



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2026 – 10:56 AM UTC

PDB ID : 1HHS / pdb_00001hhs
Title : RNA dependent RNA polymerase from dsRNA bacteriophage phi6
Authors : Grimes, J.M.; Butcher, S.J.; Makeyev, E.V.; Bamford, D.H.; Stuart, D.I.
Deposited on : 2000-12-28
Resolution : 2.00 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 types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

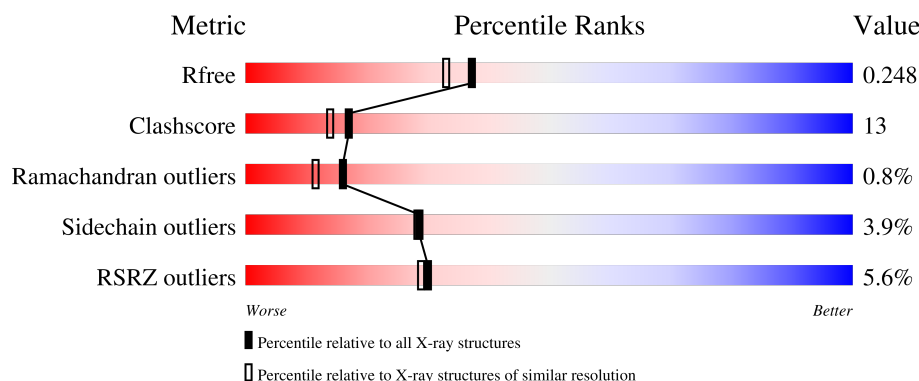
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 $\leq 5\%$. 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	664	5% 78% 19% .
1	B	664	8% 78% 19% .
1	C	664	5% 77% 20% .

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18563 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
1	A	664	Total	C	N	O	S	0	0	0
			5265	3342	914	977	32			
1	B	664	Total	C	N	O	S	0	0	0
			5265	3342	914	977	32			
1	C	664	Total	C	N	O	S	0	0	0
			5265	3342	914	977	32			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	456	MET	ILE	conflict	UNP P11124
B	456	MET	ILE	conflict	UNP P11124
C	456	MET	ILE	conflict	UNP P11124

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mn	0	0
			1	1		
2	B	1	Total	Mn	0	0
			1	1		
2	C	1	Total	Mn	0	0
			1	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	890	Total	O	0	0
			890	890		
3	B	938	Total	O	0	0
			938	938		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	937	Total 937	O 937	0	0

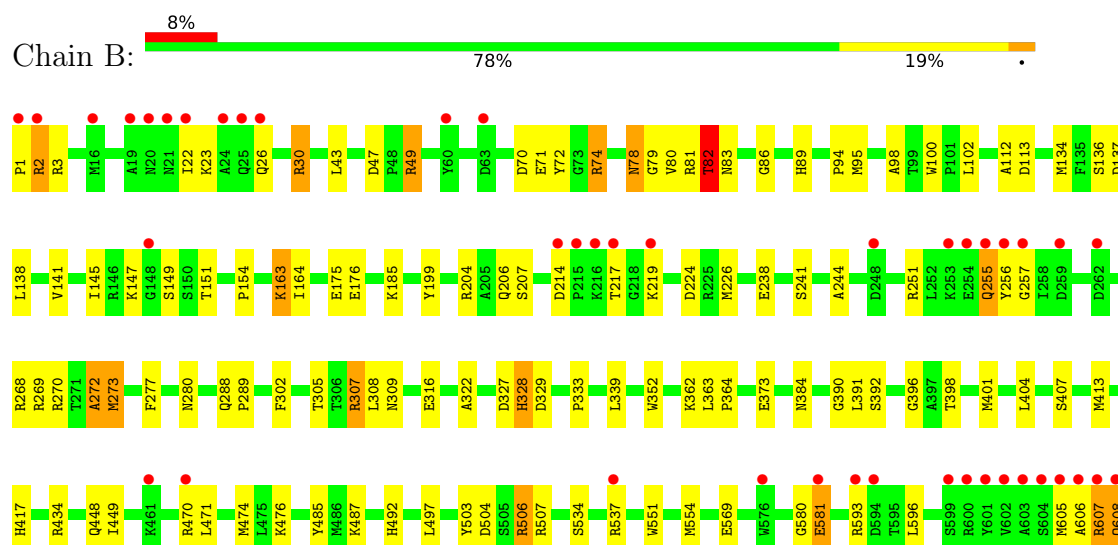
3 Residue-property plots

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

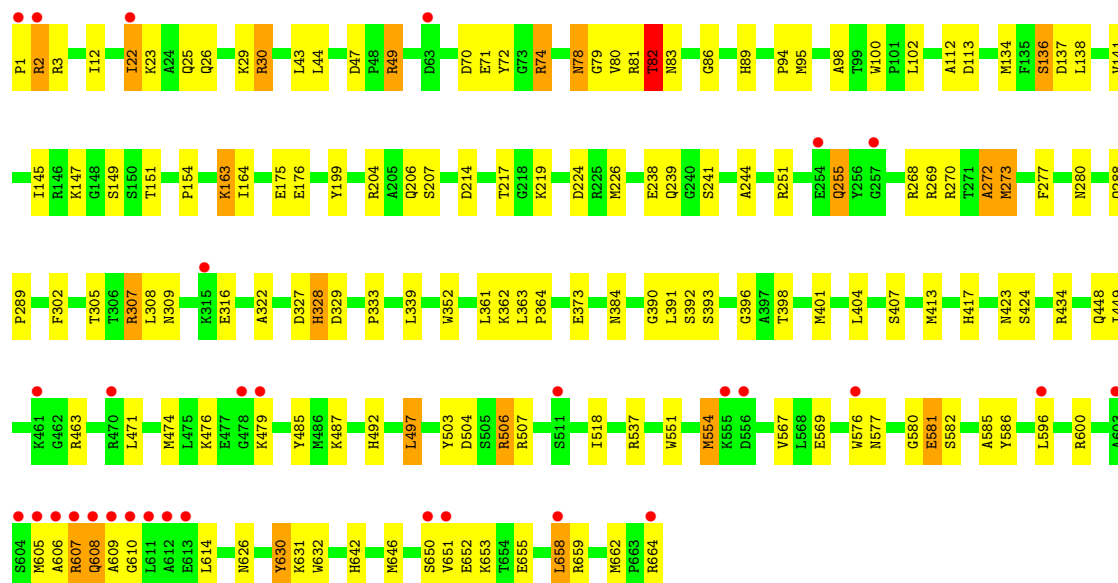
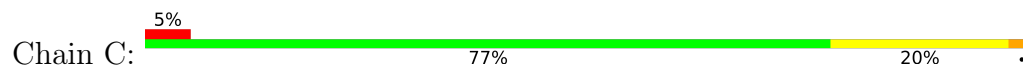


• Molecule 1: RNA-DIRECTED RNA POLYMERASE





● Molecule 1: RNA-DIRECTED RNA POLYMERASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.41Å 93.36Å 141.20Å 90.00° 101.25° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 20.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-2.00) 99.8 (20.00-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 2.00Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.221 , 0.249 0.220 , 0.248	Depositor DCC
R_{free} test set	9067 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	32.2	Xtriage
Anisotropy	0.619	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 62.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	18563	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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

