Full wwPDB X-ray Structure Validation Report (i)

Apr 28, 2024 – 05:41 pm BST

PDB ID	:	2JL9
Title	:	Structural explanation for the role of Mn in the activity of phi6 RNA- dependent RNA polymerase
Authors	:	Poranen, M.M.; Salgado, P.S.; Koivunen, M.R.L.; Wright, S.; Bamford, D.H.; Stuart, D.I.; Grimes, J.M.
Deposited on	:	2008-09-05
Resolution	:	3.20 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

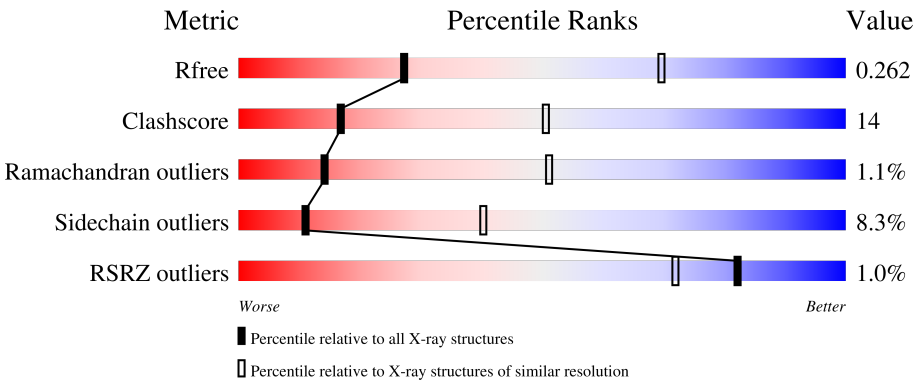
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

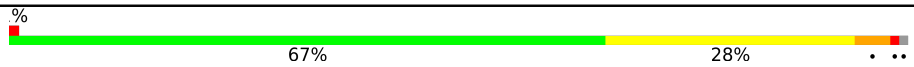
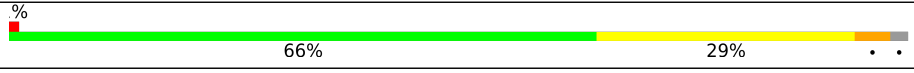
The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 of 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 <=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	665	
1	B	665	
1	C	665	

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 15629 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 RNA-DIRECTED RNA POLYMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	661	5235	3325	906	972	32	0	0	0
1	B	656	5201	3306	897	966	32	0	0	0
1	C	655	5193	3300	896	965	32	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

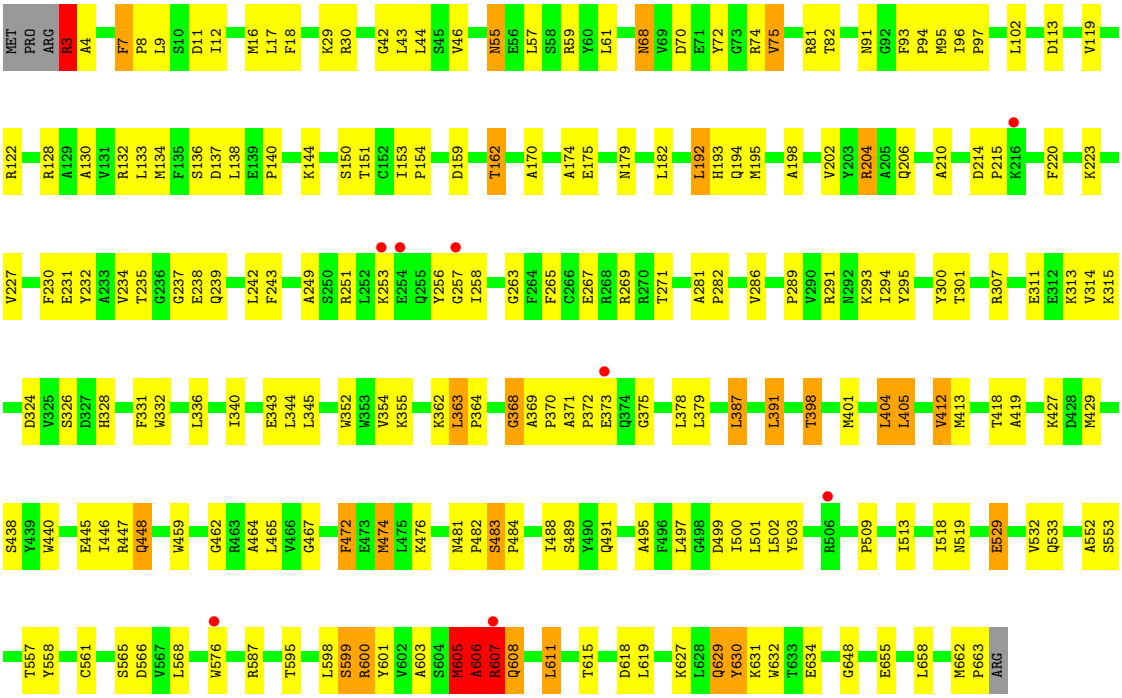
Chain	Residue	Modelled	Actual	Comment	Reference
A	491	GLN	GLU	engineered mutation	UNP P11124
B	491	GLN	GLU	engineered mutation	UNP P11124
C	491	GLN	GLU	engineered mutation	UNP P11124
A	456	MET	ILE	conflict	UNP P11124
B	456	MET	ILE	conflict	UNP P11124
C	456	MET	ILE	conflict	UNP P11124

3 Residue-property plots (i)

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

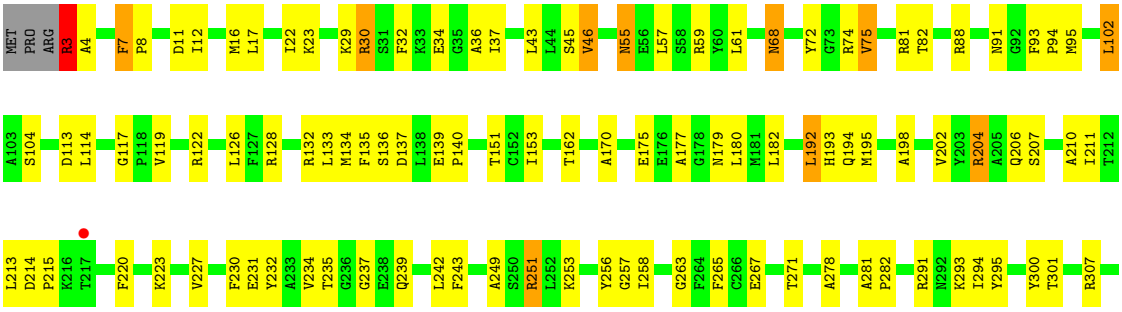
• Molecule 1: RNA-DIRECTED RNA POLYMERASE

