



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:52 PM UTC

PDB ID : 2R7R / pdb_00002r7r
Title : Crystal Structure of Rotavirus SA11 VP1/RNA (UGUGACC) complex
Authors : Lu, X.; Harrison, S.C.; Tao, Y.J.; Patton, J.T.; Nibert, M.L.
Deposited on : 2007-09-09
Resolution : 2.60 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 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

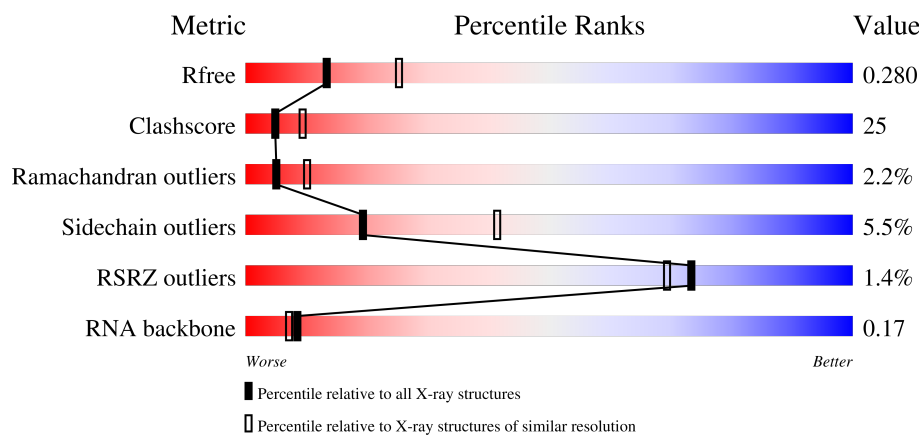
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	180053	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)
RNA backbone	3983	1014 (2.84-2.36)

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	X	7	29% 29% 43%
2	A	1095	% 53% 40% 6% .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8844 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 RNA chain called RNA (5'-R(*UP*GP*UP*GP*AP*CP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	X	7	Total	C	N	O	P	0	0	0
			145	66	25	48	6			

- Molecule 2 is a protein called RNA-dependent RNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	1073	Total	C	N	O	S	0	0	0
			8699	5579	1448	1634	38			

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.

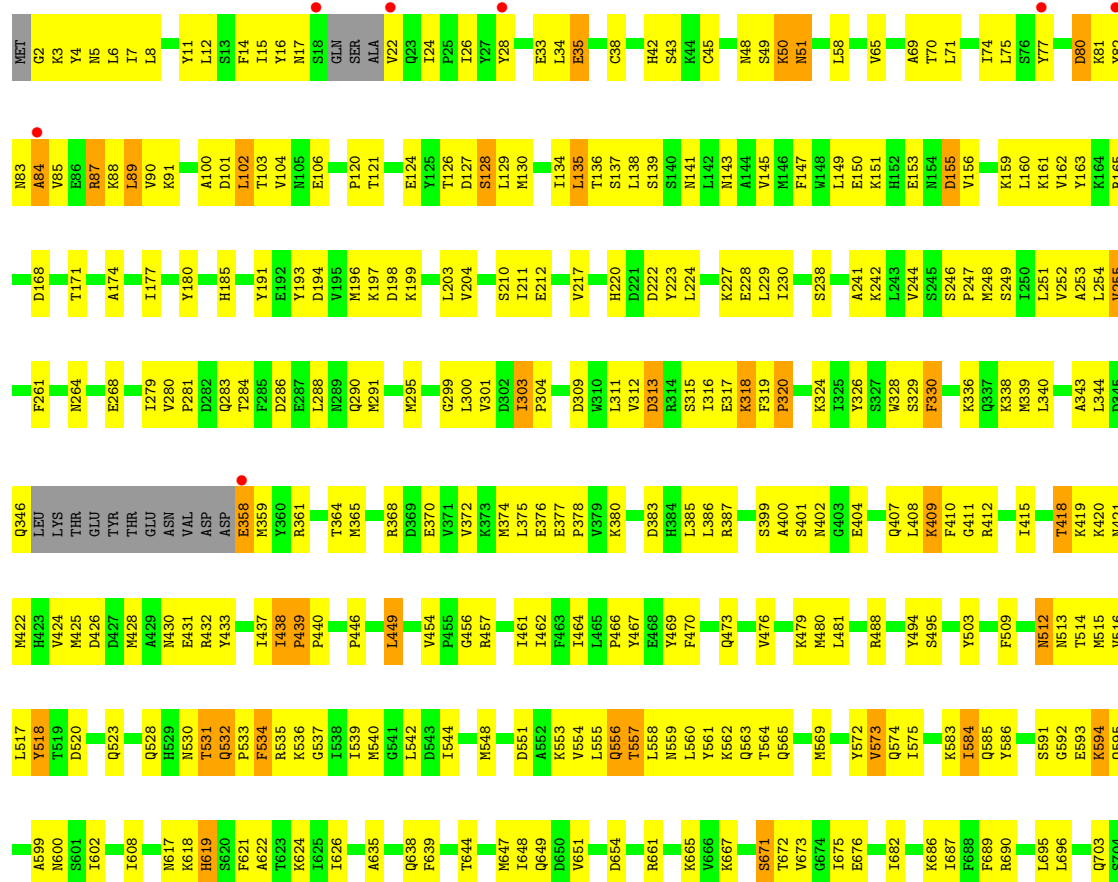
- Molecule 1: RNA (5'-R(*UP*GP*UP*GP*AP*CP*C)-3')

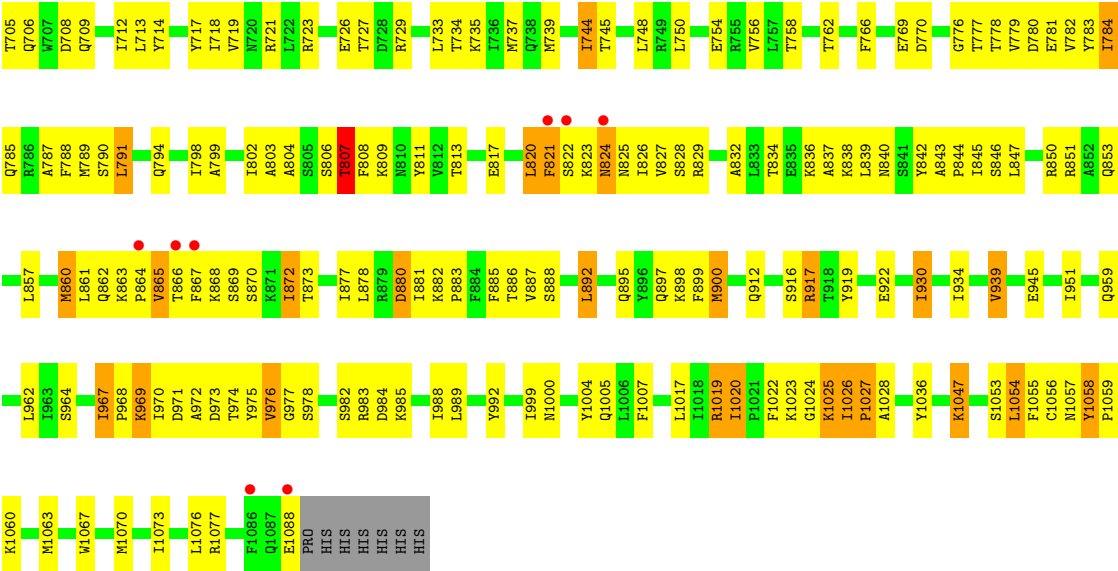
Chain X: 



