:ARG:O	2.21	0.40
1:A:348:ALA:O	1:A:355:PRO:HA	2.21	0.40
1:A:622:ARG:O	1:A:623:ILE:HD12	2.21	0.40
1:C:287:ASN:HB3	1:C:290:LEU:HD22	2.02	0.40
1:D:263:PRO:HG3	1:D:504:SER:HA	2.02	0.40
1:D:36:LEU:HD23	1:D:37:PRO:O	2.21	0.40
1:E:363:ASP:O	1:E:561:LEU:HB3	2.21	0.40
1:A:126:VAL:O	1:A:165:LEU:HG	2.21	0.40
1:A:431:ASN:O	1:A:432:SER:HB2	2.21	0.40
1:A:681:ILE:H	1:A:681:ILE:HG13	1.70	0.40
1:C:195:LEU:O	1:C:199:LEU:HG	2.22	0.40
1:C:402:ALA:HB3	1:C:403:PRO:HD3	2.03	0.40
1:D:131:ILE:HD11	1:D:151:THR:OG1	2.22	0.40
1:D:707:LEU:HD23	1:D:707:LEU:HA	1.78	0.40
1:A:59:GLY:HA2	1:A:152:ASP:HB2	2.03	0.40
1:B:36:LEU:HD13	1:B:263:PRO:HA	2.03	0.40
1:C:235:THR:HA	1:C:238:GLU:HG2	2.03	0.40
1:C:30:SER:HB3	1:C:517:TYR:CE2	2.57	0.40
1:C:59:GLY:HA3	1:C:60:ASN:HA	1.84	0.40
1:D:111:THR:HA	1:D:112:GLY:HA2	1.78	0.40
1:D:534:ALA:H	1:D:540:ILE:HD11	1.85	0.40
1:D:390:GLU:OE1	1:D:618:ARG:NH1	2.55	0.40
1:D:71:PHE:CD2	1:D:330:PRO:HG3	2.57	0.40
1:E:66:TYR:OH	1:E:152:ASP:OD2	2.40	0.40
1:E:336:ILE:O	1:E:339:THR:HG22	2.21	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:523:ARG:O	1:D:523:ARG:NH2[8_455]	2.12	0.08
1:D:655:ARG:O	1:E:27:ASN:ND2[4_555]	2.18	0.02

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	758/775 (98%)	717 (95%)	41 (5%)	0	100	100
1	B	758/775 (98%)	720 (95%)	38 (5%)	0	100	100
1	C	758/775 (98%)	718 (95%)	40 (5%)	0	100	100
1	D	758/775 (98%)	717 (95%)	41 (5%)	0	100	100
1	E	758/775 (98%)	722 (95%)	35 (5%)	1 (0%)	51	83
All	All	3790/3875 (98%)	3594 (95%)	195 (5%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	61	ILE

5.3.2 Protein sidechains ⓘ

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	618/643 (96%)	575 (93%)	43 (7%)	15	48
1	B	618/643 (96%)	576 (93%)	42 (7%)	16	50
1	C	618/643 (96%)	579 (94%)	39 (6%)	18	53
1	D	618/643 (96%)	572 (93%)	46 (7%)	13	46
1	E	618/643 (96%)	569 (92%)	49 (8%)	12	44
All	All	3090/3215 (96%)	2871 (93%)	219 (7%)	14	48

All (219) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	25	LEU
1	A	29	LEU
1	A	41	THR

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Mol	Chain	Res	Type
1	A	71	PHE
1	A	73	TYR
1	A	82	VAL
1	A	86	VAL
1	A	131	ILE
1	A	141	SER
1	A	154	VAL
1	A	159	SER
1	A	161	LEU
1	A	163	PHE
1	A	171	VAL
1	A	206	ASP
1	A	210	LEU
1	A	256	ILE
1	A	306	VAL
1	A	309	SER
1	A	316	THR
1	A	317	ILE
1	A	359	VAL
1	A	366	PHE
1	A	371	THR
1	A	378	LEU
1	A	380	ASN
1	A	389	VAL
1	A	394	SER
1	A	429	THR
1	A	439	LEU
1	A	471	LEU
1	A	518	LEU
1	A	524	THR
1	A	526	LEU
1	A	532	TYR
1	A	553	LYS
1	A	614	LEU
1	A	628	VAL
1	A	643	ASP
1	A	684	THR
1	A	716	VAL
1	A	748	LYS
1	B	4	LEU
1	B	25	LEU
1	B	29	LEU

