



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:22 AM GMT

PDB ID : 3I7K
Title : Crystal Structure of DDB1 in Complex with the H-Box Motif of WHX
Authors : Li, T.; Robert, E.I.; Breugel, P.C.V.; Strubin, M.; Zheng, N.
Deposited on : 2009-07-08
Resolution : 2.80 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

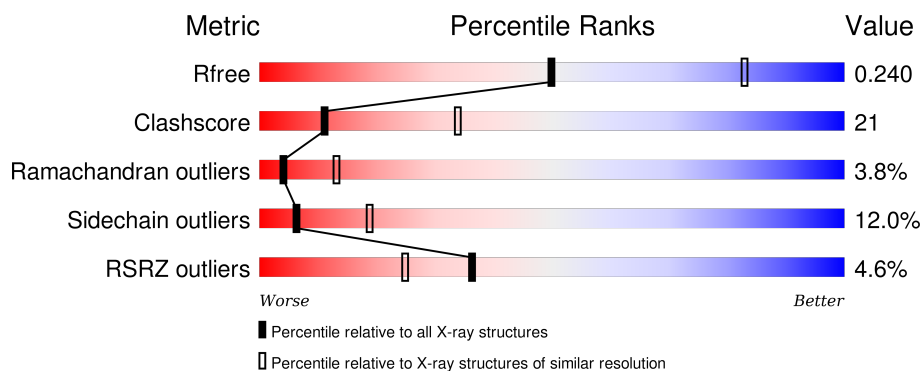
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.80 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}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	1143	 4% 56% 34% 7% . .
2	B	14	 7% 71% 29%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8843 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 DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1114	Total	C	N	O	S	0	0	0
			8726	5529	1472	1677	48			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	EXPRESSION TAG	UNP Q16531
A	-1	SER	-	EXPRESSION TAG	UNP Q16531
A	0	HIS	-	EXPRESSION TAG	UNP Q16531
A	422	TYR	ASP	SEE REMARK 999	UNP Q16531
A	898	ASP	GLU	SEE REMARK 999	UNP Q16531
A	899	VAL	LEU	SEE REMARK 999	UNP Q16531

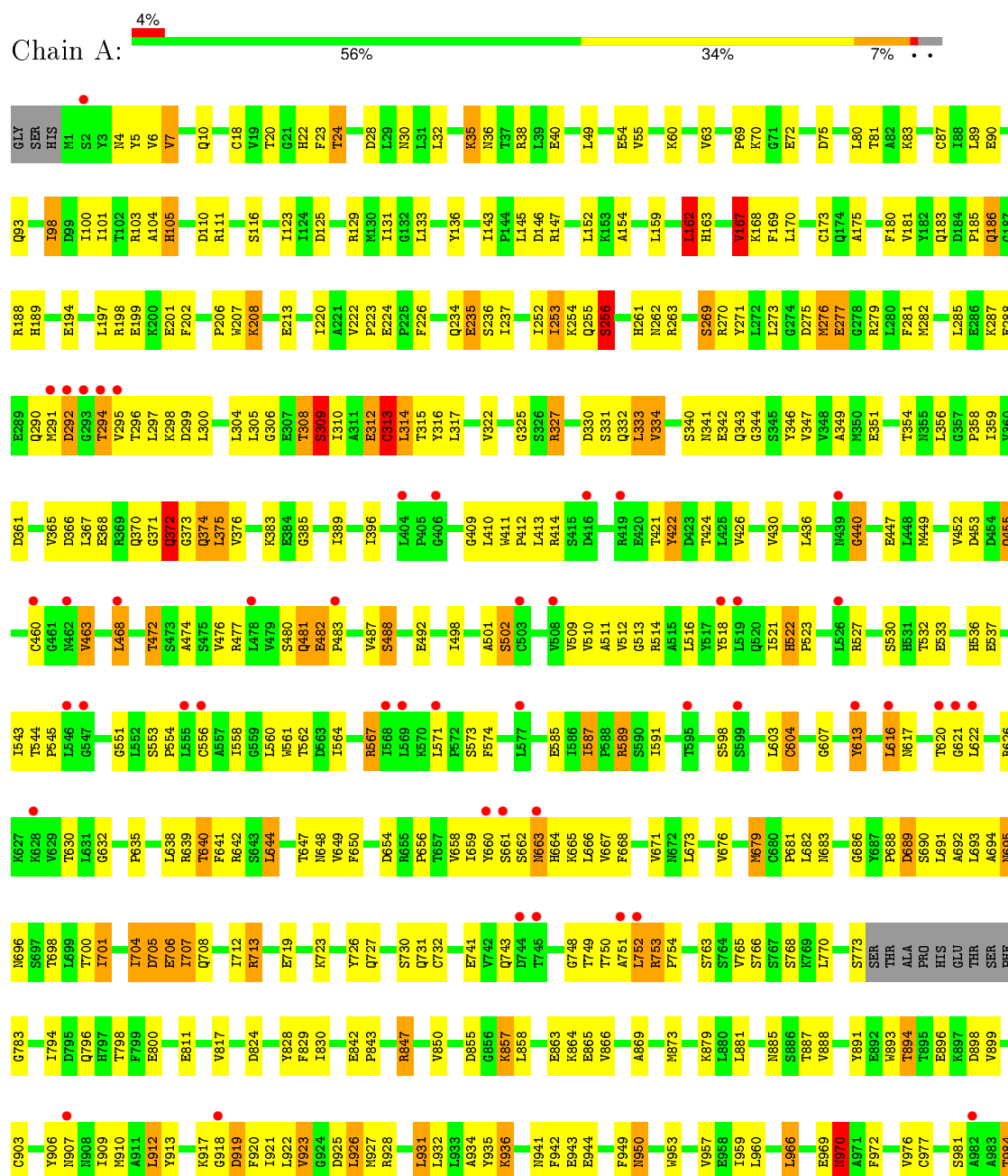
- Molecule 2 is a protein called X protein.

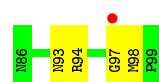
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	14	Total	C	N	O	S	0	0	0
			117	74	23	19	1			

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: DNA damage-binding protein 1





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.08Å 132.22Å 184.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.03 – 2.80 46.01 – 2.79	Depositor EDS
% Data completeness (in resolution range)	94.0 (46.03-2.80) 93.7 (46.01-2.79)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.230 , 0.271 0.233 , 0.240	Depositor DCC