- Molecule 2: RNA-dependent RNA polymerase

Chain A: 





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.35Å 112.75Å 143.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.60 50.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	84.5 (50.00-2.60) 84.5 (50.00-2.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 2.61Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.237 , 0.287 0.232 , 0.280	Depositor DCC
R_{free} test set	3030 reflections (7.88%)	wwPDB-VP
Wilson B-factor (Å ²)	52.0	Xtriage
Anisotropy	0.351	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 41.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8844	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.88% 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	X	0.42	0/161	1.12	3/249 (1.2%)
2	A	0.56	1/8870 (0.0%)	0.98	34/11989 (0.3%)
All	All	0.56	1/9031 (0.0%)	0.98	37/12238 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	303	ILE	CA-CB	5.56	1.56	1.54

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1020	ILE	N-CA-C	7.68	115.75	108.15
2	A	1026	ILE	CA-C-N	7.36	129.04	119.84
2	A	1026	ILE	C-N-CA	7.36	129.04	119.84
1	X	1103	U	C2'-C3'-O3'	6.81	119.71	109.50
2	A	939	VAL	N-CA-C	-6.32	105.53	112.80
2	A	744	ILE	N-CA-C	-6.32	104.88	111.58
2	A	449	LEU	N-CA-C	6.28	119.76	109.72
2	A	900	MET	CA-C-N	6.22	126.41	119.32
2	A	900	MET	C-N-CA	6.22	126.41	119.32
2	A	80	ASP	N-CA-C	-6.07	97.87	110.80
2	A	344	LEU	N-CA-C	5.97	117.79	111.28
2	A	573	VAL	N-CA-C	5.86	117.88	108.85
1	X	1102	G	C2'-C3'-O3'	5.75	118.12	109.50
2	A	1058	TYR	CA-C-N	5.64	125.95	119.92
2	A	1058	TYR	C-N-CA	5.64	125.95	119.92
2	A	89	LEU	N-CA-C	5.63	118.18	111.71
2	A	969	LYS	N-CA-C	5.58	117.81	111.11
2	A	1007	PHE	N-CA-C	5.58	118.33	110.23
2	A	255	VAL	N-CA-C	5.56	116.25	109.30
2	A	820	LEU	N-CA-C	5.50	117.62	110.53
2	A	138	LEU	N-CA-C	-5.44	105.00	111.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	881	ILE	N-CA-C	5.42	115.62	110.42
2	A	594	LYS	N-CA-C	-5.27	105.59	112.23
2	A	402	ASN	N-CA-C	-5.27	107.02	113.50
2	A	494	TYR	N-CA-C	5.25	117.92	110.10
2	A	967	ILE	CA-C-N	5.25	125.17	119.76
2	A	967	ILE	C-N-CA	5.25	125.17	119.76
2	A	162	VAL	N-CA-C	-5.25	105.28	111.00
2	A	330	PHE	N-CA-C	5.23	117.89	111.82
2	A	438	ILE	CA-C-N	5.21	125.75	120.38
2	A	438	ILE	C-N-CA	5.21	125.75	120.38
1	X	1101	U	C2'-C3'-O3'	5.17	117.26	109.50
2	A	488	ARG	N-CA-C	5.17	117.81	111.82
2	A	682	ILE	N-CA-C	5.13	114.96	107.37
2	A	727	THR	N-CA-C	-5.12	101.34	109.59
2	A	531	THR	N-CA-C	5.04	118.20	111.75
2	A	196	MET	N-CA-C	5.01	118.54	112.23

There are no chirality outliers.

There are no planarity outliers.

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	X	145	0	77	15	0
2	A	8699	0	8793	440	0
All	All	8844	0	8870	448	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 25.