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

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	0.83	2/5396 (0.0%)	1.09	26/7297 (0.4%)
1	B	0.84	2/5396 (0.0%)	1.09	25/7297 (0.3%)
1	C	0.84	2/5396 (0.0%)	1.09	26/7297 (0.4%)
All	All	0.83	6/16188 (0.0%)	1.09	77/21891 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
All	All	0	3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	273	MET	SD-CE	-8.39	1.58	1.79
1	A	273	MET	SD-CE	-8.38	1.58	1.79
1	B	273	MET	SD-CE	-8.37	1.58	1.79
1	B	413	MET	SD-CE	-6.48	1.63	1.79
1	A	413	MET	SD-CE	-6.47	1.63	1.79
1	C	413	MET	SD-CE	-6.46	1.63	1.79

All (77) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	302	PHE	N-CA-C	8.14	124.39	113.97

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	302	PHE	N-CA-C	8.14	124.39	113.97
1	A	302	PHE	N-CA-C	8.13	124.37	113.97
1	A	333	PRO	N-CA-C	7.71	123.12	110.55
1	C	333	PRO	N-CA-C	7.70	123.11	110.55
1	B	333	PRO	N-CA-C	7.70	123.10	110.55
1	B	206	GLN	N-CA-C	-7.57	92.71	107.62
1	C	206	GLN	N-CA-C	-7.56	92.72	107.62
1	A	206	GLN	N-CA-C	-7.55	92.75	107.62
1	B	207	SER	N-CA-C	7.32	120.12	111.71
1	C	207	SER	N-CA-C	7.30	120.11	111.71
1	A	207	SER	N-CA-C	7.30	120.10	111.71
1	B	485	TYR	N-CA-C	7.19	122.44	112.45
1	B	100	TRP	N-CA-C	-7.17	101.03	109.93
1	C	485	TYR	N-CA-C	7.17	122.42	112.45
1	A	485	TYR	N-CA-C	7.17	122.42	112.45
1	C	100	TRP	N-CA-C	-7.16	101.05	109.93
1	A	100	TRP	N-CA-C	-7.16	101.06	109.93
1	B	141	VAL	CA-C-N	-6.91	112.88	119.85
1	B	141	VAL	C-N-CA	-6.91	112.88	119.85
1	C	141	VAL	CA-C-N	-6.91	112.88	119.85
1	C	141	VAL	C-N-CA	-6.91	112.88	119.85
1	A	141	VAL	CA-C-N	-6.90	112.88	119.85
1	A	141	VAL	C-N-CA	-6.90	112.88	119.85
1	B	363	LEU	N-CA-C	6.81	119.48	110.08
1	A	363	LEU	N-CA-C	6.80	119.47	110.08
1	C	363	LEU	N-CA-C	6.80	119.46	110.08
1	A	82	THR	CB-CA-C	-6.60	98.31	111.91
1	C	82	THR	CB-CA-C	-6.59	98.33	111.91
1	B	82	THR	CB-CA-C	-6.59	98.33	111.91
1	C	22	ILE	N-CA-C	6.32	117.07	110.62
1	A	22	ILE	N-CA-C	6.31	117.05	110.62
1	B	22	ILE	N-CA-C	6.28	117.03	110.62
1	C	241	SER	N-CA-C	6.12	118.48	109.24
1	B	241	SER	N-CA-C	6.11	118.47	109.24
1	A	241	SER	N-CA-C	6.11	118.46	109.24
1	B	98	ALA	N-CA-C	-5.99	102.81	110.53
1	C	98	ALA	N-CA-C	-5.99	102.81	110.53
1	C	328	HIS	N-CA-C	5.97	118.28	111.11
1	A	98	ALA	N-CA-C	-5.96	102.84	110.53
1	A	328	HIS	N-CA-C	5.95	118.25	111.11
1	B	328	HIS	N-CA-C	5.94	118.24	111.11
1	A	280	ASN	N-CA-C	5.94	117.75	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	280	ASN	N-CA-C	5.92	117.73	111.28
1	B	280	ASN	N-CA-C	5.91	117.72	111.28
1	C	95	MET	N-CA-C	-5.86	102.75	110.43
1	B	95	MET	N-CA-C	-5.85	102.76	110.43
1	A	95	MET	N-CA-C	-5.84	102.78	110.43
1	C	390	GLY	N-CA-C	-5.78	104.34	111.45
1	B	390	GLY	N-CA-C	-5.78	104.34	111.45
1	A	390	GLY	N-CA-C	-5.77	104.35	111.45
1	B	94	PRO	N-CA-C	5.73	120.29	111.57
1	A	94	PRO	N-CA-C	5.72	120.26	111.57
1	C	94	PRO	N-CA-C	5.72	120.26	111.57
1	B	396	GLY	N-CA-C	5.52	120.52	114.40
1	A	396	GLY	N-CA-C	5.48	120.48	114.40
1	C	277	PHE	N-CA-C	5.47	117.25	111.28
1	B	277	PHE	N-CA-C	5.46	117.23	111.28
1	C	396	GLY	N-CA-C	5.45	120.45	114.40
1	A	277	PHE	N-CA-C	5.45	117.22	111.28
1	A	255	GLN	N-CA-C	5.37	118.30	111.69
1	B	255	GLN	N-CA-C	5.35	118.27	111.69
1	C	255	GLN	N-CA-C	5.34	118.26	111.69
1	C	134	MET	N-CA-C	5.33	117.17	111.36
1	A	134	MET	N-CA-C	5.31	117.15	111.36
1	B	614	LEU	N-CA-C	5.31	118.59	110.20
1	A	614	LEU	N-CA-C	5.30	118.57	110.20
1	C	614	LEU	N-CA-C	5.29	118.56	110.20
1	B	134	MET	N-CA-C	5.29	117.12	111.36
1	B	449	ILE	N-CA-C	-5.28	100.51	108.12
1	C	449	ILE	N-CA-C	-5.28	100.52	108.12
1	A	449	ILE	N-CA-C	-5.27	100.53	108.12
1	B	272	ALA	N-CA-C	-5.25	101.09	109.23
1	A	272	ALA	N-CA-C	-5.23	101.12	109.23
1	C	272	ALA	N-CA-C	-5.23	101.13	109.23
1	C	554	MET	N-CA-C	5.02	117.13	111.11
1	A	554	MET	N-CA-C	5.00	117.11	111.11

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	199	TYR	Sidechain
1	B	199	TYR	Sidechain
1	C	199	TYR	Sidechain

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	5265	0	5165	132	3
1	B	5265	0	5165	126	2
1	C	5265	0	5165	153	13
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	890	0	0	37	3
3	B	938	0	0	40	5
3	C	937	0	0	63	7
All	All	18563	0	15495	398	21

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 13.