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Mol	Chain	Res	Type
1	B	41	THR
1	B	48	MET
1	B	71	PHE
1	B	82	VAL
1	B	131	ILE
1	B	141	SER
1	B	154	VAL
1	B	159	SER
1	B	163	PHE
1	B	171	VAL
1	B	210	LEU
1	B	306	VAL
1	B	309	SER
1	B	317	ILE
1	B	358	VAL
1	B	359	VAL
1	B	366	PHE
1	B	371	THR
1	B	374	THR
1	B	378	LEU
1	B	380	ASN
1	B	381	ASN
1	B	394	SER
1	B	429	THR
1	B	439	LEU
1	B	471	LEU
1	B	518	LEU
1	B	524	THR
1	B	526	LEU
1	B	532	TYR
1	B	533	ASN
1	B	553	LYS
1	B	614	LEU
1	B	628	VAL
1	B	634	GLN
1	B	684	THR
1	B	707	LEU
1	B	716	VAL
1	B	748	LYS
1	C	25	LEU
1	C	29	LEU
1	C	41	THR

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Mol	Chain	Res	Type
1	C	71	PHE
1	C	73	TYR
1	C	82	VAL
1	C	131	ILE
1	C	141	SER
1	C	154	VAL
1	C	159	SER
1	C	163	PHE
1	C	171	VAL
1	C	210	LEU
1	C	306	VAL
1	C	309	SER
1	C	316	THR
1	C	317	ILE
1	C	359	VAL
1	C	366	PHE
1	C	371	THR
1	C	374	THR
1	C	378	LEU
1	C	380	ASN
1	C	381	ASN
1	C	389	VAL
1	C	394	SER
1	C	429	THR
1	C	439	LEU
1	C	518	LEU
1	C	524	THR
1	C	526	LEU
1	C	532	TYR
1	C	553	LYS
1	C	614	LEU
1	C	628	VAL
1	C	684	THR
1	C	707	LEU
1	C	716	VAL
1	C	748	LYS
1	D	25	LEU
1	D	29	LEU
1	D	41	THR
1	D	48	MET
1	D	61	ILE
1	D	71	PHE

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Mol	Chain	Res	Type
1	D	73	TYR
1	D	82	VAL
1	D	131	ILE
1	D	141	SER
1	D	154	VAL
1	D	159	SER
1	D	163	PHE
1	D	171	VAL
1	D	210	LEU
1	D	306	VAL
1	D	309	SER
1	D	316	THR
1	D	317	ILE
1	D	359	VAL
1	D	366	PHE
1	D	371	THR
1	D	374	THR
1	D	378	LEU
1	D	380	ASN
1	D	381	ASN
1	D	389	VAL
1	D	394	SER
1	D	429	THR
1	D	439	LEU
1	D	471	LEU
1	D	497	HIS
1	D	524	THR
1	D	525	GLU
1	D	526	LEU
1	D	532	TYR
1	D	553	LYS
1	D	576	HIS
1	D	614	LEU
1	D	624	LEU
1	D	628	VAL
1	D	643	ASP
1	D	684	THR
1	D	705	ARG
1	D	707	LEU
1	D	748	LYS
1	E	4	LEU
1	E	25	LEU

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Mol	Chain	Res	Type
1	E	29	LEU
1	E	41	THR
1	E	48	MET
1	E	60	ASN
1	E	71	PHE
1	E	73	TYR
1	E	82	VAL
1	E	86	VAL
1	E	131	ILE
1	E	149	ILE
1	E	154	VAL
1	E	159	SER
1	E	161	LEU
1	E	164	ILE
1	E	167	ASP
1	E	171	VAL
1	E	202	LEU
1	E	210	LEU
1	E	256	ILE
1	E	306	VAL
1	E	309	SER
1	E	312	GLU
1	E	317	ILE
1	E	366	PHE
1	E	371	THR
1	E	374	THR
1	E	378	LEU
1	E	380	ASN
1	E	381	ASN
1	E	394	SER
1	E	429	THR
1	E	439	LEU
1	E	464	THR
1	E	471	LEU
1	E	518	LEU
1	E	524	THR
1	E	526	LEU
1	E	533	ASN
1	E	553	LYS
1	E	614	LEU
1	E	624	LEU
1	E	628	VAL