All (448) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:520:ASP:HB3	2:A:667:LYS:HG2	1.33	1.07
2:A:865:VAL:HG22	2:A:866:THR:H	1.22	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:385:LEU:HD23	2:A:479:LYS:HE2	1.38	1.01
2:A:101:ASP:OD1	2:A:103:THR:HG22	1.66	0.96
2:A:556:GLN:HA	2:A:556:GLN:HE21	1.29	0.94
2:A:866:THR:HG22	2:A:867:PHE:H	1.34	0.91
1:X:1105:A:H5'	2:A:400:ALA:HB1	1.57	0.87
2:A:503:TYR:HB2	2:A:687:ILE:HD13	1.57	0.85
2:A:824:ASN:ND2	2:A:827:VAL:HB	1.92	0.85
2:A:24:ILE:HB	2:A:75:LEU:HB2	1.58	0.84
2:A:945:GLU:HG2	2:A:992:TYR:HE1	1.44	0.82
2:A:87:ARG:O	2:A:90:VAL:HG22	1.79	0.81
2:A:283:GLN:OE1	2:A:649:GLN:HG3	1.79	0.81
2:A:365:MET:HE1	2:A:540:MET:HE1	1.63	0.81
2:A:892:LEU:HD22	2:A:1017:LEU:HD11	1.64	0.80
2:A:515:MET:HE3	2:A:639:PHE:CE2	2.18	0.79
2:A:254:LEU:HD23	2:A:280:VAL:HG21	1.65	0.78
2:A:161:LYS:O	2:A:165:ARG:HG3	1.85	0.77
2:A:386:LEU:O	2:A:557:THR:HG21	1.85	0.77
2:A:84:ALA:HB1	2:A:88:LYS:NZ	2.01	0.76
2:A:573:VAL:HG12	2:A:575:ILE:HG13	1.68	0.74
2:A:438:ILE:HD12	2:A:563:GLN:HB3	1.69	0.74
2:A:865:VAL:HG22	2:A:866:THR:N	2.00	0.74
2:A:708:ASP:O	2:A:712:ILE:HG13	1.88	0.74
2:A:734:THR:HA	2:A:737:MET:HE3	1.69	0.73
2:A:820:LEU:H	2:A:820:LEU:HD23	1.53	0.73
2:A:667:LYS:HG3	2:A:667:LYS:O	1.89	0.73
2:A:446:PRO:HG2	2:A:583:LYS:HD3	1.70	0.72
2:A:622:ALA:HB3	2:A:638:GLN:HB3	1.71	0.72
2:A:866:THR:HG22	2:A:867:PHE:N	2.05	0.71
2:A:286:ASP:O	2:A:290:GLN:HG3	1.90	0.71
2:A:824:ASN:HD21	2:A:827:VAL:HB	1.56	0.71
2:A:885:PHE:CE1	2:A:1056:CYS:HB2	2.24	0.71
2:A:461:ILE:HD11	2:A:586:TYR:CZ	2.26	0.71
2:A:618:LYS:HD2	2:A:654:ASP:OD2	1.90	0.70
2:A:777:THR:HG21	2:A:882:LYS:HE3	1.72	0.69
2:A:1059:PRO:O	2:A:1063:MET:HG3	1.93	0.69
2:A:102:LEU:HD22	2:A:102:LEU:H	1.55	0.69
2:A:135:LEU:HD22	2:A:709:GLN:NE2	2.08	0.69
2:A:1019:ARG:HD2	2:A:1053:SER:OG	1.92	0.68
2:A:253:ALA:HB1	2:A:671:SER:HB2	1.76	0.68
2:A:343:ALA:O	2:A:346:GLN:HG3	1.93	0.68
1:X:1105:A:H5'	2:A:400:ALA:CB	2.22	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:80:ASP:O	2:A:81:LYS:HG3	1.94	0.68
2:A:217:VAL:HG13	2:A:222:ASP:HB2	1.74	0.68
2:A:553:LYS:O	2:A:557:THR:HG22	1.94	0.68
2:A:975:TYR:O	2:A:977:GLY:N	2.27	0.67
2:A:558:LEU:O	2:A:558:LEU:HD23	1.94	0.67
2:A:804:ALA:HA	2:A:809:LYS:HE3	1.74	0.67
2:A:84:ALA:HB1	2:A:88:LYS:HZ1	1.59	0.67
2:A:377:GLU:HB2	2:A:378:PRO:HD3	1.77	0.67
2:A:778:THR:O	2:A:782:VAL:HG23	1.95	0.67
2:A:865:VAL:CG2	2:A:866:THR:H	2.04	0.66
2:A:50:LYS:HG2	2:A:50:LYS:O	1.94	0.66
2:A:473:GLN:HG2	2:A:561:TYR:CE1	2.30	0.66
2:A:385:LEU:HD23	2:A:479:LYS:CE	2.21	0.66
2:A:1023:LYS:O	2:A:1060:LYS:HG2	1.95	0.66
2:A:120:PRO:HD2	2:A:124:GLU:OE2	1.96	0.66
2:A:419:LYS:HB2	2:A:422:MET:HG3	1.78	0.66
1:X:1104:G:H5'	2:A:401:SER:HB2	1.78	0.65
2:A:823:LYS:HE3	2:A:825:ASN:HD22	1.62	0.65
2:A:882:LYS:HB3	2:A:883:PRO:HD3	1.78	0.65
2:A:177:ILE:HD13	2:A:203:LEU:HD11	1.78	0.64
2:A:324:LYS:O	2:A:328:TRP:HD1	1.81	0.64
2:A:520:ASP:CB	2:A:667:LYS:HG2	2.21	0.64
2:A:528:GLN:O	2:A:531:THR:HG22	1.97	0.63
2:A:644:THR:OG1	2:A:647:MET:HG3	1.99	0.63
2:A:264:ASN:HD21	2:A:268:GLU:HG3	1.62	0.63
2:A:886:THR:OG1	2:A:1055:PHE:HB3	1.98	0.63
2:A:744:ILE:HD13	2:A:748:LEU:HD22	1.80	0.63
2:A:3:LYS:HA	2:A:6:LEU:HD23	1.80	0.62
2:A:644:THR:HG1	2:A:647:MET:HG3	1.64	0.62
2:A:820:LEU:HB2	2:A:964:SER:O	1.98	0.62
2:A:346:GLN:HG2	2:A:586:TYR:CE1	2.35	0.62
2:A:823:LYS:HE3	2:A:825:ASN:ND2	2.15	0.62
2:A:312:VAL:HG23	2:A:313:ASP:OD2	2.00	0.62
2:A:976:VAL:O	2:A:976:VAL:HG12	2.00	0.62
2:A:851:ARG:HH11	2:A:851:ARG:HG2	1.63	0.62
2:A:248:MET:HE1	2:A:319:PHE:CZ	2.35	0.62
2:A:248:MET:HE1	2:A:319:PHE:HZ	1.65	0.62
2:A:309:ASP:O	2:A:312:VAL:HG22	2.00	0.61
2:A:193:TYR:CE2	2:A:197:LYS:HD2	2.36	0.61
2:A:824:ASN:OD1	2:A:828:SER:HB2	2.00	0.61
2:A:860:MET:HE2	2:A:860:MET:HA	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:608:ILE:HD13	2:A:626:ILE:HG23	1.83	0.61
2:A:945:GLU:HG2	2:A:992:TYR:CE1	2.33	0.61
2:A:972:ALA:O	2:A:976:VAL:HG23	2.01	0.61
2:A:180:TYR:HB3	2:A:199:LYS:HG3	1.82	0.60
2:A:199:LYS:H	2:A:199:LYS:HD2	1.65	0.60
2:A:878:LEU:HD22	2:A:1036:TYR:HD1	1.65	0.60
2:A:821:PHE:N	2:A:821:PHE:CD2	2.68	0.60
2:A:556:GLN:HE21	2:A:556:GLN:CA	2.05	0.60
2:A:217:VAL:HG13	2:A:222:ASP:CB	2.32	0.60
1:X:1106:C:H2'	1:X:1107:C:O4'	2.02	0.60
2:A:135:LEU:HD22	2:A:709:GLN:HE21	1.67	0.59
2:A:719:VAL:HG12	2:A:723:ARG:HD2	1.84	0.59
2:A:85:VAL:HG21	2:A:139:SER:OG	2.03	0.59
2:A:165:ARG:HE	2:A:220:HIS:HA	1.66	0.59
2:A:516:VAL:HG21	2:A:675:ILE:CG2	2.33	0.59
2:A:1024:GLY:O	2:A:1025:LYS:CB	2.50	0.59
1:X:1105:A:C5'	2:A:400:ALA:HB1	2.29	0.59
2:A:191:TYR:CE2	2:A:204:VAL:HG11	2.37	0.59
2:A:301:VAL:C	2:A:304:PRO:HD2	2.27	0.59
2:A:984:ASP:O	2:A:988:ILE:HG12	2.03	0.59
2:A:318:LYS:HB2	2:A:318:LYS:NZ	2.18	0.58
2:A:518:TYR:H	2:A:518:TYR:HD2	1.48	0.58
2:A:212:GLU:HB2	2:A:696:LEU:HD12	1.85	0.58
2:A:798:ILE:O	2:A:802:ILE:HG22	2.02	0.58
2:A:1000:ASN:O	2:A:1005:GLN:HB3	2.03	0.58
2:A:385:LEU:CD2	2:A:479:LYS:HE2	2.25	0.58