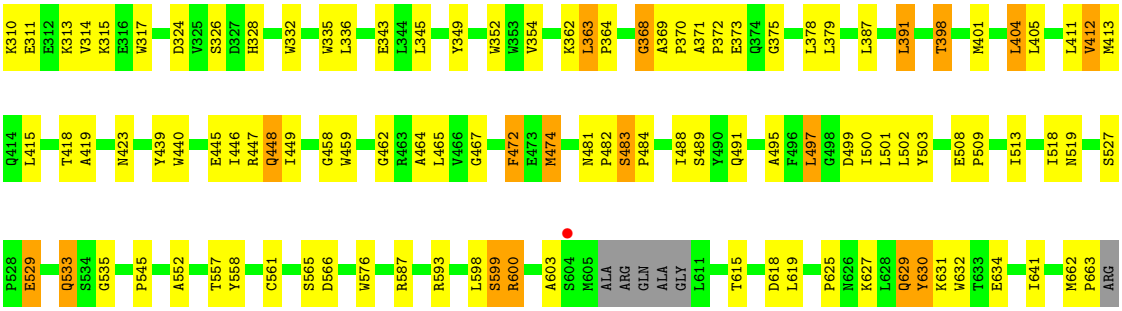
Chain A:



• Molecule 1: RNA-DIRECTED RNA POLYMERASE

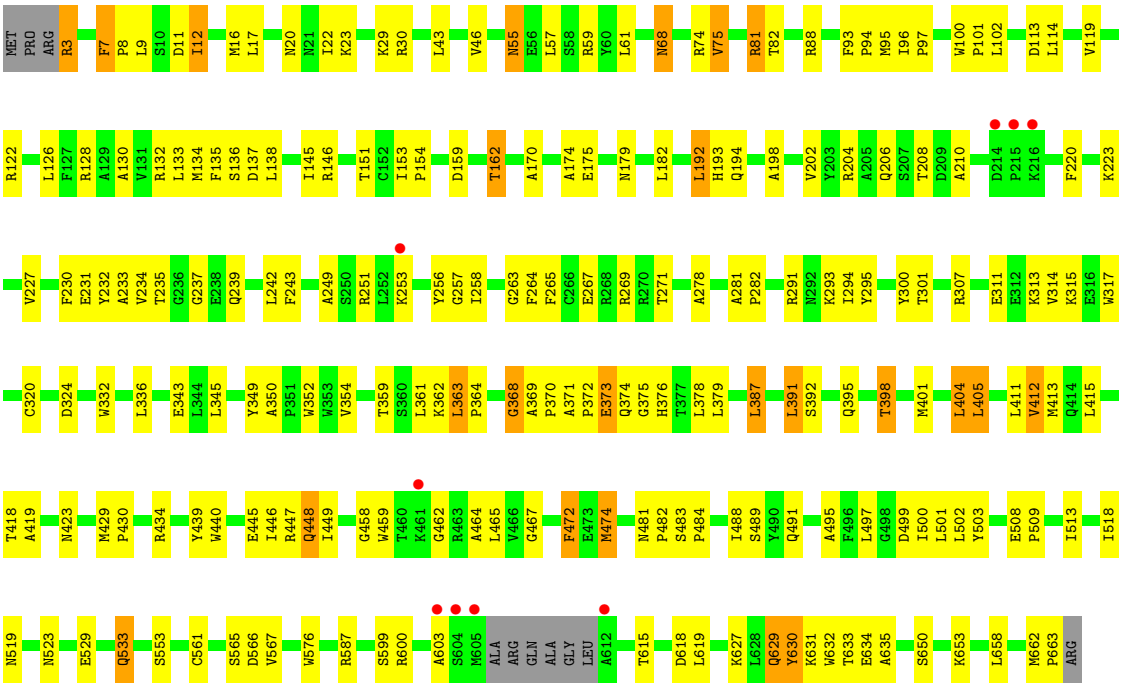
Chain B:





- Molecule 1: RNA-DIRECTED RNA POLYMERASE

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	106.52Å 91.60Å 142.71Å 90.00° 101.64° 90.00°	Depositor
Resolution (Å)	19.91 – 3.20 19.91 – 3.20	Depositor EDS
% Data completeness (in resolution range)	90.1 (19.91-3.20) 90.2 (19.91-3.20)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.95 (at 3.22Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.215 , 0.272 0.205 , 0.262	Depositor DCC
R_{free} test set	2038 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	52.5	Xtriage
Anisotropy	0.137	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 33.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	15629	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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)

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	0.51	0/5365	0.65	1/7258 (0.0%)
1	B	0.50	0/5330	0.65	2/7210 (0.0%)
1	C	0.51	0/5322	0.64	1/7199 (0.0%)
All	All	0.50	0/16017	0.65	4/21667 (0.0%)

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	2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	3	ARG	NE-CZ-NH2	-6.39	117.10	120.30
1	A	3	ARG	NE-CZ-NH2	-6.05	117.27	120.30
1	C	3	ARG	NE-CZ-NH2	-5.51	117.55	120.30
1	B	3	ARG	NE-CZ-NH1	5.26	122.93	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	605	MET	Peptide
1	A	606	ALA	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5235	0	5131	153	0
1	B	5201	0	5096	141	0
1	C	5193	0	5085	148	0
All	All	15629	0	15312	435	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 14.