All (398) 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:576:TRP:CE3	3:C:2822:HOH:O	1.87	1.25
1:C:664:ARG:HB3	3:C:2932:HOH:O	1.15	1.25
1:C:44:LEU:CD2	3:C:2120:HOH:O	1.83	1.24
1:C:463:ARG:HD2	3:C:2691:HOH:O	1.37	1.24
1:B:2:ARG:HA	3:B:2012:HOH:O	1.10	1.23
1:C:239:GLN:HG2	3:C:2494:HOH:O	1.41	1.21
1:B:470:ARG:HD2	3:B:2700:HOH:O	1.49	1.12
1:A:137:ASP:N	3:A:2284:HOH:O	1.86	1.09
1:C:137:ASP:N	3:C:2306:HOH:O	1.86	1.09
1:B:137:ASP:N	3:B:2301:HOH:O	1.86	1.09
1:C:44:LEU:HD22	3:C:2120:HOH:O	1.47	1.05
1:C:664:ARG:CB	3:C:2932:HOH:O	1.78	1.05
1:C:2:ARG:HD3	3:C:2005:HOH:O	1.58	1.02
1:A:564:TYR:CZ	3:A:2767:HOH:O	2.10	1.01
1:A:555:LYS:HD3	3:A:2767:HOH:O	1.58	0.99
1:A:316:GLU:HG2	3:A:2529:HOH:O	1.67	0.95
1:C:316:GLU:HG2	3:C:2563:HOH:O	1.67	0.95
1:A:608:GLN:HE22	1:B:593:ARG:CZ	1.80	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:316:GLU:HG2	3:B:2561:HOH:O	1.67	0.92
1:A:608:GLN:HE22	1:B:593:ARG:NH1	1.67	0.91
1:A:555:LYS:CD	3:A:2767:HOH:O	2.17	0.91
1:C:2:ARG:NH1	3:C:2008:HOH:O	2.08	0.87
1:A:427:LYS:HE3	1:C:12:ILE:HG21	1.58	0.85
1:C:82:THR:HG23	3:C:2102:HOH:O	1.78	0.83
1:A:82:THR:HG23	3:A:2092:HOH:O	1.78	0.83
1:A:556:ASP:OD2	3:A:2759:HOH:O	1.96	0.83
1:C:217:THR:HG23	1:C:219:LYS:H	1.43	0.82
1:B:82:THR:HG23	3:B:2096:HOH:O	1.78	0.82
1:B:217:THR:HG23	1:B:219:LYS:H	1.43	0.81
1:C:576:TRP:NE1	3:C:2824:HOH:O	2.11	0.81
1:A:217:THR:HG23	1:A:219:LYS:H	1.43	0.81
1:A:307:ARG:HG2	3:A:2518:HOH:O	1.81	0.80
1:A:564:TYR:CE1	3:A:2767:HOH:O	2.28	0.80
1:A:63:ASP:HA	3:A:2165:HOH:O	1.79	0.80
1:B:307:ARG:HG2	3:B:2549:HOH:O	1.81	0.79
1:A:427:LYS:HE3	1:C:12:ILE:CG2	2.13	0.78
1:C:586:TYR:N	3:C:2831:HOH:O	1.86	0.78
1:B:251:ARG:HH11	1:B:255:GLN:HE22	1.31	0.78
1:C:307:ARG:HG2	3:C:2552:HOH:O	1.81	0.78
1:C:251:ARG:HH11	1:C:255:GLN:HE22	1.31	0.78
1:C:609:ALA:HA	3:C:2875:HOH:O	1.84	0.78
1:A:26:GLN:HG2	3:A:2038:HOH:O	1.85	0.77
1:B:163:LYS:HD3	3:B:2318:HOH:O	1.85	0.77
1:C:226:MET:HE1	1:C:244:ALA:HB2	1.67	0.77
1:A:163:LYS:HD3	3:A:2302:HOH:O	1.85	0.76
1:C:26:GLN:HG2	3:C:2047:HOH:O	1.84	0.76
1:C:82:THR:HG21	3:C:2107:HOH:O	1.86	0.76
1:A:226:MET:HE1	1:A:244:ALA:HB2	1.67	0.76
1:B:26:GLN:HG2	3:B:2041:HOH:O	1.85	0.75
1:B:47:ASP:OD2	1:B:49:ARG:HD3	1.87	0.75
1:B:226:MET:HE1	1:B:244:ALA:HB2	1.67	0.75
1:C:163:LYS:HD3	3:C:2324:HOH:O	1.85	0.75
1:A:251:ARG:HH11	1:A:255:GLN:HE22	1.31	0.75
1:C:47:ASP:OD2	1:C:49:ARG:HD3	1.87	0.74
1:A:82:THR:HG21	3:A:2097:HOH:O	1.86	0.74
1:B:82:THR:HG21	3:B:2102:HOH:O	1.86	0.74
1:C:214:ASP:HB3	1:C:217:THR:HG22	1.70	0.74
1:A:72:TYR:CE1	1:A:476:LYS:HD3	2.23	0.73
1:A:47:ASP:OD2	1:A:49:ARG:HD3	1.86	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:72:TYR:CE1	1:B:476:LYS:HD3	2.23	0.73
1:C:72:TYR:CE1	1:C:476:LYS:HD3	2.23	0.73
1:B:214:ASP:HB3	1:B:217:THR:HG22	1.70	0.73
1:A:214:ASP:HB3	1:A:217:THR:HG22	1.70	0.73
1:B:268:ARG:NH1	1:B:270:ARG:HH21	1.88	0.72
1:B:506:ARG:HH11	1:B:506:ARG:HB2	1.55	0.72
1:A:506:ARG:HH11	1:A:506:ARG:HB2	1.55	0.71
1:C:609:ALA:CB	3:C:2875:HOH:O	2.38	0.71
1:C:82:THR:HG22	1:C:83:ASN:H	1.54	0.71
1:A:82:THR:HG22	1:A:83:ASN:H	1.54	0.71
1:A:194:GLN:OE1	3:A:2391:HOH:O	2.08	0.71
1:B:82:THR:HG22	1:B:83:ASN:H	1.54	0.71
1:C:268:ARG:NH1	1:C:270:ARG:HH21	1.88	0.71
1:A:608:GLN:NE2	1:B:593:ARG:NH1	2.39	0.71
1:A:268:ARG:NH1	1:A:270:ARG:HH21	1.88	0.71
1:C:506:ARG:HH11	1:C:506:ARG:HB2	1.55	0.71
1:B:655:GLU:HG2	1:B:659:ARG:NH1	2.06	0.70
1:C:576:TRP:HE3	3:C:2822:HOH:O	1.44	0.70
1:A:655:GLU:HG2	1:A:659:ARG:NH1	2.06	0.70
1:C:226:MET:HE3	3:C:2473:HOH:O	1.91	0.70
1:B:534:SER:OG	3:B:2773:HOH:O	2.10	0.69
1:C:655:GLU:HG2	1:C:659:ARG:NH1	2.06	0.69
1:C:2:ARG:HB3	3:C:2005:HOH:O	1.91	0.69
1:B:607:ARG:O	1:B:608:GLN:HG3	1.93	0.68
1:A:607:ARG:O	1:A:608:GLN:HG3	1.93	0.68
1:C:607:ARG:O	1:C:608:GLN:HG3	1.93	0.68
1:B:149:SER:O	1:B:163:LYS:HE2	1.94	0.68
1:A:149:SER:O	1:A:163:LYS:HE2	1.94	0.68
1:A:569:GLU:HG2	3:A:2402:HOH:O	1.94	0.67
1:C:149:SER:O	1:C:163:LYS:HE2	1.94	0.67
1:C:176:GLU:OE1	3:C:2386:HOH:O	2.13	0.66
1:B:176:GLU:OE1	3:B:2378:HOH:O	2.13	0.66
1:A:176:GLU:OE1	3:A:2358:HOH:O	2.13	0.66
1:B:581:GLU:OE1	3:B:2829:HOH:O	2.14	0.65
1:C:569:GLU:HG2	3:C:2435:HOH:O	1.94	0.65
1:B:569:GLU:HG2	3:B:2429:HOH:O	1.94	0.65
1:C:70:ASP:OD1	1:C:74:ARG:HD2	1.97	0.65
1:A:204:ARG:HH22	1:A:626:ASN:HD21	1.45	0.65
1:C:650:SER:HB2	1:C:652:GLU:OE1	1.97	0.65
1:C:29:LYS:CE	3:C:2098:HOH:O	2.45	0.65
1:B:204:ARG:HH22	1:B:626:ASN:HD21	1.45	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:537:ARG:HD3	3:A:2734:HOH:O	1.95	0.64
1:B:70:ASP:OD1	1:B:74:ARG:HD2	1.97	0.64
1:C:537:ARG:HD3	3:C:2769:HOH:O	1.96	0.64
1:A:650:SER:HB2	1:A:652:GLU:OE1	1.97	0.64
1:C:151:THR:HG22	1:C:163:LYS:HG3	1.80	0.64
1:B:151:THR:HG22	1:B:163:LYS:HG3	1.80	0.64
1:C:204:ARG:HH22	1:C:626:ASN:HD21	1.45	0.64
1:B:650:SER:HB2	1:B:652:GLU:OE1	1.98	0.63
1:C:664:ARG:OXT	3:C:2932:HOH:O	2.15	0.63
1:A:70:ASP:OD1	1:A:74:ARG:HD2	1.97	0.63
1:A:392:SER:O	1:A:398:THR:HG21	1.99	0.63
1:C:392:SER:O	1:C:398:THR:HG21	1.98	0.63
1:C:22:ILE:HG12	3:C:2076:HOH:O	1.98	0.63
1:A:214:ASP:HB3	1:A:217:THR:CG2	2.29	0.63
1:A:427:LYS:CE	1:C:12:ILE:HG21	2.28	0.63
1:A:564:TYR:OH	3:A:2767:HOH:O	1.71	0.63
1:C:3:ARG:HD3	3:C:2028:HOH:O	1.99	0.63
1:B:3:ARG:O	3:B:2009:HOH:O	0.63	0.63
1:B:214:ASP:HB3	1:B:217:THR:CG2	2.28	0.63
1:C:214:ASP:HB3	1:C:217:THR:CG2	2.28	0.62
1:C:609:ALA:CA	3:C:2875:HOH:O	2.44	0.62
1:B:392:SER:O	1:B:398:THR:HG21	1.98	0.62
1:A:3:ARG:HD3	3:A:2021:HOH:O	1.99	0.62
1:C:585:ALA:N	3:C:2831:HOH:O	2.33	0.61
1:A:29:LYS:NZ	3:A:2091:HOH:O	2.27	0.61
1:A:151:THR:HG22	1:A:163:LYS:HG3	1.80	0.61
1:B:3:ARG:HD3	3:B:2021:HOH:O	1.99	0.60
1:B:581:GLU:HG3	3:B:2831:HOH:O	2.02	0.60
1:C:607:ARG:NH2	3:C:2869:HOH:O	1.98	0.60
1:A:655:GLU:HG2	1:A:659:ARG:HH12	1.67	0.59
1:C:655:GLU:HG2	1:C:659:ARG:HH12	1.67	0.59