R_{free} test set	1927 reflections (5.48%)	DCC
Wilson B-factor (Å ²)	55.8	Xtriage
Anisotropy	0.219	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 67.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 38701 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8843	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.94% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.65	1/8885 (0.0%)	0.86	18/12034 (0.1%)
2	B	0.90	0/121	1.64	2/162 (1.2%)
All	All	0.66	1/9006 (0.0%)	0.88	20/12196 (0.2%)

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	313	CYS	CB-SG	-7.51	1.69	1.82

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	290	GLN	CB-CA-C	20.20	150.81	110.40
1	A	309	SER	N-CA-CB	-17.48	84.28	110.50
1	A	291	MET	N-CA-C	-15.56	68.99	111.00
1	A	291	MET	CB-CA-C	-15.31	79.78	110.40
2	B	98	MET	N-CA-CB	-14.38	84.72	110.60
1	A	290	GLN	N-CA-C	-9.86	84.38	111.00
1	A	514	ARG	N-CA-CB	-9.56	93.38	110.60
2	B	98	MET	N-CA-C	8.54	134.06	111.00
1	A	308	THR	CB-CA-C	8.22	133.80	111.60
1	A	292	ASP	N-CA-C	7.53	131.33	111.00
1	A	1129	LEU	CA-CB-CG	6.58	130.42	115.30
1	A	992	LEU	CA-CB-CG	6.19	129.55	115.30
1	A	1000	LEU	CA-CB-CG	6.14	129.43	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	327	ARG	NE-CZ-NH1	5.95	123.28	120.30
1	A	829	PHE	N-CA-C	-5.83	95.27	111.00
1	A	167	VAL	CB-CA-C	-5.82	100.34	111.40
1	A	330	ASP	CB-CG-OD1	5.44	123.19	118.30
1	A	926	LEU	CA-CB-CG	5.41	127.74	115.30
1	A	865	GLU	N-CA-C	-5.34	96.58	111.00
1	A	314	LEU	CB-CG-CD2	-5.01	102.49	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	312	GLU	Peptide
1	A	522	HIS	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8726	0	8706	364	0
2	B	117	0	107	3	0
All	All	8843	0	8813	367	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 21.