All (435) 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:A:605:MET:O	1:A:606:ALA:HB3	1.75	0.87
1:A:607:ARG:O	1:A:608:GLN:HB2	1.81	0.81
1:B:465:LEU:HD12	1:B:465:LEU:O	1.80	0.81
1:A:122:ARG:HH21	1:C:20:ASN:ND2	1.77	0.81
1:C:553:SER:HB3	1:C:619:LEU:HD12	1.68	0.75
1:A:605:MET:O	1:A:606:ALA:CB	2.34	0.75
1:A:465:LEU:HD12	1:A:465:LEU:O	1.87	0.74
1:A:599:SER:CB	1:A:606:ALA:HA	2.18	0.73
1:A:553:SER:HB3	1:A:619:LEU:HD12	1.71	0.73
1:A:74:ARG:HB3	1:A:503:TYR:CD2	2.24	0.72
1:A:122:ARG:NH2	1:C:20:ASN:ND2	2.38	0.71
1:C:133:LEU:O	1:C:293:LYS:HE2	1.90	0.71
1:C:57:LEU:HD12	1:C:57:LEU:O	1.91	0.70
1:C:465:LEU:HD12	1:C:465:LEU:O	1.91	0.69
1:C:74:ARG:HB3	1:C:503:TYR:CD2	2.27	0.69
1:A:57:LEU:HD12	1:A:57:LEU:O	1.93	0.68
1:B:133:LEU:O	1:B:293:LYS:HE2	1.94	0.68
1:B:495:ALA:HB1	1:B:499:ASP:O	1.94	0.68
1:A:599:SER:HB2	1:A:606:ALA:HA	1.75	0.67
1:C:132:ARG:NH1	1:C:343:GLU:OE2	2.27	0.67
1:C:281:ALA:HB3	1:C:282:PRO:HD3	1.78	0.66
1:B:88:ARG:HB2	1:B:211:ILE:HD12	1.77	0.66
1:C:179:ASN:HA	1:C:182:LEU:HD12	1.78	0.66
1:A:8:PRO:HD2	1:A:11:ASP:HB2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:132:ARG:O	1:B:136:SER:HB3	1.96	0.65
1:B:8:PRO:HD2	1:B:11:ASP:HB2	1.78	0.65
1:C:95:MET:CE	1:C:269:ARG:H	2.09	0.65
1:B:74:ARG:HB3	1:B:503:TYR:CD2	2.32	0.65
1:A:130:ALA:HB1	1:A:404:LEU:HD13	1.79	0.64
1:A:553:SER:HB3	1:A:619:LEU:HB2	1.79	0.64
1:C:391:LEU:HD22	1:C:398:THR:HG22	1.79	0.64
1:B:404:LEU:O	1:B:404:LEU:HD12	1.97	0.64
1:B:281:ALA:HB3	1:B:282:PRO:HD3	1.79	0.64
1:C:301:THR:HG22	1:C:448:GLN:O	1.98	0.63
1:C:8:PRO:HD2	1:C:11:ASP:HB2	1.79	0.62
1:A:391:LEU:HD22	1:A:398:THR:HG22	1.81	0.62
1:A:42:GLY:HA2	1:B:256:TYR:O	1.99	0.62
1:A:301:THR:HG22	1:A:448:GLN:O	2.00	0.62
1:B:301:THR:HG22	1:B:448:GLN:O	1.99	0.62
1:A:132:ARG:O	1:A:136:SER:HB3	2.00	0.62
1:A:607:ARG:O	1:A:608:GLN:CB	2.48	0.62
1:C:518:ILE:HB	1:C:561:CYS:SG	2.40	0.62
1:A:132:ARG:NH1	1:A:343:GLU:OE2	2.33	0.61
1:C:138:LEU:HD12	1:C:662:MET:SD	2.40	0.61
1:A:179:ASN:HA	1:A:182:LEU:HD12	1.83	0.61
1:A:253:LYS:O	1:A:257:GLY:HA2	2.01	0.61
1:B:17:LEU:O	1:B:153:ILE:HG23	2.01	0.61
1:C:132:ARG:O	1:C:136:SER:HB3	2.00	0.61
1:B:198:ALA:HA	1:B:363:LEU:HD23	1.82	0.61
1:A:232:TYR:CE2	1:A:237:GLY:HA2	2.36	0.60
1:A:599:SER:HB3	1:A:606:ALA:HA	1.83	0.59
1:C:210:ALA:HB3	1:C:223:LYS:HB2	1.84	0.59
1:C:17:LEU:O	1:C:153:ILE:HG23	2.02	0.59
1:C:253:LYS:O	1:C:257:GLY:HA2	2.02	0.59
1:B:134:MET:HG2	1:B:294:ILE:HG21	1.85	0.59
1:C:198:ALA:HA	1:C:363:LEU:HD23	1.85	0.59
1:C:74:ARG:HB3	1:C:503:TYR:HD2	1.68	0.58
1:C:364:PRO:HB3	1:C:379:LEU:O	2.03	0.58
1:A:130:ALA:CB	1:A:404:LEU:HD13	2.34	0.58
1:B:405:LEU:O	1:B:405:LEU:HG	2.01	0.58
1:C:495:ALA:HB1	1:C:499:ASP:O	2.04	0.58
1:B:364:PRO:HB3	1:B:379:LEU:O	2.04	0.58
1:B:391:LEU:HD22	1:B:398:THR:HG22	1.86	0.57
1:C:404:LEU:HD12	1:C:404:LEU:O	2.04	0.57
1:B:253:LYS:O	1:B:257:GLY:HA2	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:114:LEU:HA	1:B:484:PRO:O	2.04	0.57
1:B:495:ALA:CB	1:B:500:ILE:HA	2.34	0.57
1:B:419:ALA:HB2	1:B:464:ALA:HB2	1.87	0.57
1:A:210:ALA:HB3	1:A:223:LYS:HB2	1.86	0.56
1:A:446:ILE:O	1:A:447:ARG:HG3	2.04	0.56
1:B:132:ARG:NH1	1:B:343:GLU:OE2	2.37	0.56
1:C:553:SER:HB3	1:C:619:LEU:CD1	2.34	0.56
1:B:179:ASN:HA	1:B:182:LEU:HD12	1.87	0.56
1:C:101:PRO:O	1:C:233:ALA:HB1	2.05	0.56
1:A:552:ALA:HB3	1:A:619:LEU:HD13	1.88	0.56
1:A:220:PHE:CD2	1:A:263:GLY:HA3	2.40	0.56
1:A:404:LEU:HD12	1:A:404:LEU:O	2.06	0.56
1:A:662:MET:HB3	1:A:663:PRO:CD	2.36	0.56
1:B:55:ASN:HD21	1:B:59:ARG:HE	1.51	0.56
1:A:227:VAL:HG22	1:A:243:PHE:O	2.06	0.56
1:B:336:LEU:HD23	1:B:405:LEU:HB2	1.88	0.55
1:B:495:ALA:HB2	1:B:500:ILE:HA	1.87	0.55
1:A:495:ALA:HB1	1:A:499:ASP:O	2.07	0.55
1:C:662:MET:HB3	1:C:663:PRO:CD	2.37	0.55
1:A:132:ARG:HD2	1:A:429:MET:CE	2.37	0.55
1:C:391:LEU:CD2	1:C:398:THR:HG22	2.37	0.55
1:A:553:SER:HB3	1:A:619:LEU:CD1	2.37	0.55