1:B:288:GLN:HB3	1:B:289:PRO:HD3	1.85	0.59
1:A:606:ALA:H	1:A:609:ALA:HB2	1.69	0.58
1:B:606:ALA:H	1:B:609:ALA:HB2	1.68	0.58
1:C:78:ASN:C	1:C:78:ASN:HD22	2.12	0.58
1:C:577:ASN:OD1	3:C:2825:HOH:O	2.17	0.58
1:B:581:GLU:CG	3:B:2831:HOH:O	2.51	0.58
1:A:288:GLN:HB3	1:A:289:PRO:HD3	1.85	0.57
1:B:470:ARG:NH2	3:B:2695:HOH:O	2.37	0.57
1:C:606:ALA:H	1:C:609:ALA:HB2	1.69	0.57
1:B:650:SER:HB2	1:B:652:GLU:CD	2.30	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:HIS:CE1	1:A:474:MET:HE1	2.40	0.57
1:C:288:GLN:HB3	1:C:289:PRO:HD3	1.85	0.57
1:B:417:HIS:CE1	1:B:474:MET:HE1	2.40	0.57
1:B:655:GLU:HG2	1:B:659:ARG:HH12	1.67	0.57
1:A:362:LYS:HD2	3:A:2595:HOH:O	2.05	0.57
1:A:401:MET:HE2	1:A:401:MET:HA	1.87	0.57
1:B:78:ASN:C	1:B:78:ASN:HD22	2.12	0.57
1:C:650:SER:HB2	1:C:652:GLU:CD	2.30	0.57
1:C:417:HIS:CE1	1:C:474:MET:HE1	2.40	0.57
1:A:328:HIS:HD2	1:A:329:ASP:OD1	1.89	0.56
1:B:328:HIS:HD2	1:B:329:ASP:OD1	1.89	0.56
1:B:492:HIS:HD2	3:B:2721:HOH:O	1.88	0.56
1:C:30:ARG:HD2	3:C:2106:HOH:O	2.05	0.56
1:C:328:HIS:HD2	1:C:329:ASP:OD1	1.89	0.56
1:B:401:MET:HA	1:B:401:MET:HE2	1.87	0.56
1:A:78:ASN:C	1:A:78:ASN:HD22	2.12	0.56
1:A:650:SER:HB2	1:A:652:GLU:CD	2.30	0.56
1:C:147:LYS:HD3	3:C:2780:HOH:O	2.06	0.56
1:A:30:ARG:HD2	3:A:2096:HOH:O	2.05	0.56
1:B:147:LYS:HD3	3:B:2785:HOH:O	2.06	0.56
1:B:362:LYS:HD2	3:B:2627:HOH:O	2.05	0.56
1:B:470:ARG:CD	3:B:2700:HOH:O	2.26	0.56
1:C:362:LYS:HD2	3:C:2630:HOH:O	2.05	0.56
1:B:30:ARG:HD2	3:B:2097:HOH:O	2.05	0.56
1:B:407:SER:HA	1:B:448:GLN:HE22	1.71	0.56
1:A:147:LYS:HD3	3:A:2743:HOH:O	2.06	0.55
1:C:407:SER:HA	1:C:448:GLN:HE22	1.72	0.55
1:A:407:SER:HA	1:A:448:GLN:HE22	1.71	0.55
1:C:585:ALA:CA	3:C:2831:HOH:O	2.54	0.55
1:A:251:ARG:HH11	1:A:255:GLN:NE2	2.03	0.55
1:C:401:MET:HE2	1:C:401:MET:HA	1.87	0.55
1:A:44:LEU:HD21	1:B:257:GLY:HA3	1.89	0.55
1:C:576:TRP:CD2	3:C:2822:HOH:O	2.35	0.55
1:C:1:PRO:HG2	1:C:238:GLU:OE1	2.07	0.55
1:B:1:PRO:HG2	1:B:238:GLU:OE1	2.07	0.55
1:A:504:ASP:CG	1:A:506:ARG:HH12	2.15	0.55
1:C:492:HIS:HD2	3:C:2718:HOH:O	1.88	0.55
1:C:506:ARG:HH11	1:C:506:ARG:CB	2.20	0.55
1:C:251:ARG:HH11	1:C:255:GLN:NE2	2.03	0.54
1:C:504:ASP:CG	1:C:506:ARG:HH12	2.15	0.54
1:A:492:HIS:HD2	3:A:2682:HOH:O	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:PRO:HG2	1:A:238:GLU:OE1	2.07	0.54
1:B:504:ASP:CG	1:B:506:ARG:HH12	2.15	0.54
1:C:580:GLY:C	1:C:581:GLU:HG2	2.34	0.53
1:A:119:VAL:HG22	1:C:22:ILE:HD11	1.90	0.53
1:C:78:ASN:HD22	1:C:79:GLY:N	2.07	0.53
1:A:78:ASN:HD22	1:A:79:GLY:N	2.07	0.53
1:B:2:ARG:CA	3:B:2012:HOH:O	1.97	0.53
1:B:78:ASN:ND2	1:B:80:VAL:H	2.06	0.53
1:C:25:GLN:NE2	3:C:2086:HOH:O	2.37	0.53
1:C:78:ASN:ND2	1:C:80:VAL:H	2.06	0.53
1:A:29:LYS:CE	3:A:2091:HOH:O	2.57	0.53
1:A:506:ARG:HH11	1:A:506:ARG:CB	2.20	0.53
1:C:650:SER:OG	1:C:653:LYS:HG3	2.09	0.53
1:A:650:SER:OG	1:A:653:LYS:HG3	2.09	0.53
1:B:74:ARG:HB3	1:B:503:TYR:CD2	2.44	0.53
1:C:585:ALA:HB3	3:C:2831:HOH:O	2.08	0.53
1:A:74:ARG:HB3	1:A:503:TYR:CD2	2.44	0.53
1:B:650:SER:OG	1:B:653:LYS:HG3	2.09	0.53
1:A:78:ASN:ND2	1:A:80:VAL:H	2.06	0.52
1:C:74:ARG:HB3	1:C:503:TYR:CD2	2.44	0.52
1:A:580:GLY:C	1:A:581:GLU:HG2	2.34	0.52
1:B:70:ASP:OD1	1:B:74:ARG:CD	2.58	0.52
1:A:70:ASP:OD1	1:A:74:ARG:CD	2.58	0.52
1:B:580:GLY:C	1:B:581:GLU:HG2	2.33	0.52
1:B:664:ARG:HG2	1:B:664:ARG:HH11	1.75	0.52
1:B:78:ASN:HD22	1:B:79:GLY:N	2.07	0.52
1:B:339:LEU:HD23	1:B:339:LEU:C	2.35	0.52
1:A:339:LEU:C	1:A:339:LEU:HD23	2.35	0.52
1:A:658:LEU:HG	1:A:662:MET:HE2	1.93	0.51
1:C:339:LEU:C	1:C:339:LEU:HD23	2.35	0.51
1:C:658:LEU:HG	1:C:662:MET:HE2	1.93	0.51
1:B:251:ARG:HH11	1:B:255:GLN:NE2	2.03	0.51
1:C:70:ASP:OD1	1:C:74:ARG:CD	2.58	0.51
1:C:664:ARG:HA	3:C:2933:HOH:O	2.11	0.51
1:B:658:LEU:HG	1:B:662:MET:HE2	1.92	0.51
1:A:664:ARG:HG2	1:A:664:ARG:HH11	1.75	0.51
1:A:138:LEU:HB2	1:A:662:MET:SD	2.51	0.51
1:A:204:ARG:HG3	1:A:272:ALA:HB2	1.92	0.50
1:C:576:TRP:HB3	3:C:2822:HOH:O	2.11	0.50
1:C:138:LEU:HB2	1:C:662:MET:SD	2.51	0.50
1:A:600:ARG:HD3	3:B:2832:HOH:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:ALA:HB1	1:A:487:LYS:HE2	1.94	0.50
1:B:138:LEU:HB2	1:B:662:MET:SD	2.51	0.50
1:B:492:HIS:CD2	3:B:2721:HOH:O	2.64	0.50
1:B:204:ARG:HG3	1:B:272:ALA:HB2	1.92	0.50
1:C:664:ARG:HG2	1:C:664:ARG:HH11	1.75	0.50
1:C:112:ALA:HB1	1:C:487:LYS:HE2	1.94	0.50
1:C:392:SER:O	1:C:398:THR:CG2	2.60	0.50
1:A:214:ASP:CB	1:A:217:THR:HG22	2.40	0.50
1:B:506:ARG:HH11	1:B:506:ARG:CB	2.20	0.50
1:B:581:GLU:CB	3:B:2831:HOH:O	2.59	0.50
1:C:145:ILE:HG21	1:C:163:LYS:HD2	1.94	0.50
1:A:1:PRO:O	1:A:2:ARG:HB2	2.12	0.49
1:A:322:ALA:HB3	3:A:2685:HOH:O	2.12	0.49
1:A:392:SER:O	1:A:398:THR:CG2	2.60	0.49
1:A:631:LYS:HE3	1:A:632:TRP:CZ2	2.47	0.49
1:B:631:LYS:HE3	1:B:632:TRP:CZ2	2.47	0.49
1:A:506:ARG:HH11	1:A:506:ARG:CG	2.26	0.49
1:B:1:PRO:O	1:B:2:ARG:HB2	2.12	0.49
1:C:204:ARG:HG3	1:C:272:ALA:HB2	1.92	0.49
1:C:631:LYS:HE3	1:C:632:TRP:CZ2	2.47	0.49
1:A:492:HIS:CD2	3:A:2682:HOH:O	2.64	0.49
1:B:392:SER:O	1:B:398:THR:CG2	2.60	0.49
1:C:1:PRO:O	1:C:2:ARG:HB2	2.12	0.49
1:A:608:GLN:NE2	1:B:593:ARG:CZ	2.62	0.49
1:B:506:ARG:HH11	1:B:506:ARG:CG	2.26	0.49
1:C:506:ARG:HH11	1:C:506:ARG:CG	2.26	0.49
1:A:145:ILE:HG21	1:A:163:LYS:HD2	1.94	0.49
1:B:322:ALA:HB3	3:B:2722:HOH:O	2.12	0.49
1:C:29:LYS:HE2	3:C:2101:HOH:O	2.12	0.49
1:C:72:TYR:CZ	1:C:476:LYS:HD3	2.49	0.48
1:C:600:ARG:HD3	3:C:2861:HOH:O	2.11	0.48
1:C:610:GLY:HA3	3:C:2874:HOH:O	2.14	0.48
1:A:504:ASP:HB2	3:A:2701:HOH:O	2.14	0.48
1:A:610:GLY:HA3	3:A:2827:HOH:O	2.14	0.48
1:C:423:ASN:HB2	3:C:2654:HOH:O	2.11	0.48
1:C:504:ASP:HB2	3:C:2735:HOH:O	2.14	0.48
1:A:119:VAL:O	1:C:25:GLN:HG3	2.14	0.48
1:B:610:GLY:HA3	3:B:2873:HOH:O	2.14	0.48
1:A:269:ARG:NH2	3:A:2488:HOH:O	2.43	0.48
1:B:112:ALA:HB1	1:B:487:LYS:HE2	1.94	0.48
1:B:145:ILE:HG21	1:B:163:LYS:HD2	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:651:VAL:O	1:B:655:GLU:HB2	2.14	0.48