All (367) 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:907:ASN:HB2	1:A:942:PHE:CZ	1.77	1.19
1:A:22:HIS:HD2	1:A:28:ASP:O	1.38	1.04
1:A:587:ILE:HD13	1:A:587:ILE:H	1.23	1.04
1:A:750:THR:HG22	1:A:751:ALA:N	1.71	1.03
1:A:750:THR:HG22	1:A:751:ALA:H	0.90	1.03
1:A:907:ASN:HB2	1:A:942:PHE:CE2	1.99	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:522:HIS:HB2	1:A:527:ARG:HH12	1.28	0.94
1:A:753:ARG:HG3	1:A:754:PRO:HD2	1.50	0.93
1:A:907:ASN:CB	1:A:942:PHE:CZ	2.52	0.93
1:A:907:ASN:HA	1:A:942:PHE:HZ	1.37	0.90
1:A:413:LEU:HB3	1:A:424:THR:HB	1.54	0.90
1:A:277:GLU:OE1	1:A:279:ARG:NH1	2.05	0.89
1:A:1051:LEU:HD22	1:A:1094:ILE:HD13	1.54	0.87
1:A:22:HIS:CD2	1:A:28:ASP:O	2.28	0.85
1:A:921:ILE:HG22	1:A:922:LEU:H	1.41	0.85
1:A:589:ARG:HG3	1:A:635:PRO:HB2	1.59	0.84
1:A:282:MET:HB2	1:A:305:LEU:HD21	1.61	0.82
1:A:750:THR:CG2	1:A:751:ALA:H	1.75	0.82
1:A:907:ASN:CA	1:A:942:PHE:HZ	1.94	0.81
1:A:753:ARG:CG	1:A:754:PRO:HD2	2.09	0.81
1:A:1061:VAL:HG21	1:A:1108:VAL:HG22	1.63	0.80
1:A:587:ILE:H	1:A:587:ILE:CD1	1.95	0.79
1:A:262:ASN:ND2	1:A:316:TYR:H	1.81	0.79
1:A:482:GLU:HB3	1:A:483:PRO:HD3	1.65	0.78
1:A:910:MET:O	1:A:910:MET:HG3	1.84	0.77
1:A:731:GLN:O	1:A:796:GLN:HG2	1.85	0.77
1:A:24:THR:H	1:A:30:ASN:HD21	1.30	0.77
1:A:480:SER:HB3	1:A:483:PRO:HD2	1.66	0.77
1:A:522:HIS:HB2	1:A:527:ARG:NH1	1.99	0.77
1:A:110:ASP:HB2	1:A:136:TYR:CE1	2.20	0.76
1:A:185:PRO:O	1:A:186:GLN:HB2	1.84	0.76
1:A:752:LEU:O	1:A:753:ARG:HB2	1.85	0.76
1:A:864:LYS:HE2	1:A:899:VAL:O	1.86	0.76
2:B:94:ARG:HA	2:B:97:GLY:O	1.87	0.75
1:A:907:ASN:HD21	1:A:909:ILE:HG13	1.50	0.74
1:A:285:LEU:HD22	1:A:300:LEU:HD22	1.69	0.74
1:A:383:LYS:HB3	1:A:753:ARG:NH2	2.03	0.73
1:A:1026:GLY:O	1:A:1041:THR:HG23	1.88	0.73
1:A:1032:THR:HB	1:A:1036:MET:H	1.53	0.73
1:A:613:TYR:H	1:A:613:TYR:HD2	1.34	0.73
1:A:752:LEU:O	1:A:753:ARG:CB	2.37	0.73
1:A:83:LYS:NZ	1:A:1077:HIS:HB3	2.03	0.73
1:A:1123:GLU:O	1:A:1124:ALA:HB3	1.89	0.72