1:B:227:VAL:HG22	1:B:243:PHE:O	2.07	0.55
1:A:391:LEU:CD2	1:A:398:THR:HG22	2.37	0.55
1:B:122:ARG:NH1	1:B:423:ASN:OD1	2.40	0.55
1:C:232:TYR:CE2	1:C:237:GLY:HA2	2.43	0.54
1:C:301:THR:HG23	1:C:440:TRP:O	2.08	0.54
1:A:29:LYS:O	1:A:30:ARG:C	2.46	0.54
1:C:194:GLN:O	1:C:278:ALA:HB3	2.08	0.54
1:C:488:ILE:HG22	1:C:489:SER:N	2.23	0.54
1:A:629:GLN:O	1:A:630:TYR:HB3	2.08	0.54
1:C:194:GLN:HB2	1:C:278:ALA:HB2	1.89	0.54
1:B:57:LEU:O	1:B:57:LEU:HD12	2.08	0.53
1:B:495:ALA:HB2	1:B:500:ILE:HG12	1.91	0.53
1:B:175:GLU:HA	1:B:352:TRP:CE3	2.44	0.53
1:B:232:TYR:CE2	1:B:237:GLY:HA2	2.43	0.53
1:C:446:ILE:O	1:C:447:ARG:HG3	2.08	0.53
1:A:281:ALA:HB3	1:A:282:PRO:HD3	1.90	0.53
1:A:198:ALA:HA	1:A:363:LEU:HD23	1.90	0.53
1:B:210:ALA:HB3	1:B:223:LYS:HB2	1.91	0.53
1:C:249:ALA:HB2	1:C:265:PHE:HA	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:ARG:NH2	1:A:529:GLU:OE2	2.42	0.52
1:C:615:THR:O	1:C:618:ASP:HB2	2.09	0.52
1:A:17:LEU:O	1:A:153:ILE:HG23	2.09	0.52
1:B:68:ASN:N	1:B:68:ASN:HD22	2.07	0.52
1:A:340:ILE:O	1:A:344:LEU:HD12	2.10	0.52
1:A:336:LEU:HD23	1:A:405:LEU:HB2	1.91	0.52
1:A:488:ILE:HG22	1:A:489:SER:N	2.25	0.52
1:C:29:LYS:O	1:C:30:ARG:C	2.48	0.52
1:A:518:ILE:HB	1:A:561:CYS:SG	2.50	0.52
1:B:518:ILE:HB	1:B:561:CYS:SG	2.49	0.52
1:C:227:VAL:HG22	1:C:243:PHE:O	2.10	0.52
1:C:95:MET:HE3	1:C:269:ARG:H	1.75	0.52
1:C:17:LEU:HD11	1:C:378:LEU:HD13	1.92	0.52
1:B:391:LEU:CD2	1:B:398:THR:HG22	2.39	0.52
1:A:133:LEU:O	1:A:293:LYS:HE2	2.10	0.51
1:A:418:THR:HG22	1:A:467:GLY:C	2.29	0.51
1:C:392:SER:O	1:C:398:THR:CG2	2.58	0.51
1:A:175:GLU:HA	1:A:352:TRP:CE3	2.45	0.51
1:B:220:PHE:CD2	1:B:263:GLY:HA3	2.46	0.51
1:C:175:GLU:HA	1:C:352:TRP:CE3	2.45	0.51
1:A:81:ARG:O	1:A:82:THR:HB	2.10	0.51
1:A:495:ALA:HB2	1:A:500:ILE:HA	1.92	0.51
1:B:411:LEU:HB2	1:B:439:TYR:CE1	2.46	0.51
1:A:68:ASN:N	1:A:68:ASN:HD22	2.08	0.51
1:A:194:GLN:CD	1:A:194:GLN:N	2.64	0.51
1:C:88:ARG:HA	1:C:264:PHE:CE2	2.45	0.51
1:C:55:ASN:HD21	1:C:59:ARG:HE	1.58	0.51
1:A:94:PRO:HB3	1:A:269:ARG:HG3	1.92	0.51
1:B:445:GLU:OE2	1:B:462:GLY:HA3	2.10	0.51
1:C:95:MET:HE2	1:C:269:ARG:H	1.76	0.51
1:C:68:ASN:HD22	1:C:68:ASN:N	2.08	0.51
1:C:192:LEU:C	1:C:193:HIS:CG	2.84	0.51
1:C:220:PHE:CD2	1:C:263:GLY:HA3	2.45	0.51
1:C:336:LEU:HD23	1:C:405:LEU:HB2	1.93	0.51
1:C:495:ALA:HB2	1:C:500:ILE:HA	1.93	0.51
1:C:629:GLN:O	1:C:630:TYR:HB3	2.09	0.51
1:A:74:ARG:HB3	1:A:503:TYR:HD2	1.74	0.50
1:B:194:GLN:N	1:B:194:GLN:CD	2.64	0.50
1:A:336:LEU:O	1:A:336:LEU:HD12	2.12	0.50
1:C:128:ARG:O	1:C:132:ARG:HG3	2.11	0.50
1:C:136:SER:OG	1:C:137:ASP:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:404:LEU:HD12	1:B:404:LEU:C	2.31	0.50
1:C:231:GLU:O	1:C:235:THR:HG23	2.12	0.50
1:A:495:ALA:CB	1:A:500:ILE:HA	2.42	0.50
1:B:192:LEU:C	1:B:193:HIS:CG	2.85	0.50
1:A:332:TRP:CZ2	1:A:401:MET:HB3	2.46	0.50
1:B:488:ILE:HG22	1:B:489:SER:N	2.27	0.50
1:B:207:SER:HB2	1:B:527:SER:HB3	1.93	0.49
1:C:405:LEU:O	1:C:405:LEU:HG	2.08	0.49
1:B:662:MET:HB3	1:B:663:PRO:CD	2.42	0.49
1:C:94:PRO:HB3	1:C:269:ARG:HG3	1.94	0.49
1:C:495:ALA:CB	1:C:500:ILE:HA	2.42	0.49
1:A:17:LEU:HB3	1:A:153:ILE:HD13	1.95	0.49
1:B:75:VAL:HG13	1:B:501:LEU:O	2.12	0.49
1:A:364:PRO:HB3	1:A:379:LEU:O	2.13	0.49
1:C:134:MET:HG2	1:C:294:ILE:HG21	1.93	0.49
1:B:3:ARG:HD3	1:B:4:ALA:H	1.77	0.49
1:B:332:TRP:CZ2	1:B:401:MET:HB3	2.47	0.49
1:B:446:ILE:O	1:B:447:ARG:HG3	2.12	0.49
1:B:231:GLU:O	1:B:235:THR:HG23	2.11	0.49
1:B:301:THR:HG23	1:B:440:TRP:O	2.12	0.49
1:B:310:LYS:NZ	1:B:499:ASP:OD2	2.38	0.49
1:C:495:ALA:HB2	1:C:500:ILE:HG12	1.95	0.49
1:A:301:THR:HG23	1:A:440:TRP:O	2.13	0.49
1:A:446:ILE:C	1:A:447:ARG:HG3	2.34	0.49
1:C:419:ALA:HB2	1:C:464:ALA:HB2	1.95	0.49
1:A:324:ASP:HB2	1:A:491:GLN:HG2	1.95	0.48
1:B:204:ARG:NH2	1:B:529:GLU:OE2	2.46	0.48
1:C:95:MET:HG2	1:C:267:GLU:O	2.12	0.48
1:C:311:GLU:OE1	1:C:513:ILE:HG22	2.13	0.48