1:B:504:ASP:HB2	3:B:2739:HOH:O	2.14	0.48
1:A:651:VAL:O	1:A:655:GLU:HB2	2.14	0.47
1:B:214:ASP:CB	1:B:217:THR:HG22	2.41	0.47
1:C:322:ALA:HB3	3:C:2720:HOH:O	2.12	0.47
1:A:72:TYR:CZ	1:A:476:LYS:HD3	2.49	0.47
1:B:71:GLU:H	1:B:71:GLU:CD	2.23	0.47
1:B:269:ARG:NH2	3:B:2520:HOH:O	2.43	0.47
1:C:424:SER:N	3:C:2654:HOH:O	2.40	0.47
1:B:72:TYR:CZ	1:B:476:LYS:HD3	2.49	0.47
1:B:384:ASN:HB3	3:B:2618:HOH:O	2.15	0.47
1:C:226:MET:HE1	1:C:244:ALA:CB	2.41	0.47
1:A:642:HIS:CE1	1:A:646:MET:HG3	2.50	0.47
1:B:470:ARG:NH1	3:B:2699:HOH:O	2.47	0.47
1:B:650:SER:HG	1:B:653:LYS:HG3	1.80	0.47
1:C:70:ASP:CG	1:C:74:ARG:HD2	2.40	0.47
1:C:214:ASP:CB	1:C:217:THR:HG22	2.41	0.47
1:A:42:GLY:O	1:B:256:TYR:HB3	2.15	0.47
1:A:70:ASP:CG	1:A:74:ARG:HD2	2.40	0.47
1:B:642:HIS:CE1	1:B:646:MET:HG3	2.50	0.47
1:B:70:ASP:CG	1:B:74:ARG:HD2	2.40	0.47
1:C:642:HIS:CE1	1:C:646:MET:HG3	2.50	0.47
1:C:492:HIS:CD2	3:C:2718:HOH:O	2.64	0.47
1:A:492:HIS:HE1	3:A:2198:HOH:O	1.98	0.46
1:C:224:ASP:HB3	1:C:226:MET:CE	2.45	0.46
1:C:651:VAL:O	1:C:655:GLU:HB2	2.14	0.46
1:C:71:GLU:CD	1:C:71:GLU:H	2.23	0.46
1:A:224:ASP:HB3	1:A:226:MET:CE	2.45	0.46
1:B:86:GLY:O	1:B:89:HIS:HD2	1.99	0.46
1:A:71:GLU:CD	1:A:71:GLU:H	2.23	0.46
1:C:630:TYR:CD1	1:C:630:TYR:C	2.94	0.46
1:A:551:TRP:CH2	1:A:554:MET:HE1	2.51	0.46
1:B:226:MET:HE1	1:B:244:ALA:CB	2.41	0.46
1:A:86:GLY:O	1:A:89:HIS:HD2	1.99	0.46
1:B:492:HIS:HE1	3:B:2213:HOH:O	1.99	0.46
1:A:384:ASN:HB3	3:A:2586:HOH:O	2.15	0.46
1:C:551:TRP:CH2	1:C:554:MET:HE1	2.51	0.46
1:B:224:ASP:HB3	1:B:226:MET:CE	2.45	0.46
1:C:384:ASN:HB3	3:C:2620:HOH:O	2.15	0.46
1:A:268:ARG:HH12	1:A:270:ARG:HH21	1.62	0.46
1:C:606:ALA:N	1:C:609:ALA:HB2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:THR:CG2	1:A:163:LYS:HG3	2.46	0.45
1:C:471:LEU:CD1	1:C:474:MET:HE3	2.47	0.45
1:A:471:LEU:CD1	1:A:474:MET:HE3	2.47	0.45
1:A:630:TYR:CD1	1:A:630:TYR:C	2.94	0.45
1:B:551:TRP:CH2	1:B:554:MET:HE1	2.51	0.45
1:C:86:GLY:O	1:C:89:HIS:HD2	1.99	0.45
1:C:434:ARG:NH1	3:C:2663:HOH:O	2.50	0.45
1:C:492:HIS:HE1	3:C:2223:HOH:O	1.98	0.45
1:A:650:SER:HG	1:A:653:LYS:HG3	1.81	0.45
1:A:175:GLU:HA	1:A:352:TRP:CE3	2.52	0.45
1:B:273:MET:HE3	1:B:392:SER:HB3	1.99	0.45
1:B:630:TYR:CD1	1:B:630:TYR:C	2.94	0.45
1:C:29:LYS:HE3	3:C:2098:HOH:O	2.12	0.45
1:C:305:THR:H	1:C:309:ASN:ND2	2.15	0.45
1:A:305:THR:H	1:A:309:ASN:ND2	2.15	0.45
1:C:268:ARG:HH12	1:C:270:ARG:HH21	1.62	0.45
1:B:471:LEU:CD1	1:B:474:MET:HE3	2.47	0.44
1:C:82:THR:HG22	1:C:83:ASN:N	2.28	0.44
1:A:497:LEU:HD12	1:A:497:LEU:HA	1.87	0.44
1:A:606:ALA:N	1:A:609:ALA:HB2	2.31	0.44
1:C:175:GLU:HA	1:C:352:TRP:CE3	2.52	0.44
1:A:434:ARG:NH1	3:A:2630:HOH:O	2.50	0.44
1:B:474:MET:HE2	3:B:2646:HOH:O	2.16	0.44
1:C:136:SER:C	3:C:2306:HOH:O	2.47	0.44
1:C:151:THR:CG2	1:C:163:LYS:HG3	2.46	0.44
1:C:273:MET:HE3	1:C:392:SER:HB3	1.99	0.44
1:B:175:GLU:HA	1:B:352:TRP:CE3	2.52	0.44
1:B:305:THR:H	1:B:309:ASN:ND2	2.15	0.44
1:C:474:MET:HE2	3:C:2647:HOH:O	2.16	0.44
1:B:470:ARG:CZ	3:B:2699:HOH:O	2.65	0.44
1:B:434:ARG:NH1	3:B:2661:HOH:O	2.50	0.43
1:B:23:LYS:HB3	1:B:23:LYS:HE2	1.80	0.43
1:B:606:ALA:N	1:B:609:ALA:HB2	2.31	0.43
1:A:474:MET:HE2	3:A:2614:HOH:O	2.16	0.43
1:C:471:LEU:HD12	1:C:474:MET:HE3	2.00	0.43
1:C:74:ARG:HD3	1:C:507:ARG:HD2	2.01	0.43
1:A:273:MET:HE3	1:A:392:SER:HB3	1.99	0.43
1:B:151:THR:CG2	1:B:163:LYS:HG3	2.46	0.43
1:A:74:ARG:HD3	1:A:507:ARG:HD2	2.01	0.43
1:B:74:ARG:HD3	1:B:507:ARG:HD2	2.01	0.43
1:C:269:ARG:NH2	3:C:2525:HOH:O	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:MET:HE1	1:A:244:ALA:CB	2.41	0.43
1:C:497:LEU:HD12	1:C:497:LEU:HA	1.87	0.43
1:B:204:ARG:HG3	1:B:272:ALA:CB	2.49	0.43
1:B:607:ARG:NH1	3:B:2868:HOH:O	2.52	0.43
1:A:605:MET:HE3	1:A:610:GLY:O	2.19	0.42
1:B:268:ARG:HH12	1:B:270:ARG:HH21	1.62	0.42
1:C:204:ARG:HG3	1:C:272:ALA:CB	2.49	0.42
1:B:82:THR:HG22	1:B:83:ASN:N	2.28	0.42
1:A:204:ARG:HG3	1:A:272:ALA:CB	2.49	0.42
1:B:175:GLU:HA	1:B:352:TRP:CD2	2.55	0.42
1:B:652:GLU:CD	1:B:652:GLU:H	2.28	0.42
1:C:175:GLU:HA	1:C:352:TRP:CD2	2.55	0.42
1:A:471:LEU:HD12	1:A:474:MET:HE3	2.00	0.42
1:B:471:LEU:HD12	1:B:474:MET:HE3	2.00	0.42
1:C:23:LYS:HE2	1:C:23:LYS:HB3	1.80	0.42
1:A:136:SER:C	3:A:2284:HOH:O	2.47	0.42
1:C:652:GLU:CD	1:C:652:GLU:H	2.28	0.42
1:A:662:MET:HE3	3:A:2447:HOH:O	2.19	0.42
1:B:605:MET:HE3	1:B:610:GLY:O	2.20	0.42
1:A:119:VAL:HG13	1:C:22:ILE:HD13	2.02	0.42
1:C:662:MET:HE3	3:C:2483:HOH:O	2.19	0.41
1:A:163:LYS:HB2	1:A:163:LYS:HE3	1.74	0.41
1:A:175:GLU:HA	1:A:352:TRP:CD2	2.55	0.41
1:B:185:LYS:HG2	3:B:2186:HOH:O	2.19	0.41
1:A:607:ARG:H	1:A:607:ARG:HE	1.68	0.41
1:C:605:MET:HE3	1:C:610:GLY:O	2.19	0.41
1:C:607:ARG:H	1:C:607:ARG:HE	1.68	0.41
1:A:506:ARG:CG	1:A:506:ARG:NH1	2.84	0.41
1:B:86:GLY:O	1:B:89:HIS:CD2	2.74	0.41
1:B:596:LEU:CD2	1:B:608:GLN:HG2	2.51	0.41
1:C:145:ILE:HD12	1:C:164:ILE:HD13	2.02	0.41
1:A:652:GLU:CD	1:A:652:GLU:H	2.28	0.41
1:A:86:GLY:O	1:A:89:HIS:CD2	2.74	0.41
1:C:273:MET:H	1:C:393:SER:HG	1.68	0.41
1:A:361:LEU:C	1:A:362:LYS:HG2	2.45	0.41
1:A:596:LEU:CD2	1:A:608:GLN:HG2	2.51	0.41
1:C:506:ARG:CG	1:C:506:ARG:NH1	2.84	0.41
1:C:664:ARG:HB2	3:C:2932:HOH:O	1.77	0.41
1:A:78:ASN:C	1:A:78:ASN:ND2	2.79	0.41
1:A:89:HIS:HE1	3:A:2466:HOH:O	2.04	0.41
1:C:2:ARG:CD	3:C:2005:HOH:O	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:596:LEU:CD2	1:C:608:GLN:HG2	2.51	0.41
1:B:145:ILE:HD12	1:B:164:ILE:HD13	2.03	0.40
1:B:662:MET:HE3	3:B:2475:HOH:O	2.19	0.40
1:C:89:HIS:HE1	3:C:2502:HOH:O	2.04	0.40
1:C:361:LEU:C	1:C:362:LYS:HG2	2.45	0.40
1:B:664:ARG:HG2	1:B:664:ARG:NH1	2.36	0.40
1:C:664:ARG:HG2	1:C:664:ARG:NH1	2.36	0.40
1:A:608:GLN:HE22	1:B:593:ARG:NE	2.16	0.40
1:B:163:LYS:HB2	1:B:163:LYS:HE3	1.74	0.40
1:C:86:GLY:O	1:C:89:HIS:CD2	2.74	0.40
1:C:518:ILE:HG12	1:C:567:VAL:HG21	2.03	0.40