2:A:279:ILE:HG22	2:A:648:ILE:HD12	1.84	0.58
2:A:255:VAL:HG11	2:A:316:ILE:HB	1.84	0.57
2:A:312:VAL:HG23	2:A:313:ASP:N	2.19	0.57
2:A:83:ASN:O	2:A:85:VAL:N	2.35	0.57
2:A:261:PHE:HD2	2:A:899:PHE:HB3	1.69	0.57
2:A:313:ASP:OD2	2:A:313:ASP:N	2.36	0.57
2:A:542:LEU:HD11	2:A:561:TYR:HD2	1.70	0.57
2:A:129:LEU:HD22	2:A:336:LYS:O	2.05	0.57
2:A:975:TYR:C	2:A:977:GLY:H	2.13	0.56
2:A:12:LEU:HD22	2:A:16:TYR:HE2	1.70	0.56
2:A:368:ARG:O	2:A:372:VAL:HG23	2.05	0.56
2:A:897:GLN:N	2:A:897:GLN:OE1	2.38	0.56
1:X:1103:U:O2'	1:X:1104:G:H5''	2.05	0.56
2:A:4:TYR:HD1	2:A:733:LEU:HD22	1.71	0.56
2:A:781:GLU:O	2:A:785:GLN:HG3	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:744:ILE:HD11	2:A:750:LEU:HB2	1.88	0.56
2:A:820:LEU:HD13	2:A:824:ASN:ND2	2.20	0.56
2:A:22:VAL:HG22	2:A:77:TYR:HB2	1.87	0.56
2:A:530:ASN:O	2:A:533:PRO:HD2	2.06	0.55
2:A:473:GLN:HE21	2:A:594:LYS:HB3	1.71	0.55
2:A:821:PHE:N	2:A:821:PHE:HD2	2.04	0.55
2:A:165:ARG:NE	2:A:220:HIS:HA	2.20	0.55
2:A:565:GLN:O	2:A:569:MET:HG2	2.07	0.55
2:A:261:PHE:CD2	2:A:899:PHE:HB3	2.42	0.55
2:A:617:ASN:N	2:A:617:ASN:HD22	2.04	0.55
2:A:784:ILE:HG23	2:A:788:PHE:CE2	2.41	0.55
2:A:407:GLN:O	2:A:408:LEU:HD23	2.07	0.55
2:A:102:LEU:HD22	2:A:102:LEU:N	2.22	0.54
1:X:1103:U:O2'	1:X:1104:G:P	2.65	0.54
2:A:866:THR:CG2	2:A:867:PHE:H	2.13	0.54
2:A:295:MET:HE1	2:A:303:ILE:HG22	1.89	0.54
2:A:428:MET:CE	2:A:811:TYR:HD1	2.20	0.54
2:A:8:LEU:HD13	2:A:737:MET:HG2	1.90	0.54
2:A:281:PRO:HG2	2:A:284:THR:OG1	2.07	0.54
2:A:687:ILE:HG23	2:A:900:MET:HG3	1.90	0.54
2:A:967:ILE:HD12	2:A:967:ILE:N	2.22	0.54
2:A:872:ILE:HG22	2:A:1073:ILE:HA	1.87	0.54
2:A:210:SER:OG	2:A:230:ILE:HG23	2.07	0.54
2:A:364:THR:HG23	2:A:537:GLY:CA	2.37	0.54
2:A:295:MET:O	2:A:300:LEU:HB2	2.08	0.54
2:A:762:THR:HA	2:A:1077:ARG:O	2.08	0.53
2:A:470:PHE:HE1	2:A:594:LYS:HD3	1.73	0.53
2:A:248:MET:HE2	2:A:252:VAL:CG1	2.38	0.53
2:A:6:LEU:N	2:A:6:LEU:HD22	2.24	0.53
2:A:887:VAL:HG22	2:A:1054:LEU:HD11	1.91	0.53
2:A:464:ILE:O	2:A:464:ILE:HG22	2.09	0.53
2:A:824:ASN:HB3	2:A:828:SER:HB2	1.91	0.53
2:A:837:ALA:O	2:A:840:ASN:ND2	2.41	0.53
2:A:851:ARG:HG2	2:A:851:ARG:NH1	2.24	0.53
2:A:248:MET:HE3	2:A:251:LEU:HB2	1.90	0.52
2:A:968:PRO:HG2	2:A:971:ASP:OD2	2.08	0.52
2:A:516:VAL:HG21	2:A:675:ILE:HG21	1.91	0.52
2:A:141:ASN:O	2:A:145:VAL:HG23	2.10	0.52
2:A:514:THR:HG22	2:A:638:GLN:HA	1.91	0.52
2:A:361:ARG:O	2:A:365:MET:HG2	2.09	0.52
2:A:137:SER:HB2	2:A:185:HIS:CD2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:248:MET:HE2	2:A:252:VAL:HG13	1.92	0.52
2:A:90:VAL:HG23	2:A:91:LYS:N	2.25	0.52
2:A:301:VAL:O	2:A:304:PRO:HD2	2.09	0.52
2:A:420:LYS:O	2:A:424:VAL:HG23	2.10	0.52
2:A:419:LYS:HB2	2:A:422:MET:CG	2.39	0.52
2:A:150:GLU:O	2:A:153:GLU:HB2	2.10	0.52
2:A:130:MET:HE1	2:A:191:TYR:HB2	1.92	0.51
2:A:518:TYR:CD2	2:A:518:TYR:N	2.78	0.51
2:A:647:MET:O	2:A:651:VAL:HG23	2.10	0.51
2:A:340:LEU:O	2:A:340:LEU:HD12	2.09	0.51
2:A:470:PHE:CE1	2:A:594:LYS:HD3	2.46	0.51
2:A:744:ILE:HD13	2:A:748:LEU:CD2	2.40	0.51
2:A:520:ASP:HB2	2:A:667:LYS:HE2	1.93	0.51
2:A:776:GLY:HA3	2:A:785:GLN:NE2	2.25	0.51
2:A:823:LYS:HG2	2:A:824:ASN:H	1.74	0.51
2:A:24:ILE:HD12	2:A:45:CYS:HB3	1.91	0.51
2:A:556:GLN:HA	2:A:556:GLN:NE2	2.11	0.51
2:A:820:LEU:C	2:A:821:PHE:HD2	2.18	0.51
2:A:375:LEU:C	2:A:378:PRO:HD2	2.36	0.51
2:A:242:LYS:O	2:A:246:SER:HB2	2.11	0.51
2:A:312:VAL:HG23	2:A:313:ASP:H	1.76	0.51
2:A:58:LEU:N	2:A:58:LEU:HD22	2.26	0.50
2:A:824:ASN:CG	2:A:828:SER:HB2	2.37	0.50
2:A:149:LEU:O	2:A:163:TYR:HE1	1.95	0.50
2:A:437:ILE:O	2:A:439:PRO:HD3	2.11	0.50
2:A:735:LYS:O	2:A:739:MET:HG3	2.11	0.50
2:A:860:MET:HE1	2:A:865:VAL:HG12	1.92	0.50
2:A:33:GLU:HG3	2:A:34:LEU:H	1.76	0.50
2:A:303:ILE:HB	2:A:304:PRO:HD3	1.92	0.50
2:A:466:PRO:HD2	2:A:469:TYR:CD2	2.47	0.50
2:A:703:GLN:CD	2:A:703:GLN:N	2.69	0.50
2:A:535:ARG:HH11	2:A:565:GLN:HE22	1.60	0.50
2:A:687:ILE:HG22	2:A:899:PHE:O	2.12	0.50
2:A:803:ALA:HA	2:A:808:PHE:CD2	2.46	0.50
2:A:536:LYS:O	2:A:540:MET:HG3	2.12	0.50
2:A:847:LEU:O	2:A:851:ARG:HG3	2.12	0.50
1:X:1105:A:C5	2:A:462:ILE:HD13	2.47	0.50
2:A:14:PHE:CE2	2:A:147:PHE:HB2	2.47	0.50
2:A:49:SER:C	2:A:51:ASN:H	2.20	0.50
2:A:789:MET:HE2	2:A:1076:LEU:HD21	1.93	0.50
2:A:1020:ILE:O	2:A:1020:ILE:HG22	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:288:LEU:HD21	2:A:311:LEU:HD11	1.93	0.49
2:A:370:GLU:HG2	2:A:602:ILE:HG23	1.94	0.49
2:A:512:ASN:C	2:A:512:ASN:HD22	2.19	0.49
2:A:842:TYR:CE2	2:A:844:PRO:HB2	2.47	0.49
2:A:319:PHE:N	2:A:320:PRO:CD	2.75	0.49
2:A:428:MET:HG2	2:A:433:TYR:CG	2.47	0.49
2:A:794:GLN:HG2	2:A:853:GLN:OE1	2.12	0.49
2:A:399:SER:HB3	2:A:838:LYS:HB3	1.94	0.49
2:A:1024:GLY:O	2:A:1025:LYS:HB3	2.11	0.49
2:A:126:THR:OG1	2:A:128:SER:HB3	2.12	0.49
2:A:279:ILE:O	2:A:648:ILE:HD12	2.13	0.49
2:A:523:GLN:HB2	2:A:665:LYS:O	2.12	0.49
2:A:4:TYR:HB3	2:A:754:GLU:OE1	2.13	0.49
2:A:185:HIS:CD2	2:A:185:HIS:H	2.31	0.49
2:A:100:ALA:O	2:A:102:LEU:HD22	2.13	0.49