1:A:170:ALA:O	1:A:174:ALA:HB2	2.13	0.48
1:B:46:VAL:HG11	1:B:93:PHE:HE1	1.77	0.48
1:A:446:ILE:HG22	1:A:459:TRP:CD1	2.49	0.48
1:B:265:PHE:CD1	1:B:265:PHE:N	2.82	0.48
1:B:474:MET:O	1:B:474:MET:HG3	2.11	0.48
1:C:445:GLU:OE2	1:C:462:GLY:HA3	2.14	0.48
1:C:95:MET:HE2	1:C:269:ARG:N	2.28	0.48
1:C:114:LEU:HA	1:C:484:PRO:O	2.13	0.48
1:A:138:LEU:HD12	1:A:662:MET:SD	2.54	0.48
1:A:314:VAL:HG12	1:A:314:VAL:O	2.13	0.48
1:A:300:TYR:HA	1:A:313:LYS:HE2	1.96	0.47
1:B:412:VAL:HG12	1:B:413:MET:N	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:133:LEU:N	1:C:133:LEU:HD23	2.29	0.47
1:A:95:MET:C	1:A:96:ILE:HD13	2.34	0.47
1:A:95:MET:O	1:A:96:ILE:HD13	2.15	0.47
1:A:220:PHE:HD2	1:A:263:GLY:HA3	1.78	0.47
1:A:404:LEU:HD12	1:A:404:LEU:C	2.35	0.47
1:A:495:ALA:HB2	1:A:500:ILE:HG12	1.95	0.47
1:C:7:PHE:CD1	1:C:7:PHE:N	2.81	0.47
1:C:130:ALA:CB	1:C:404:LEU:HD13	2.45	0.47
1:C:22:ILE:O	1:C:23:LYS:C	2.52	0.47
1:C:230:PHE:O	1:C:234:VAL:HG22	2.14	0.47
1:A:9:LEU:O	1:A:9:LEU:HD12	2.14	0.47
1:A:136:SER:OG	1:A:137:ASP:N	2.47	0.47
1:B:641:ILE:HD13	1:B:641:ILE:HA	1.70	0.47
1:C:336:LEU:O	1:C:336:LEU:HD12	2.15	0.47
1:C:369:ALA:HA	1:C:370:PRO:HD3	1.73	0.47
1:C:418:THR:HG22	1:C:467:GLY:C	2.35	0.47
1:A:231:GLU:O	1:A:235:THR:HG23	2.14	0.47
1:B:629:GLN:O	1:B:630:TYR:HB3	2.14	0.47
1:C:130:ALA:HB1	1:C:404:LEU:HD13	1.96	0.47
1:C:132:ARG:HD2	1:C:429:MET:CE	2.45	0.47
1:C:208:THR:HG21	1:C:523:ASN:OD1	2.15	0.47
1:B:345:LEU:HG	1:B:354:VAL:HG11	1.96	0.47
1:C:81:ARG:O	1:C:82:THR:HB	2.15	0.47
1:A:445:GLU:OE2	1:A:462:GLY:HA3	2.14	0.46
1:B:235:THR:HG21	1:B:239:GLN:HB2	1.96	0.46
1:B:122:ARG:HD2	1:B:415:LEU:HD12	1.97	0.46
1:C:88:ARG:O	1:C:264:PHE:HA	2.16	0.46
1:B:3:ARG:HD3	1:B:4:ALA:N	2.31	0.46
1:C:194:GLN:CD	1:C:194:GLN:N	2.67	0.46
1:C:430:PRO:O	1:C:434:ARG:HG3	2.15	0.46
1:C:650:SER:OG	1:C:653:LYS:HG3	2.16	0.46
1:A:7:PHE:CD1	1:A:7:PHE:N	2.82	0.46
1:A:256:TYR:HB2	1:A:258:ILE:HG13	1.97	0.46
1:A:474:MET:HG3	1:A:474:MET:O	2.14	0.46
1:A:595:THR:OG1	1:A:611:LEU:HD21	2.16	0.46
1:C:300:TYR:HA	1:C:313:LYS:HE2	1.97	0.46
1:C:324:ASP:HB2	1:C:491:GLN:HG2	1.98	0.46
1:C:488:ILE:HG22	1:C:489:SER:H	1.80	0.46
1:A:314:VAL:O	1:A:314:VAL:CG1	2.64	0.46
1:B:17:LEU:HB3	1:B:153:ILE:HD13	1.97	0.46
1:B:17:LEU:HD11	1:B:378:LEU:HD13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:345:LEU:HG	1:C:354:VAL:HG11	1.96	0.46
1:C:404:LEU:HD12	1:C:404:LEU:C	2.36	0.46
1:A:17:LEU:HD11	1:A:378:LEU:HD13	1.97	0.46
1:A:192:LEU:C	1:A:193:HIS:CG	2.89	0.46
1:A:568:LEU:HD23	1:A:568:LEU:HA	1.80	0.46
1:A:608:GLN:OE1	1:B:593:ARG:HD2	2.16	0.46
1:B:136:SER:OG	1:B:137:ASP:N	2.49	0.46
1:C:265:PHE:CD1	1:C:265:PHE:N	2.84	0.46
1:C:315:LYS:HA	1:C:509:PRO:O	2.15	0.46
1:A:44:LEU:HD11	1:B:257:GLY:HA3	1.99	0.45
1:B:55:ASN:O	1:B:59:ARG:HG3	2.15	0.45
1:A:631:LYS:HE3	1:A:632:TRP:CZ2	2.51	0.45
1:B:128:ARG:O	1:B:132:ARG:HG3	2.17	0.45
1:C:75:VAL:HG13	1:C:501:LEU:O	2.16	0.45
1:A:405:LEU:O	1:A:405:LEU:HG	2.07	0.45
1:B:29:LYS:O	1:B:30:ARG:C	2.54	0.45
1:B:220:PHE:HD2	1:B:263:GLY:HA3	1.81	0.45
1:C:159:ASP:HB3	1:C:162:THR:OG1	2.16	0.45
1:C:363:LEU:HG	1:C:364:PRO:HD2	1.99	0.45
1:B:363:LEU:HG	1:B:364:PRO:HD2	1.99	0.45
1:C:193:HIS:O	1:C:278:ALA:HB1	2.17	0.45
1:B:34:GLU:OE1	1:B:251:ARG:NH2	2.44	0.45
1:C:291:ARG:O	1:C:295:TYR:CD2	2.70	0.45
1:A:230:PHE:O	1:A:234:VAL:HG22	2.16	0.45
1:C:314:VAL:HG12	1:C:314:VAL:O	2.15	0.45
1:B:91:ASN:HA	1:B:267:GLU:OE1	2.17	0.45
1:A:3:ARG:HD3	1:A:4:ALA:H	1.82	0.45
1:A:412:VAL:HG12	1:A:413:MET:N	2.32	0.45
1:B:300:TYR:HA	1:B:313:LYS:HE2	1.99	0.45
1:B:37:ILE:HG12	1:B:45:SER:HB3	1.99	0.45
1:B:598:LEU:C	1:B:600:ARG:H	2.21	0.45
1:C:631:LYS:HE3	1:C:632:TRP:CZ2	2.52	0.45
1:A:128:ARG:O	1:A:132:ARG:HG3	2.17	0.45
1:B:81:ARG:O	1:B:82:THR:HB	2.16	0.45
1:B:472:PHE:HD1	1:B:472:PHE:O	2.00	0.45
1:A:55:ASN:HD21	1:A:59:ARG:HE	1.63	0.44