All (21) 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:479:LYS:NZ	1:C:607:ARG:C[2_445]	0.93	1.27
1:C:479:LYS:CE	1:C:608:GLN:N[2_445]	1.13	1.07
3:A:2392:HOH:O	3:C:2828:HOH:O[1_655]	1.43	0.77
1:C:479:LYS:NZ	1:C:608:GLN:N[2_445]	1.47	0.73
1:A:652:GLU:CG	1:C:664:ARG:NH1[2_545]	1.52	0.68
3:B:2030:HOH:O	3:C:2317:HOH:O[2_555]	1.52	0.68
1:A:566:ASP:OD2	1:C:2:ARG:CG[2_555]	1.53	0.67
1:C:479:LYS:NZ	1:C:607:ARG:O[2_445]	1.69	0.51
1:C:479:LYS:NZ	1:C:607:ARG:CA[2_445]	1.79	0.41
3:B:2046:HOH:O	3:C:2283:HOH:O[2_555]	1.81	0.39
3:A:2773:HOH:O	3:C:2005:HOH:O[2_555]	1.90	0.30
1:B:537:ARG:NH2	1:C:582:SER:N[1_655]	1.95	0.25
1:C:479:LYS:CE	1:C:607:ARG:C[2_445]	1.96	0.24
3:B:2861:HOH:O	3:C:2067:HOH:O[1_655]	1.98	0.22
1:A:65:PHE:CE2	1:C:2:ARG:NH2[2_555]	2.03	0.17
1:C:479:LYS:CE	1:C:608:GLN:CA[2_445]	2.04	0.16
1:C:479:LYS:CD	1:C:608:GLN:CB[2_445]	2.05	0.15
1:B:537:ARG:CD	1:C:581:GLU:OE1[1_655]	2.06	0.14
3:C:2426:HOH:O	3:C:2472:HOH:O[2_455]	2.11	0.09
3:B:2038:HOH:O	3:C:2327:HOH:O[2_555]	2.14	0.06
3:A:2029:HOH:O	3:B:2263:HOH:O[2_646]	2.19	0.01