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Mol	Chain	Res	Type
1	E	643	ASP
1	E	684	THR
1	E	705	ARG
1	E	707	LEU
1	E	716	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	533	ASN
1	B	228	HIS
1	D	228	HIS
1	E	156	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	760/775 (98%)	-0.24	20 (2%)	56	40	130, 172, 242, 296	0
1	B	760/775 (98%)	-0.20	20 (2%)	56	40	125, 172, 241, 296	0
1	C	760/775 (98%)	-0.21	26 (3%)	45	30	123, 170, 243, 295	0
1	D	760/775 (98%)	-0.20	23 (3%)	50	34	122, 169, 241, 293	0
1	E	760/775 (98%)	-0.20	18 (2%)	59	42	122, 168, 241, 296	0
All	All	3800/3875 (98%)	-0.21	107 (2%)	53	37	122, 171, 241, 296	0

All (107) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	425	SER	6.3
1	D	529	PRO	5.4
1	D	161	LEU	5.2
1	C	529	PRO	5.1
1	B	426	GLN	4.9
1	A	424	VAL	4.8
1	C	511	ALA	4.8
1	E	529	PRO	4.4
1	C	427	ARG	4.4
1	B	529	PRO	4.2
1	D	433	ASN	4.1
1	A	209	MET	4.1
1	E	424	VAL	4.0
1	C	428	GLY	4.0
1	B	205	VAL	3.9
1	A	166	PRO	3.8
1	D	423	ALA	3.8
1	D	427	ARG	3.8
1	C	206	ASP	3.8
1	A	425	SER	3.8

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Mol	Chain	Res	Type	RSRZ
1	C	205	VAL	3.8
1	D	510	ALA	3.8
1	C	166	PRO	3.7
1	D	509	VAL	3.5
1	E	510	ALA	3.5
1	B	424	VAL	3.4
1	B	206	ASP	3.3
1	C	510	ALA	3.3
1	E	114	SER	3.2
1	A	212	ALA	3.2
1	B	212	ALA	3.2
1	C	433	ASN	3.1
1	D	428	GLY	3.1
1	D	425	SER	3.1
1	D	162	GLY	3.1
1	E	526	LEU	3.0
1	E	421	TYR	2.9
1	E	423	ALA	2.9
1	A	208	LYS	2.9
1	C	209	MET	2.8
1	C	352	MET	2.8
1	D	227	GLN	2.8
1	D	424	VAL	2.8
1	D	432	SER	2.8
1	D	431	ASN	2.8
1	A	426	GLN	2.8
1	D	421	TYR	2.8
1	C	421	TYR	2.8
1	D	267	LYS	2.7
1	E	227	GLN	2.7
1	A	534	ALA	2.7
1	C	167	ASP	2.7
1	C	161	LEU	2.7
1	A	122	ALA	2.6
1	E	425	SER	2.6
1	D	571	HIS	2.6
1	B	423	ALA	2.6
1	C	434	GLY	2.6
1	B	572	THR	2.6
1	D	211	GLN	2.6
1	E	352	MET	2.6
1	B	208	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	E	122	ALA	2.5
1	C	429	THR	2.5
1	B	113	SER	2.5
1	B	124	GLY	2.5
1	D	114	SER	2.5
1	A	125	LYS	2.5
1	B	120	ALA	2.5
1	C	426	GLN	2.4
1	A	510	ALA	2.4
1	B	114	SER	2.4
1	C	424	VAL	2.4
1	B	123	VAL	2.4
1	A	511	ALA	2.4
1	A	705	ARG	2.4
1	E	268	GLU	2.3
1	E	660	LYS	2.3
1	B	508	GLY	2.3
1	B	433	ASN	2.3
1	B	657	ASP	2.2
1	C	114	SER	2.2
1	A	428	GLY	2.2
1	C	526	LEU	2.2
1	C	268	GLU	2.2
1	A	160	PRO	2.2
1	A	421	TYR	2.2
1	C	219	ALA	2.2
1	C	705	ARG	2.2
1	B	219	ALA	2.1
1	C	507	GLN	2.1
1	E	351	HIS	2.1
1	A	529	PRO	2.1
1	D	311	GLU	2.1
1	B	534	ALA	2.1
1	A	509	VAL	2.1
1	E	572	THR	2.1
1	E	115	ASN	2.1
1	A	268	GLU	2.1
1	C	431	ASN	2.1
1	D	572	THR	2.1
1	C	227	GLN	2.1
1	D	208	LYS	2.0
1	E	431	ASN	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	209	MET	2.0
1	E	209	MET	2.0
1	A	423	ALA	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.