1:B:72:TYR:HB3	1:B:472:PHE:CZ	2.52	0.44
1:A:96:ILE:HA	1:A:97:PRO:HA	1.76	0.44
1:A:159:ASP:HB3	1:A:162:THR:OG1	2.17	0.44
1:B:256:TYR:HB2	1:B:258:ILE:HG13	1.99	0.44
1:C:472:PHE:HD1	1:C:472:PHE:O	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:VAL:HG13	1:A:501:LEU:O	2.17	0.44
1:A:557:THR:HG22	1:A:558:TYR:N	2.31	0.44
1:B:336:LEU:HD12	1:B:336:LEU:O	2.17	0.44
1:B:627:LYS:HA	1:B:630:TYR:CE2	2.53	0.44
1:A:605:MET:HG2	1:A:606:ALA:H	1.82	0.44
1:C:235:THR:HG21	1:C:239:GLN:HB2	1.99	0.44
1:C:412:VAL:HG12	1:C:413:MET:N	2.31	0.44
1:A:57:LEU:CD1	1:A:61:LEU:HG	2.48	0.44
1:C:192:LEU:HB3	1:C:193:HIS:NE2	2.33	0.44
1:A:93:PHE:HA	1:A:94:PRO:HD3	1.87	0.44
1:B:230:PHE:O	1:B:234:VAL:HG22	2.17	0.44
1:A:474:MET:HB2	1:A:474:MET:HE2	1.83	0.44
1:A:472:PHE:HD1	1:A:472:PHE:O	2.01	0.44
1:C:17:LEU:HB3	1:C:153:ILE:HD13	2.00	0.44
1:A:286:VAL:O	1:A:289:PRO:HD2	2.17	0.44
1:B:72:TYR:HD1	1:B:472:PHE:CE1	2.36	0.44
1:C:446:ILE:C	1:C:447:ARG:HG3	2.39	0.44
1:A:235:THR:HG21	1:A:239:GLN:HB2	1.99	0.43
1:A:364:PRO:HA	1:A:387:LEU:HD22	1.99	0.43
1:C:411:LEU:HB2	1:C:439:TYR:CE1	2.53	0.43
1:C:502:LEU:HB3	1:C:513:ILE:HG13	2.00	0.43
1:A:368:GLY:O	1:A:375:GLY:HA3	2.16	0.43
1:B:57:LEU:CD1	1:B:61:LEU:HG	2.48	0.43
1:C:9:LEU:O	1:C:9:LEU:HD12	2.19	0.43
1:C:102:LEU:HA	1:C:102:LEU:HD12	1.73	0.43
1:C:368:GLY:O	1:C:375:GLY:HA3	2.19	0.43
1:A:133:LEU:N	1:A:133:LEU:HD23	2.32	0.43
1:A:587:ARG:HA	1:A:587:ARG:HD2	1.82	0.43
1:B:94:PRO:HB2	1:B:95:MET:O	2.18	0.43
1:B:117:GLY:HA2	1:B:335:TRP:CD2	2.53	0.43
1:C:220:PHE:HD2	1:C:263:GLY:HA3	1.84	0.43
1:A:57:LEU:HD12	1:A:61:LEU:HG	2.01	0.43
1:A:265:PHE:N	1:A:265:PHE:CD1	2.86	0.43
1:A:598:LEU:O	1:A:601:TYR:N	2.49	0.43
1:B:249:ALA:HB2	1:B:265:PHE:HA	2.01	0.43
1:B:449:ILE:O	1:B:449:ILE:HG13	2.18	0.43
1:B:587:ARG:HA	1:B:587:ARG:HD2	1.83	0.43
1:C:153:ILE:HA	1:C:154:PRO:HA	1.81	0.43
1:C:364:PRO:HA	1:C:387:LEU:HD22	1.99	0.43
1:A:315:LYS:HA	1:A:509:PRO:O	2.19	0.43
1:C:96:ILE:HD13	1:C:96:ILE:HA	1.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:552:ALA:HB3	1:B:619:LEU:HD13	2.01	0.43
1:C:314:VAL:O	1:C:314:VAL:CG1	2.67	0.43
1:C:627:LYS:HA	1:C:630:TYR:CE2	2.54	0.43
1:A:70:ASP:OD1	1:A:74:ARG:NH1	2.52	0.43
1:A:419:ALA:HB2	1:A:464:ALA:HB2	1.99	0.43
1:A:615:THR:O	1:A:618:ASP:HB2	2.19	0.43
1:B:36:ALA:CB	1:B:46:VAL:HG13	2.49	0.43
1:C:391:LEU:HD11	1:C:398:THR:O	2.19	0.43
1:A:91:ASN:HA	1:A:267:GLU:OE1	2.19	0.42
1:B:598:LEU:C	1:B:600:ARG:N	2.73	0.42
1:B:598:LEU:O	1:B:600:ARG:N	2.52	0.42
1:C:170:ALA:O	1:C:174:ALA:HB2	2.19	0.42
1:B:545:PRO:HD2	1:B:625:PRO:HD3	2.01	0.42
1:A:345:LEU:HG	1:A:354:VAL:HG11	2.00	0.42
1:A:369:ALA:HA	1:A:370:PRO:HD3	1.70	0.42
1:A:501:LEU:HD12	1:A:501:LEU:HA	1.79	0.42
1:B:631:LYS:HE3	1:B:632:TRP:CZ2	2.54	0.42
1:C:122:ARG:HD2	1:C:415:LEU:HD12	2.02	0.42
1:C:395:GLN:HB3	1:C:398:THR:HG23	2.00	0.42
1:A:286:VAL:C	1:A:289:PRO:HD2	2.40	0.42
1:B:418:THR:HG22	1:B:467:GLY:C	2.39	0.42
1:A:483:SER:HA	1:A:484:PRO:HD3	1.79	0.42
1:B:314:VAL:O	1:B:314:VAL:HG12	2.19	0.42
1:B:368:GLY:O	1:B:375:GLY:HA3	2.19	0.42
1:C:446:ILE:HG22	1:C:459:TRP:CD1	2.54	0.42
1:C:587:ARG:HA	1:C:587:ARG:HD2	1.80	0.42
1:B:122:ARG:HD2	1:B:415:LEU:CD1	2.50	0.42
1:C:508:GLU:HA	1:C:509:PRO:HD3	1.85	0.42
1:A:55:ASN:O	1:A:59:ARG:HG3	2.19	0.42
1:B:7:PHE:CD1	1:B:7:PHE:N	2.86	0.42
1:B:126:LEU:HA	1:B:126:LEU:HD23	1.79	0.42
1:B:483:SER:HA	1:B:484:PRO:HD3	1.81	0.42
1:B:615:THR:O	1:B:618:ASP:HB2	2.19	0.42
1:A:140:PRO:HB3	1:A:655:GLU:HA	2.02	0.42
1:B:371:ALA:HB1	1:B:372:PRO:CD	2.50	0.42
1:B:557:THR:HG22	1:B:558:TYR:N	2.35	0.42
1:C:359:THR:C	1:C:361:LEU:H	2.23	0.42
1:A:553:SER:CB	1:A:619:LEU:HB2	2.50	0.42
1:B:170:ALA:HB1	1:B:195:MET:HE3	2.01	0.42
1:B:291:ARG:O	1:B:295:TYR:CD2	2.73	0.42
1:C:122:ARG:NH1	1:C:423:ASN:OD1	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:55:ASN:ND2	1:B:59:ARG:HE	2.17	0.42