1:A:562:THR:O	1:A:564:ILE:HD12	1.90	0.72
1:A:731:GLN:HA	1:A:796:GLN:HE21	1.54	0.71
1:A:1125:THR:HB	1:A:1128:ASP:HB2	1.73	0.71
1:A:770:LEU:HD12	1:A:847:ARG:HD2	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:309:SER:HB3	1:A:332:GLN:OE1	1.93	0.69
1:A:522:HIS:CB	1:A:527:ARG:HH12	2.03	0.69
1:A:55:VAL:HG11	1:A:100:ILE:HD12	1.72	0.69
1:A:752:LEU:C	1:A:752:LEU:HD12	2.13	0.69
1:A:396:ILE:HD11	1:A:673:LEU:HD11	1.75	0.69
1:A:1125:THR:HG22	1:A:1127:ASP:H	1.57	0.68
1:A:676:VAL:HG21	1:A:693:LEU:HD23	1.75	0.68
1:A:894:THR:HG22	1:A:896:GLU:H	1.57	0.68
1:A:907:ASN:CA	1:A:942:PHE:CZ	2.75	0.68
1:A:1032:THR:HG22	1:A:1034:ASN:H	1.59	0.67
1:A:375:LEU:HD12	1:A:376:VAL:N	2.11	0.66
1:A:502:SER:HB3	1:A:509:VAL:O	1.95	0.66
1:A:468:LEU:HD21	1:A:481:GLN:HG2	1.77	0.66
1:A:24:THR:CG2	1:A:28:ASP:OD2	2.44	0.66
1:A:308:THR:HG22	1:A:347:VAL:HG11	1.76	0.66
1:A:1123:GLU:N	1:A:1123:GLU:OE1	2.30	0.65
1:A:396:ILE:CD1	1:A:673:LEU:HD11	2.27	0.65
1:A:770:LEU:HG	1:A:863:GLU:OE1	1.97	0.64
1:A:1030:PHE:CZ	1:A:1038:GLY:HA3	2.32	0.64
1:A:919:ASP:CG	1:A:920:PHE:H	2.01	0.64
1:A:411:TRP:HB3	1:A:460:CYS:O	1.99	0.63
1:A:308:THR:CG2	1:A:347:VAL:HG11	2.28	0.62
1:A:907:ASN:OD1	1:A:909:ILE:HB	2.00	0.62
1:A:24:THR:H	1:A:30:ASN:ND2	1.97	0.62
1:A:285:LEU:HD13	1:A:297:LEU:HD11	1.80	0.62
1:A:72:GLU:OE2	1:A:103:ARG:NH2	2.27	0.62
1:A:726:TYR:OH	1:A:796:GLN:NE2	2.33	0.61
1:A:185:PRO:O	1:A:186:GLN:CB	2.48	0.61
1:A:55:VAL:HG11	1:A:100:ILE:CD1	2.29	0.61
1:A:1030:PHE:O	1:A:1037:ILE:HA	1.99	0.61
1:A:263:ARG:HH11	1:A:263:ARG:HG2	1.65	0.61
1:A:921:ILE:HG22	1:A:922:LEU:N	2.14	0.60
1:A:917:LYS:HD2	1:A:921:ILE:HD12	1.83	0.60
1:A:1122:ARG:C	1:A:1123:GLU:OE1	2.39	0.60
1:A:1110:ALA:C	1:A:1111:ASN:HD22	2.05	0.60
1:A:167:VAL:HG13	1:A:180:PHE:HB3	1.84	0.60
1:A:263:ARG:HB2	1:A:271:TYR:CE2	2.37	0.60
1:A:798:THR:OG1	1:A:800:GLU:HG2	2.01	0.60
1:A:409:GLY:O	1:A:410:LEU:HD23	2.01	0.60
1:A:389:ILE:N	1:A:389:ILE:HD12	2.17	0.60