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	662/664 (100%)	645 (97%)	12 (2%)	5 (1%)	16	11
1	B	662/664 (100%)	645 (97%)	12 (2%)	5 (1%)	16	11
1	C	662/664 (100%)	645 (97%)	12 (2%)	5 (1%)	16	11
All	All	1986/1992 (100%)	1935 (97%)	36 (2%)	15 (1%)	16	11

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	136	SER
1	A	607	ARG
1	B	136	SER
1	B	607	ARG
1	C	136	SER
1	C	607	ARG
1	A	630	TYR
1	B	630	TYR
1	C	608	GLN
1	C	630	TYR
1	A	2	ARG
1	A	608	GLN
1	B	2	ARG
1	B	608	GLN
1	C	2	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	557/557 (100%)	535 (96%)	22 (4%)	28	28
1	B	557/557 (100%)	535 (96%)	22 (4%)	28	28
1	C	557/557 (100%)	535 (96%)	22 (4%)	28	28
All	All	1671/1671 (100%)	1605 (96%)	66 (4%)	28	28

All (66) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	ARG
1	A	43	LEU
1	A	49	ARG
1	A	74	ARG
1	A	78	ASN
1	A	81	ARG
1	A	82	THR
1	A	102	LEU
1	A	113	ASP
1	A	154	PRO
1	A	163	LYS
1	A	307	ARG
1	A	308	LEU
1	A	327	ASP
1	A	364	PRO
1	A	373	GLU
1	A	391	LEU
1	A	404	LEU
1	A	497	LEU
1	A	506	ARG
1	A	581	GLU
1	A	658	LEU
1	B	30	ARG
1	B	43	LEU
1	B	49	ARG
1	B	74	ARG
1	B	78	ASN
1	B	81	ARG
1	B	82	THR
1	B	102	LEU
1	B	113	ASP
1	B	154	PRO
1	B	163	LYS
1	B	307	ARG