1:B:57:LEU:HD12	1:B:61:LEU:HG	2.02	0.42
1:B:102:LEU:HD23	1:B:104:SER:O	2.20	0.42
1:B:177:ALA:O	1:B:180:LEU:HB2	2.19	0.42
1:C:350:ALA:HB1	1:C:352:TRP:NE1	2.34	0.42
1:A:170:ALA:HB1	1:A:195:MET:HE3	2.02	0.41
1:A:311:GLU:CD	1:A:513:ILE:HG22	2.41	0.41
1:A:371:ALA:HB1	1:A:372:PRO:CD	2.51	0.41
1:A:427:LYS:HE3	1:C:12:ILE:CG2	2.50	0.41
1:A:488:ILE:HG22	1:A:489:SER:H	1.83	0.41
1:B:502:LEU:HB3	1:B:513:ILE:HG13	2.02	0.41
1:C:100:TRP:HA	1:C:101:PRO:HD2	1.89	0.41
1:C:481:ASN:HA	1:C:482:PRO:HD2	1.76	0.41
1:A:214:ASP:HA	1:A:215:PRO:HD2	1.95	0.41
1:B:446:ILE:HG22	1:B:459:TRP:CD1	2.55	0.41
1:C:126:LEU:HD23	1:C:126:LEU:HA	1.79	0.41
1:C:332:TRP:CZ2	1:C:401:MET:HB3	2.55	0.41
1:C:474:MET:O	1:C:474:MET:HG3	2.20	0.41
1:A:598:LEU:C	1:A:600:ARG:H	2.23	0.41
1:A:134:MET:HG2	1:A:294:ILE:HG21	2.01	0.41
1:A:144:LYS:HD3	1:A:648:GLY:HA3	2.03	0.41
1:A:627:LYS:HA	1:A:630:TYR:CE2	2.55	0.41
1:B:22:ILE:O	1:B:23:LYS:C	2.58	0.41
1:B:195:MET:HE2	1:B:278:ALA:O	2.20	0.41
1:B:317:TRP:CD2	1:B:458:GLY:HA3	2.56	0.41
1:A:363:LEU:HG	1:A:364:PRO:HD2	2.03	0.41
1:A:418:THR:HG22	1:A:467:GLY:O	2.20	0.41
1:B:311:GLU:OE1	1:B:513:ILE:HG22	2.21	0.41
1:B:518:ILE:HD12	1:B:518:ILE:HA	1.81	0.41
1:C:61:LEU:HD13	1:C:567:VAL:HG22	2.03	0.41
1:B:315:LYS:HA	1:B:509:PRO:O	2.20	0.41
1:A:122:ARG:NH2	1:C:20:ASN:HD22	2.16	0.41
1:B:133:LEU:N	1:B:133:LEU:HD23	2.36	0.41
1:B:446:ILE:C	1:B:447:ARG:HG3	2.41	0.41
1:B:533:GLN:C	1:B:535:GLY:H	2.24	0.41
1:C:317:TRP:HE3	1:C:320:CYS:HB2	1.86	0.41
1:C:371:ALA:HB1	1:C:372:PRO:CD	2.51	0.41
1:C:633:THR:O	1:C:635:ALA:N	2.53	0.41
1:A:72:TYR:CE1	1:A:476:LYS:HD3	2.55	0.41
1:A:291:ARG:O	1:A:295:TYR:CD2	2.74	0.41
1:A:311:GLU:OE1	1:A:513:ILE:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:481:ASN:HA	1:A:482:PRO:HD2	1.79	0.41
1:A:598:LEU:O	1:A:600:ARG:N	2.53	0.41
1:A:598:LEU:C	1:A:600:ARG:N	2.74	0.41
1:B:139:GLU:HA	1:B:140:PRO:HD3	1.82	0.41
1:B:328:HIS:ND1	1:B:328:HIS:C	2.74	0.41
1:B:474:MET:HB2	1:B:474:MET:HE2	1.76	0.41
1:B:533:GLN:O	1:B:535:GLY:N	2.54	0.41
1:C:29:LYS:O	1:C:376:HIS:NE2	2.49	0.41
1:C:373:GLU:O	1:C:374:GLN:HG3	2.21	0.41
1:A:331:PHE:O	1:A:332:TRP:C	2.60	0.41
1:B:481:ASN:HA	1:B:482:PRO:HD2	1.79	0.41
1:B:508:GLU:HA	1:B:509:PRO:HD3	1.86	0.41
1:C:256:TYR:HB2	1:C:258:ILE:HG13	2.02	0.41
1:C:311:GLU:CD	1:C:513:ILE:HG22	2.41	0.41
1:C:317:TRP:CD2	1:C:458:GLY:HA3	2.56	0.41
1:A:249:ALA:HB2	1:A:265:PHE:HA	2.02	0.40
1:A:605:MET:HG2	1:A:606:ALA:N	2.36	0.40
1:B:135:PHE:HB3	1:B:349:TYR:OH	2.21	0.40
1:B:192:LEU:HB3	1:B:193:HIS:NE2	2.36	0.40
1:B:369:ALA:HA	1:B:370:PRO:HD3	1.72	0.40
1:B:497:LEU:HD12	1:B:497:LEU:HA	1.94	0.40
1:C:93:PHE:HA	1:C:94:PRO:HD3	1.86	0.40
1:C:145:ILE:HG22	1:C:146:ARG:N	2.36	0.40
1:C:192:LEU:O	1:C:193:HIS:CG	2.74	0.40
1:C:533:GLN:HE21	1:C:533:GLN:HB3	1.77	0.40
1:B:32:PHE:CD1	1:B:371:ALA:HA	2.56	0.40
1:A:328:HIS:ND1	1:A:328:HIS:C	2.73	0.40
1:B:36:ALA:HB2	1:B:46:VAL:HG13	2.04	0.40
1:C:135:PHE:HB3	1:C:349:TYR:OH	2.21	0.40
1:C:449:ILE:HG13	1:C:449:ILE:O	2.21	0.40
1:A:502:LEU:HB3	1:A:513:ILE:HG13	2.03	0.40
1:B:32:PHE:CZ	1:B:94:PRO:HG2	2.56	0.40
1:B:213:LEU:HD13	1:B:220:PHE:CE1	2.56	0.40
1:C:97:PRO:HB3	1:C:371:ALA:HB2	2.03	0.40
1:C:658:LEU:HD12	1:C:658:LEU:HA	1.88	0.40
1:A:18:PHE:CD1	1:A:18:PHE:N	2.90	0.40
1:A:153:ILE:HA	1:A:154:PRO:HA	1.84	0.40
1:A:182:LEU:HD21	1:A:355:LYS:HB2	2.04	0.40
1:A:658:LEU:HD12	1:A:658:LEU:HA	1.80	0.40
1:B:214:ASP:HA	1:B:215:PRO:HD2	1.94	0.40
1:B:324:ASP:HB2	1:B:491:GLN:HG2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:411:LEU:HD13	1:C:439:TYR:CE1	2.56	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	659/665 (99%)	599 (91%)	50 (8%)	10 (2%)	10	44
1	B	652/665 (98%)	596 (91%)	49 (8%)	7 (1%)	14	51
1	C	651/665 (98%)	598 (92%)	48 (7%)	5 (1%)	19	58
All	All	1962/1995 (98%)	1793 (91%)	147 (8%)	22 (1%)	14	51