2:A:254:LEU:CD2	2:A:280:VAL:HG21	2.40	0.49
2:A:383:ASP:O	2:A:387:ARG:HG3	2.13	0.49
2:A:462:ILE:HG23	2:A:591:SER:O	2.12	0.49
2:A:813:THR:O	2:A:817:GLU:HG3	2.13	0.49
2:A:847:LEU:HD23	2:A:850:ARG:NH1	2.27	0.49
2:A:165:ARG:HD3	2:A:223:TYR:CB	2.43	0.49
2:A:509:PHE:CD2	2:A:624:LYS:HB3	2.47	0.49
2:A:155:ASP:O	2:A:160:LEU:HD13	2.13	0.49
2:A:161:LYS:O	2:A:165:ARG:NH1	2.45	0.49
2:A:608:ILE:HD11	2:A:635:ALA:HB2	1.95	0.49
2:A:617:ASN:N	2:A:617:ASN:ND2	2.61	0.49
1:X:1103:U:O2'	1:X:1104:G:C5'	2.61	0.48
2:A:2:GLY:HA2	2:A:754:GLU:OE2	2.12	0.48
2:A:358:GLU:OE2	2:A:359:MET:HG2	2.13	0.48
2:A:823:LYS:HG2	2:A:824:ASN:N	2.29	0.48
2:A:989:LEU:HD11	2:A:1070:MET:HE3	1.94	0.48
2:A:428:MET:HG2	2:A:433:TYR:CB	2.43	0.48
2:A:721:ARG:HH11	2:A:721:ARG:CG	2.26	0.48
2:A:959:GLN:NE2	2:A:973:ASP:OD1	2.47	0.48
2:A:744:ILE:HG22	2:A:745:THR:HG23	1.95	0.48
2:A:756:VAL:HG13	2:A:788:PHE:CZ	2.49	0.48
2:A:758:THR:HG22	2:A:766:PHE:O	2.13	0.48
2:A:1028:ALA:HB1	2:A:1070:MET:HE2	1.96	0.48
2:A:134:ILE:HD13	2:A:136:THR:HG22	1.96	0.48
2:A:438:ILE:CD1	2:A:563:GLN:HB3	2.40	0.47
2:A:826:ILE:O	2:A:829:ARG:HG2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:246:SER:N	2:A:247:PRO:CD	2.78	0.47
2:A:248:MET:HE3	2:A:248:MET:O	2.14	0.47
2:A:860:MET:HE1	2:A:865:VAL:CG1	2.44	0.47
2:A:843:ALA:HB3	2:A:844:PRO:HD3	1.96	0.47
2:A:887:VAL:HG12	2:A:888:SER:N	2.29	0.47
2:A:542:LEU:O	2:A:558:LEU:HD21	2.15	0.47
2:A:917:ARG:NH1	2:A:1004:TYR:O	2.48	0.47
2:A:90:VAL:HG23	2:A:91:LYS:H	1.80	0.47
2:A:989:LEU:C	2:A:989:LEU:HD23	2.39	0.47
2:A:127:ASP:O	2:A:129:LEU:N	2.48	0.47
2:A:145:VAL:HG21	2:A:211:ILE:HG23	1.97	0.47
2:A:534:PHE:CZ	2:A:599:ALA:HB1	2.50	0.47
2:A:544:ILE:O	2:A:548:MET:HG3	2.14	0.47
2:A:794:GLN:HG2	2:A:853:GLN:CD	2.40	0.47
2:A:430:ASN:C	2:A:432:ARG:H	2.23	0.47
2:A:539:ILE:HG23	2:A:562:LYS:HE3	1.97	0.47
2:A:295:MET:HE1	2:A:303:ILE:CG2	2.45	0.47
2:A:330:PHE:CE1	2:A:690:ARG:CZ	2.98	0.47
2:A:791:LEU:HD23	2:A:791:LEU:N	2.30	0.47
2:A:619:HIS:ND1	2:A:619:HIS:N	2.63	0.46
2:A:789:MET:HE1	2:A:873:THR:HG21	1.97	0.46
1:X:1101:U:O2'	1:X:1102:G:P	2.73	0.46
2:A:102:LEU:H	2:A:102:LEU:CD2	2.24	0.46
2:A:532:GLN:HG3	2:A:536:LYS:HE3	1.97	0.46
2:A:695:LEU:HG	2:A:713:LEU:CD1	2.45	0.46
2:A:228:GLU:OE1	2:A:303:ILE:HG13	2.15	0.46
2:A:667:LYS:O	2:A:667:LYS:CG	2.60	0.46
2:A:689:PHE:HB2	2:A:723:ARG:HG2	1.97	0.46
2:A:719:VAL:CG1	2:A:723:ARG:HD2	2.46	0.46
2:A:449:LEU:CD2	2:A:573:VAL:HG11	2.45	0.46
2:A:514:THR:O	2:A:672:THR:HG22	2.15	0.46
2:A:721:ARG:HH11	2:A:721:ARG:HG3	1.80	0.46
2:A:974:THR:HG22	2:A:974:THR:O	2.14	0.46
2:A:50:LYS:O	2:A:51:ASN:OD1	2.33	0.46
2:A:880:ASP:O	2:A:883:PRO:HD2	2.16	0.46
2:A:145:VAL:CG2	2:A:211:ILE:HG23	2.46	0.46
2:A:449:LEU:HD22	2:A:573:VAL:CG1	2.46	0.46
2:A:983:ARG:O	2:A:984:ASP:C	2.59	0.46
2:A:88:LYS:HA	2:A:91:LYS:HE2	1.98	0.46
2:A:516:VAL:N	2:A:671:SER:O	2.48	0.46
2:A:703:GLN:CD	2:A:703:GLN:H	2.24	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:473:GLN:NE2	2:A:595:GLN:HG2	2.30	0.46
2:A:969:LYS:O	2:A:970:ILE:C	2.59	0.46
2:A:101:ASP:O	2:A:103:THR:N	2.49	0.46
2:A:824:ASN:HB3	2:A:825:ASN:H	1.41	0.46
2:A:824:ASN:CB	2:A:828:SER:HB2	2.46	0.46
2:A:839:LEU:HB3	2:A:845:ILE:HD12	1.96	0.46
2:A:28:TYR:CE2	2:A:70:THR:HB	2.51	0.45
2:A:33:GLU:HG3	2:A:34:LEU:N	2.32	0.45
2:A:83:ASN:HB3	2:A:84:ALA:H	1.52	0.45
2:A:338:LYS:O	2:A:339:MET:C	2.59	0.45
2:A:409:LYS:H	2:A:409:LYS:HZ2	1.64	0.45
2:A:790:SER:HB3	2:A:791:LEU:HD23	1.97	0.45
2:A:4:TYR:CD1	2:A:733:LEU:HD22	2.50	0.45
2:A:22:VAL:CG2	2:A:77:TYR:HB2	2.46	0.45
2:A:244:VAL:CG1	2:A:329:SER:HB3	2.47	0.45
2:A:729:ARG:HE	2:A:770:ASP:CG	2.23	0.45
2:A:860:MET:HA	2:A:860:MET:CE	2.44	0.45
2:A:84:ALA:HB1	2:A:88:LYS:HZ2	1.80	0.45
2:A:135:LEU:HB3	2:A:706:GLN:HG2	1.98	0.45
2:A:249:SER:HB3	2:A:676:GLU:OE1	2.16	0.45
2:A:378:PRO:O	2:A:383:ASP:HB2	2.16	0.45
2:A:982:SER:O	2:A:985:LYS:HB2	2.17	0.45
2:A:1000:ASN:C	2:A:1005:GLN:HB3	2.40	0.45
2:A:467:TYR:C	2:A:467:TYR:CD1	2.95	0.45
2:A:101:ASP:C	2:A:103:THR:H	2.25	0.45
2:A:661:ARG:O	2:A:661:ARG:HG3	2.17	0.45
2:A:886:THR:HG1	2:A:1055:PHE:HB3	1.81	0.45
2:A:721:ARG:HD2	2:A:726:GLU:HG3	1.98	0.45
2:A:898:LYS:HE2	2:A:912:GLN:NE2	2.31	0.45
2:A:951:ILE:HG13	2:A:985:LYS:HG2	1.98	0.45
2:A:376:GLU:HG2	2:A:380:LYS:HE2	1.99	0.45
2:A:473:GLN:HE22	2:A:593:GLU:HB3	1.82	0.45
2:A:734:THR:CA	2:A:737:MET:HE3	2.43	0.45
2:A:1023:LYS:HD2	2:A:1058:TYR:O	2.17	0.45
2:A:88:LYS:O	2:A:91:LYS:HG3	2.17	0.44
2:A:665:LYS:HD3	2:A:665:LYS:HA	1.84	0.44
2:A:168:ASP:OD2	2:A:223:TYR:OH	2.24	0.44
2:A:476:VAL:O	2:A:480:MET:HG3	2.18	0.44
2:A:558:LEU:HD23	2:A:558:LEU:C	2.42	0.44
2:A:962:LEU:O	2:A:967:ILE:HD13	2.17	0.44
2:A:428:MET:HE2	2:A:811:TYR:HD1	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:198:ASP:HB2	2:A:199:LYS:HD2	2.00	0.44
2:A:806:SER:O	2:A:807:THR:C	2.60	0.44
1:X:1102:G:O2'	1:X:1103:U:P	2.75	0.44
2:A:11:TYR:O	2:A:14:PHE:HB3	2.18	0.44
2:A:199:LYS:H	2:A:199:LYS:CD	2.29	0.44
2:A:515:MET:HG2	2:A:639:PHE:HE2	1.82	0.44