1:A:1032:THR:HG22	1:A:1034:ASN:N	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:879:LYS:HB3	1:A:891:TYR:O	2.02	0.59
1:A:1057:ARG:HD3	1:A:1108:VAL:O	2.03	0.59
1:A:985:THR:HG22	1:A:989:ARG:HD3	1.84	0.59
1:A:660:TYR:HB2	1:A:667:VAL:HB	1.83	0.59
1:A:370:GLN:HB2	1:A:372:GLN:HG3	1.84	0.59
1:A:23:PHE:H	1:A:30:ASN:ND2	1.99	0.59
1:A:24:THR:HG21	1:A:28:ASP:OD2	2.02	0.59
1:A:38:ARG:HD2	1:A:54:GLU:OE1	2.03	0.59
1:A:1125:THR:HG22	1:A:1126:ALA:N	2.18	0.59
1:A:587:ILE:HD13	1:A:587:ILE:N	2.07	0.58
1:A:731:GLN:C	1:A:796:GLN:HG2	2.22	0.58
1:A:917:LYS:O	1:A:919:ASP:N	2.37	0.58
1:A:90:GLU:HB3	1:A:101:ILE:CG2	2.34	0.58
1:A:315:THR:HG22	1:A:317:LEU:HD23	1.84	0.58
1:A:1055:GLN:HE21	1:A:1089:ILE:HG23	1.68	0.58
1:A:226:PHE:HZ	1:A:287:LYS:HG2	1.67	0.58
1:A:917:LYS:HG2	1:A:959:ILE:HG21	1.86	0.58
1:A:1050:LEU:O	1:A:1053:ASP:HB3	2.03	0.58
1:A:662:SER:OG	1:A:663:ASN:N	2.37	0.57
1:A:1055:GLN:HE22	1:A:1089:ILE:HA	1.69	0.57
1:A:732:CYS:HB2	1:A:794:ILE:O	2.02	0.57
1:A:659:ILE:HG12	1:A:668:PHE:CE1	2.39	0.57
1:A:960:LEU:HD21	1:A:966:LEU:HB2	1.86	0.57
1:A:365:VAL:O	1:A:374:GLN:HB2	2.03	0.57
1:A:676:VAL:CG2	1:A:693:LEU:HD23	2.35	0.57
1:A:312:GLU:HG3	1:A:327:ARG:HD3	1.86	0.57
1:A:953:TRP:HB2	1:A:970:ASN:HB2	1.86	0.57
1:A:1122:ARG:C	1:A:1123:GLU:CD	2.63	0.57
1:A:705:ASP:O	1:A:706:GLU:O	2.22	0.57
1:A:642:ARG:HA	1:A:647:THR:HB	1.85	0.57
1:A:1123:GLU:O	1:A:1124:ALA:CB	2.52	0.57
1:A:926:LEU:HB3	1:A:931:LEU:HD11	1.86	0.56
1:A:90:GLU:HB3	1:A:101:ILE:HG22	1.87	0.56
1:A:741:GLU:HB3	1:A:749:THR:HB	1.87	0.56
1:A:888:VAL:HB	1:A:907:ASN:OD1	2.05	0.56
1:A:613:TYR:CD2	1:A:613:TYR:N	2.73	0.56
1:A:234:GLN:O	1:A:236:SER:N	2.38	0.56
1:A:558:ILE:HG23	1:A:567:ARG:HG2	1.87	0.56
1:A:1102:ARG:NH2	1:A:1126:ALA:HB1	2.19	0.56
1:A:691:LEU:O	1:A:701:ILE:HA	2.06	0.56
1:A:811:GLU:OE1	1:A:847:ARG:NH1	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:341:ASN:OD1	1:A:342:GLU:O	2.24	0.56
1:A:342:GLU:C	1:A:344:GLY:H	2.09	0.56