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	606	ALA
1	A	607	ARG
1	A	608	GLN
1	A	630	TYR
1	B	630	TYR
1	C	630	TYR
1	A	634	GLU
1	B	30	ARG
1	B	368	GLY
1	B	634	GLU
1	C	368	GLY
1	C	634	GLU
1	B	251	ARG
1	A	368	GLY
1	B	599	SER
1	B	603	ALA

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Mol	Chain	Res	Type
1	C	251	ARG
1	C	603	ALA
1	A	238	GLU
1	A	603	ALA
1	A	605	MET
1	A	251	ARG

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	554/558 (99%)	504 (91%)	50 (9%)	9 34
1	B	552/558 (99%)	508 (92%)	44 (8%)	12 42
1	C	551/558 (99%)	507 (92%)	44 (8%)	12 42
All	All	1657/1674 (99%)	1519 (92%)	138 (8%)	11 40

All (138) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	7	PHE
1	A	12	ILE
1	A	16	MET
1	A	43	LEU
1	A	46	VAL
1	A	55	ASN
1	A	68	ASN
1	A	75	VAL
1	A	102	LEU
1	A	113	ASP
1	A	119	VAL
1	A	150	SER
1	A	151	THR
1	A	162	THR
1	A	192	LEU

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Mol	Chain	Res	Type
1	A	202	VAL
1	A	204	ARG
1	A	206	GLN
1	A	242	LEU
1	A	271	THR
1	A	307	ARG
1	A	326	SER
1	A	362	LYS
1	A	363	LEU
1	A	373	GLU
1	A	387	LEU
1	A	391	LEU
1	A	398	THR
1	A	404	LEU
1	A	405	LEU
1	A	412	VAL
1	A	438	SER
1	A	448	GLN
1	A	472	PHE
1	A	474	MET
1	A	483	SER
1	A	497	LEU
1	A	519	ASN
1	A	529	GLU
1	A	532	VAL
1	A	533	GLN
1	A	565	SER
1	A	566	ASP
1	A	576	TRP
1	A	599	SER
1	A	600	ARG
1	A	607	ARG
1	A	611	LEU
1	A	629	GLN
1	B	3	ARG
1	B	7	PHE
1	B	12	ILE
1	B	16	MET
1	B	43	LEU
1	B	46	VAL
1	B	55	ASN
1	B	68	ASN

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Mol	Chain	Res	Type
1	B	75	VAL
1	B	102	LEU
1	B	113	ASP
1	B	119	VAL
1	B	151	THR
1	B	162	THR
1	B	192	LEU
1	B	202	VAL
1	B	204	ARG
1	B	206	GLN
1	B	242	LEU
1	B	271	THR
1	B	307	ARG
1	B	326	SER
1	B	362	LYS
1	B	363	LEU
1	B	373	GLU
1	B	387	LEU
1	B	391	LEU
1	B	398	THR
1	B	404	LEU
1	B	412	VAL
1	B	448	GLN
1	B	472	PHE
1	B	474	MET
1	B	483	SER
1	B	497	LEU
1	B	519	ASN
1	B	529	GLU
1	B	533	GLN
1	B	565	SER
1	B	566	ASP
1	B	576	TRP
1	B	599	SER
1	B	600	ARG
1	B	629	GLN
1	C	3	ARG
1	C	7	PHE
1	C	12	ILE
1	C	16	MET
1	C	43	LEU
1	C	46	VAL

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Mol	Chain	Res	Type
1	C	55	ASN
1	C	68	ASN
1	C	75	VAL
1	C	81	ARG
1	C	113	ASP
1	C	119	VAL
1	C	151	THR
1	C	162	THR
1	C	192	LEU
1	C	202	VAL
1	C	204	ARG
1	C	206	GLN
1	C	242	LEU
1	C	271	THR
1	C	307	ARG
1	C	362	LYS
1	C	363	LEU
1	C	373	GLU
1	C	387	LEU
1	C	391	LEU
1	C	398	THR
1	C	404	LEU
1	C	405	LEU
1	C	412	VAL
1	C	448	GLN
1	C	472	PHE
1	C	474	MET
1	C	483	SER
1	C	497	LEU
1	C	519	ASN
1	C	529	GLU
1	C	533	GLN
1	C	565	SER
1	C	566	ASP
1	C	576	TRP
1	C	599	SER
1	C	600	ARG
1	C	629	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	ASN
1	A	68	ASN
1	A	194	GLN
1	B	55	ASN
1	B	68	ASN
1	B	417	HIS
1	C	55	ASN
1	C	68	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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	661/665 (99%)	-0.49	8 (1%)	79	67	23, 45, 76, 107	0
1	B	656/665 (98%)	-0.51	2 (0%)	94	92	22, 45, 73, 103	0
1	C	655/665 (98%)	-0.36	9 (1%)	75	63	20, 47, 77, 108	0
All	All	1972/1995 (98%)	-0.45	19 (0%)	82	72	20, 46, 76, 108	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	604	SER	6.6
1	C	603	ALA	3.9
1	C	216	LYS	3.7
1	C	215	PRO	3.2
1	A	216	LYS	3.2
1	A	607	ARG	3.1
1	A	254	GLU	3.1
1	A	257	GLY	3.0
1	B	217	THR	2.7
1	C	612	ALA	2.7
1	B	604	SER	2.6
1	A	253	LYS	2.5
1	A	373	GLU	2.4
1	C	214	ASP	2.2
1	A	576	TRP	2.2
1	A	506	ARG	2.2
1	C	461	LYS	2.2
1	C	605	MET	2.0
1	C	253	LYS	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 monosaccharides 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.