2:A:551:ASP:HB3	2:A:554:VAL:HB	1.99	0.44
2:A:621:PHE:HA	2:A:638:GLN:O	2.18	0.44
2:A:412:ARG:O	2:A:412:ARG:HG2	2.18	0.44
2:A:534:PHE:HZ	2:A:599:ALA:HB1	1.81	0.44
2:A:860:MET:C	2:A:862:GLN:H	2.26	0.44
2:A:930:ILE:O	2:A:934:ILE:HG13	2.16	0.44
2:A:1026:ILE:HD11	2:A:1067:TRP:CG	2.53	0.44
2:A:87:ARG:H	2:A:87:ARG:HG2	1.42	0.44
2:A:165:ARG:HB3	2:A:223:TYR:HB2	1.98	0.44
2:A:532:GLN:CB	2:A:533:PRO:HD3	2.48	0.44
2:A:857:LEU:O	2:A:861:LEU:HD13	2.17	0.44
2:A:3:LYS:O	2:A:7:ILE:HG12	2.17	0.44
2:A:408:LEU:HD22	2:A:426:ASP:CG	2.43	0.44
2:A:421:ASN:O	2:A:425:MET:HG3	2.18	0.44
2:A:5:ASN:CG	2:A:71:LEU:HD23	2.43	0.43
2:A:248:MET:HG2	2:A:326:TYR:CD1	2.53	0.43
2:A:420:LYS:HG2	2:A:467:TYR:HB3	1.99	0.43
2:A:572:TYR:CE1	2:A:585:GLN:HB2	2.53	0.43
2:A:193:TYR:CZ	2:A:197:LYS:HD2	2.53	0.43
2:A:834:THR:O	2:A:838:LYS:HG3	2.19	0.43
2:A:11:TYR:HA	2:A:147:PHE:CE1	2.54	0.43
2:A:255:VAL:O	2:A:673:VAL:HG21	2.18	0.43
2:A:1023:LYS:HZ1	2:A:1057:ASN:HA	1.83	0.43
2:A:555:LEU:O	2:A:559:ASN:HB2	2.19	0.43
2:A:705:THR:O	2:A:709:GLN:HG3	2.19	0.43
2:A:315:SER:C	2:A:317:GLU:N	2.74	0.43
2:A:409:LYS:HB2	2:A:409:LYS:NZ	2.34	0.43
2:A:832:ALA:O	2:A:836:LYS:HG3	2.19	0.43
2:A:89:LEU:HD11	2:A:174:ALA:CB	2.48	0.43
2:A:446:PRO:HB2	2:A:574:GLN:CG	2.48	0.43
2:A:449:LEU:HD21	2:A:573:VAL:HG11	2.01	0.43
2:A:469:TYR:CD1	2:A:564:THR:HG22	2.53	0.43
2:A:1058:TYR:HA	2:A:1059:PRO:HD3	1.87	0.43
2:A:454:VAL:CG1	2:A:457:ARG:HB3	2.49	0.43
2:A:853:GLN:NE2	2:A:853:GLN:HA	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:35:GLU:O	2:A:38:CYS:HB2	2.19	0.43
2:A:358:GLU:OE2	2:A:359:MET:CG	2.67	0.43
2:A:999:ILE:HD12	2:A:999:ILE:HA	1.88	0.43
2:A:877:ILE:O	2:A:880:ASP:HB2	2.19	0.42
2:A:424:VAL:HG22	2:A:467:TYR:CD2	2.54	0.42
2:A:481:LEU:HD23	2:A:481:LEU:HA	1.86	0.42
2:A:532:GLN:HB3	2:A:533:PRO:HD3	2.01	0.42
2:A:843:ALA:O	2:A:844:PRO:C	2.62	0.42
2:A:584:ILE:HD12	2:A:585:GLN:C	2.44	0.42
2:A:919:TYR:CD1	2:A:919:TYR:C	2.97	0.42
2:A:1047:LYS:HB2	2:A:1047:LYS:NZ	2.34	0.42
2:A:241:ALA:HB3	2:A:456:GLY:HA2	2.00	0.42
2:A:410:PHE:CE1	2:A:425:MET:HE3	2.55	0.42
2:A:244:VAL:HA	2:A:295:MET:HE3	2.01	0.42
2:A:404:GLU:C	2:A:418:THR:HG23	2.44	0.42
2:A:410:PHE:HE1	2:A:425:MET:HE3	1.84	0.42
2:A:779:VAL:HG23	2:A:780:ASP:N	2.34	0.42
2:A:959:GLN:CD	2:A:973:ASP:OD1	2.63	0.42
2:A:24:ILE:HG22	2:A:26:ILE:HD11	2.01	0.42
2:A:721:ARG:CG	2:A:721:ARG:NH1	2.83	0.42
2:A:744:ILE:CD1	2:A:748:LEU:HD22	2.48	0.42
2:A:161:LYS:HG2	2:A:165:ARG:CZ	2.50	0.42
2:A:512:ASN:HD22	2:A:513:ASN:N	2.18	0.42
2:A:130:MET:SD	2:A:130:MET:C	3.02	0.42
2:A:165:ARG:HD3	2:A:223:TYR:HB2	2.01	0.42
2:A:283:GLN:OE1	2:A:649:GLN:CG	2.59	0.42
2:A:428:MET:HE1	2:A:811:TYR:HD1	1.83	0.42
2:A:975:TYR:C	2:A:977:GLY:N	2.75	0.42
2:A:1023:LYS:NZ	2:A:1057:ASN:HA	2.34	0.42
2:A:8:LEU:HD23	2:A:74:ILE:HD12	2.02	0.42
2:A:769:GLU:HG2	2:A:1047:LYS:HZ2	1.84	0.42
2:A:617:ASN:ND2	2:A:617:ASN:H	2.18	0.41
2:A:244:VAL:HG12	2:A:329:SER:HB3	2.01	0.41
1:X:1103:U:O2'	1:X:1104:G:O5'	2.39	0.41
1:X:1107:C:OP1	2:A:594:LYS:NZ	2.49	0.41
2:A:28:TYR:HA	2:A:35:GLU:OE2	2.20	0.41
2:A:370:GLU:O	2:A:374:MET:HG3	2.20	0.41
2:A:438:ILE:HD11	2:A:560:LEU:HB3	2.01	0.41
2:A:806:SER:O	2:A:808:PHE:N	2.53	0.41
2:A:65:VAL:O	2:A:69:ALA:HB3	2.19	0.41
2:A:799:ALA:HB2	2:A:845:ILE:HD13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:1101:U:O2'	1:X:1102:G:OP1	2.35	0.41
2:A:101:ASP:O	2:A:104:VAL:HG13	2.21	0.41
2:A:324:LYS:O	2:A:328:TRP:CD1	2.66	0.41
2:A:863:LYS:HG3	2:A:863:LYS:O	2.21	0.41
2:A:8:LEU:HA	2:A:737:MET:SD	2.61	0.41
2:A:42:HIS:O	2:A:43:SER:C	2.64	0.41
2:A:319:PHE:N	2:A:320:PRO:HD2	2.36	0.41
2:A:473:GLN:HE22	2:A:595:GLN:H	1.67	0.41
2:A:744:ILE:CG1	2:A:748:LEU:HD22	2.51	0.41
2:A:803:ALA:HA	2:A:808:PHE:CE2	2.56	0.41
2:A:147:PHE:O	2:A:151:LYS:HG2	2.21	0.41
2:A:291:MET:O	2:A:295:MET:HG3	2.21	0.41
2:A:376:GLU:CG	2:A:380:LYS:HE2	2.51	0.41
2:A:449:LEU:HD13	2:A:573:VAL:HG13	2.03	0.41
2:A:842:TYR:CZ	2:A:844:PRO:HG2	2.56	0.41
2:A:15:ILE:HG22	2:A:16:TYR:CD1	2.55	0.41
2:A:430:ASN:O	2:A:432:ARG:N	2.54	0.41
2:A:769:GLU:HG2	2:A:1047:LYS:NZ	2.36	0.41
2:A:866:THR:O	2:A:867:PHE:HB2	2.21	0.41
2:A:199:LYS:HD2	2:A:199:LYS:N	2.32	0.40
2:A:299:GLY:O	2:A:301:VAL:HG23	2.21	0.40
2:A:714:TYR:O	2:A:717:TYR:HB3	2.21	0.40
2:A:824:ASN:O	2:A:825:ASN:HB2	2.21	0.40
2:A:846:SER:OG	2:A:850:ARG:NH2	2.54	0.40
2:A:253:ALA:CB	2:A:671:SER:HB2	2.47	0.40
2:A:439:PRO:HA	2:A:440:PRO:HD3	1.85	0.40
2:A:584:ILE:HD12	2:A:584:ILE:C	2.46	0.40
2:A:780:ASP:O	2:A:783:TYR:HB3	2.21	0.40
2:A:806:SER:C	2:A:808:PHE:N	2.80	0.40
2:A:168:ASP:O	2:A:171:THR:N	2.48	0.40
1:X:1105:A:C6	2:A:462:ILE:HD13	2.56	0.40
2:A:126:THR:O	2:A:126:THR:HG23	2.22	0.40
2:A:686:LYS:HD2	2:A:899:PHE:HA	2.02	0.40
2:A:714:TYR:CZ	2:A:718:ILE:HD11	2.57	0.40
2:A:787:ALA:O	2:A:790:SER:HB3	2.21	0.40
2:A:318:LYS:HB2	2:A:318:LYS:HZ2	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	
2	A	1067/1095 (97%)	949 (89%)	95 (9%)	23 (2%)	5	10