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Mol	Chain	Res	Type
1	B	308	LEU
1	B	327	ASP
1	B	364	PRO
1	B	373	GLU
1	B	391	LEU
1	B	404	LEU
1	B	497	LEU
1	B	506	ARG
1	B	581	GLU
1	B	658	LEU
1	C	30	ARG
1	C	43	LEU
1	C	49	ARG
1	C	74	ARG
1	C	78	ASN
1	C	81	ARG
1	C	82	THR
1	C	102	LEU
1	C	113	ASP
1	C	154	PRO
1	C	163	LYS
1	C	307	ARG
1	C	308	LEU
1	C	327	ASP
1	C	364	PRO
1	C	373	GLU
1	C	391	LEU
1	C	404	LEU
1	C	497	LEU
1	C	506	ARG
1	C	581	GLU
1	C	658	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	A	26	GLN
1	A	78	ASN
1	A	89	HIS
1	A	91	ASN
1	A	191	GLN

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Mol	Chain	Res	Type
1	A	255	GLN
1	A	309	ASN
1	A	328	HIS
1	A	448	GLN
1	A	519	ASN
1	A	525	GLN
1	A	608	GLN
1	A	626	ASN
1	B	15	GLN
1	B	26	GLN
1	B	78	ASN
1	B	89	HIS
1	B	91	ASN
1	B	191	GLN
1	B	255	GLN
1	B	309	ASN
1	B	328	HIS
1	B	448	GLN
1	B	492	HIS
1	B	519	ASN
1	B	525	GLN
1	B	626	ASN
1	C	15	GLN
1	C	26	GLN
1	C	78	ASN
1	C	89	HIS
1	C	91	ASN
1	C	255	GLN
1	C	309	ASN
1	C	328	HIS
1	C	448	GLN
1	C	492	HIS
1	C	519	ASN
1	C	525	GLN
1	C	626	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	664/664 (100%)	0.33	31 (4%)	36	35	25, 37, 72, 159	0
1	B	664/664 (100%)	0.45	50 (7%)	20	19	25, 37, 72, 159	0
1	C	664/664 (100%)	0.37	31 (4%)	36	35	25, 37, 72, 159	0
All	All	1992/1992 (100%)	0.38	112 (5%)	30	29	25, 37, 72, 159	0

All (112) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	606	ALA	10.2
1	B	22	ILE	6.6
1	B	257	GLY	6.6
1	B	606	ALA	6.3
1	B	1	PRO	6.3
1	C	606	ALA	6.1
1	C	609	ALA	6.0
1	A	603	ALA	5.7
1	A	257	GLY	5.6
1	A	609	ALA	5.3
1	C	2	ARG	5.3
1	C	607	ARG	4.9
1	A	610	GLY	4.9
1	B	607	ARG	4.6
1	C	610	GLY	4.6
1	C	612	ALA	4.5
1	B	609	ALA	4.5
1	A	608	GLN	4.4
1	A	605	MET	4.3
1	C	1	PRO	4.3
1	B	20	ASN	4.2
1	B	217	THR	4.2
1	C	576	TRP	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	24	ALA	4.0
1	A	537	ARG	4.0
1	A	576	TRP	3.8
1	B	19	ALA	3.8
1	B	603	ALA	3.7
1	C	608	GLN	3.6
1	A	602	VAL	3.6
1	C	596	LEU	3.6
1	B	253	LYS	3.5
1	C	605	MET	3.5
1	C	664	ARG	3.5
1	A	599	SER	3.5
1	C	603	ALA	3.5
1	A	607	ARG	3.5
1	B	610	GLY	3.4
1	C	63	ASP	3.4
1	A	600	ARG	3.4
1	A	612	ALA	3.4
1	B	611	LEU	3.4
1	B	605	MET	3.3
1	A	581	GLU	3.3
1	A	629	GLN	3.3
1	C	470	ARG	3.2
1	B	254	GLU	3.2
1	B	256	TYR	3.1
1	A	148	GLY	3.1
1	A	1	PRO	3.1
1	B	600	ARG	3.1
1	B	21	ASN	3.1
1	C	479	LYS	3.1
1	A	604	SER	3.1
1	B	219	LYS	3.0
1	B	604	SER	3.0
1	B	26	GLN	3.0
1	C	315	LYS	2.9
1	C	478	GLY	2.9
1	B	63	ASP	2.9
1	C	22	ILE	2.9
1	A	22	ILE	2.8
1	C	650	SER	2.8
1	B	608	GLN	2.7
1	B	214	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	581	GLU	2.7
1	A	664	ARG	2.7
1	C	257	GLY	2.7
1	B	664	ARG	2.6
1	A	427	LYS	2.6
1	A	256	TYR	2.6
1	C	254	GLU	2.5
1	B	599	SER	2.5
1	B	629	GLN	2.4
1	B	16	MET	2.4
1	A	315	LYS	2.4
1	B	216	LYS	2.4
1	B	612	ALA	2.4
1	A	630	TYR	2.3
1	C	611	LEU	2.3
1	B	537	ARG	2.3
1	A	611	LEU	2.3
1	C	651	VAL	2.3
1	B	2	ARG	2.3
1	B	593	ARG	2.3
1	A	596	LEU	2.3
1	A	613	GLU	2.2
1	B	148	GLY	2.2
1	A	136	SER	2.2
1	C	556	ASP	2.2
1	B	576	TRP	2.2
1	B	262	ASP	2.2
1	B	602	VAL	2.2
1	B	60	TYR	2.2
1	B	594	ASP	2.2
1	B	25	GLN	2.1
1	B	255	GLN	2.1
1	B	470	ARG	2.1
1	C	511	SER	2.1
1	C	461	LYS	2.1
1	C	613	GLU	2.1
1	A	589	ASP	2.1
1	B	601	TYR	2.1
1	B	215	PRO	2.1
1	A	592	LYS	2.1
1	B	461	LYS	2.1
1	B	248	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	259	ASP	2.0
1	B	633	THR	2.0
1	C	555	LYS	2.0
1	C	604	SER	2.0
1	C	658	LEU	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MN	B	665	1/1	0.97	0.04	32,32,32,32	0
2	MN	C	665	1/1	0.98	0.04	32,32,32,32	0
2	MN	A	665	1/1	0.99	0.03	32,32,32,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.