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	102	LEU
2	A	106	GLU
2	A	128	SER
2	A	865	VAL
2	A	976	VAL
2	A	978	SER
2	A	1025	LYS
2	A	822	SER
2	A	1027	PRO
2	A	82	TYR
2	A	84	ALA
2	A	870	SER
2	A	592	GLY
2	A	807	THR
2	A	238	SER
2	A	431	GLU
2	A	864	PRO
2	A	51	ASN
2	A	439	PRO
2	A	495	SER
2	A	534	PHE
2	A	869	SER
2	A	411	GLY

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	
2	A	975/996 (98%)	921 (94%)	54 (6%)	19	41

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	17	ASN
2	A	35	GLU
2	A	48	ASN
2	A	50	LYS
2	A	87	ARG
2	A	121	THR
2	A	135	LEU
2	A	143	ASN
2	A	155	ASP
2	A	156	VAL
2	A	159	LYS
2	A	194	ASP
2	A	224	LEU
2	A	227	LYS
2	A	229	LEU
2	A	313	ASP
2	A	318	LYS
2	A	320	PRO
2	A	358	GLU
2	A	409	LYS
2	A	415	ILE
2	A	418	THR
2	A	512	ASN
2	A	517	LEU
2	A	518	TYR
2	A	532	GLN
2	A	556	GLN
2	A	557	THR
2	A	584	ILE
2	A	600	ASN

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Mol	Chain	Res	Type
2	A	619	HIS
2	A	671	SER
2	A	784	ILE
2	A	791	LEU
2	A	807	THR
2	A	821	PHE
2	A	824	ASN
2	A	860	MET
2	A	868	LYS
2	A	872	ILE
2	A	880	ASP
2	A	892	LEU
2	A	895	GLN
2	A	916	SER
2	A	917	ARG
2	A	922	GLU
2	A	930	ILE
2	A	939	VAL
2	A	1019	ARG
2	A	1022	PHE
2	A	1027	PRO
2	A	1047	LYS
2	A	1054	LEU
2	A	1088	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	36	ASN
2	A	48	ASN
2	A	63	ASN
2	A	143	ASN
2	A	154	ASN
2	A	185	HIS
2	A	220	HIS
2	A	289	ASN
2	A	308	GLN
2	A	337	GLN
2	A	473	GLN
2	A	496	GLN
2	A	512	ASN
2	A	528	GLN

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Mol	Chain	Res	Type
2	A	529	HIS
2	A	530	ASN
2	A	556	GLN
2	A	563	GLN
2	A	565	GLN
2	A	574	GLN
2	A	579	ASN
2	A	617	ASN
2	A	646	GLN
2	A	653	ASN
2	A	698	ASN
2	A	709	GLN
2	A	760	ASN
2	A	810	ASN
2	A	824	ASN
2	A	825	ASN
2	A	853	GLN
2	A	895	GLN
2	A	908	GLN
2	A	912	GLN
2	A	959	GLN
2	A	1034	HIS
2	A	1043	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	X	7/7 (100%)	4 (57%)	3 (42%)

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	X	1102	G
1	X	1103	U
1	X	1104	G
1	X	1105	A

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	X	1101	U

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Mol	Chain	Res	Type
1	X	1102	G
1	X	1103	U

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](#)

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	X	7/7 (100%)	0.33	0 100 100	47, 63, 76, 81	0
2	A	1073/1095 (97%)	0.03	15 (1%) 73 69	16, 51, 80, 122	0
All	All	1080/1102 (98%)	0.04	15 (1%) 73 69	16, 51, 80, 122	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	824	ASN	4.7
2	A	1086	PHE	3.6
2	A	82	TYR	3.3
2	A	22	VAL	3.2
2	A	867	PHE	2.6
2	A	358	GLU	2.6
2	A	18	SER	2.5
2	A	866	THR	2.3
2	A	1088	GLU	2.3
2	A	84	ALA	2.2
2	A	28	TYR	2.2
2	A	864	PRO	2.2
2	A	77	TYR	2.1
2	A	821	PHE	2.1
2	A	822	SER	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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.