1:A:660:TYR:CE1	1:A:707:ILE:HA	2.40	0.56
1:A:322:VAL:HB	1:A:334:VAL:HG12	1.88	0.56
1:A:312:GLU:HG3	1:A:327:ARG:HB2	1.88	0.56
1:A:925:ASP:OD1	1:A:925:ASP:C	2.44	0.56
1:A:7:VAL:HG13	1:A:1091:GLY:HA3	1.88	0.55
1:A:907:ASN:HD21	1:A:909:ILE:CG1	2.19	0.55
1:A:607:GLY:HA2	1:A:635:PRO:HB3	1.88	0.55
1:A:270:ARG:HB3	1:A:282:MET:CE	2.36	0.55
1:A:926:LEU:HG	1:A:927:MET:N	2.21	0.55
1:A:1048:TYR:O	1:A:1052:LEU:HB2	2.07	0.55
1:A:617:ASN:HB2	1:A:620:THR:H	1.72	0.55
1:A:170:LEU:HD13	1:A:207:TRP:CH2	2.42	0.55
1:A:313:CYS:HB3	1:A:325:GLY:HA3	1.89	0.54
1:A:613:TYR:HD2	1:A:613:TYR:N	2.02	0.54
1:A:468:LEU:CD2	1:A:481:GLN:HG2	2.36	0.54
1:A:367:LEU:HB2	1:A:374:GLN:HG3	1.89	0.54
1:A:752:LEU:C	1:A:752:LEU:CD1	2.75	0.54
1:A:1047:TRP:HZ3	1:A:1132:VAL:HG13	1.72	0.54
1:A:375:LEU:HD12	1:A:376:VAL:H	1.71	0.54
1:A:917:LYS:HG3	1:A:959:ILE:HD13	1.91	0.53
1:A:591:ILE:HG13	1:A:604:CYS:HB2	1.90	0.53
1:A:511:ALA:HB2	1:A:516:LEU:HD23	1.90	0.53
1:A:220:ILE:HG12	1:A:261:HIS:CE1	2.43	0.53
1:A:573:SER:O	1:A:574:PHE:HB2	2.08	0.53
1:A:206:PRO:O	1:A:207:TRP:HB3	2.09	0.53
1:A:396:ILE:HG22	1:A:704:ILE:HG12	1.89	0.53
1:A:22:HIS:O	1:A:75:ASP:HB2	2.08	0.53
1:A:385:GLY:HA3	1:A:719:GLU:O	2.09	0.53
1:A:1039:LEU:HD21	1:A:1139:ILE:HG23	1.89	0.53
1:A:6:VAL:HG22	1:A:1040:VAL:HG22	1.91	0.53
1:A:935:TYR:CD1	1:A:941:ASN:O	2.61	0.53
1:A:498:ILE:HG23	1:A:510:VAL:HB	1.91	0.53
1:A:1045:GLU:HG2	1:A:1046:SER:N	2.23	0.53
1:A:24:THR:HG22	1:A:28:ASP:OD2	2.09	0.53
1:A:383:LYS:CB	1:A:753:ARG:NH2	2.72	0.53
1:A:543:ILE:HD12	1:A:543:ILE:O	2.10	0.53
1:A:372:GLN:OE1	1:A:373:GLY:N	2.40	0.53
1:A:1136:LEU:O	1:A:1139:ILE:HB	2.08	0.53
1:A:129:ARG:NH2	1:A:197:LEU:HD21	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:532:THR:HG22	1:A:533:GLU:N	2.24	0.52
1:A:907:ASN:HA	1:A:942:PHE:CZ	2.29	0.52
1:A:492:GLU:HG3	1:A:512:VAL:HG21	1.92	0.52
1:A:235:GLU:HA	1:A:253:ILE:HG22	1.91	0.52
1:A:894:THR:HG22	1:A:896:GLU:N	2.25	0.52
1:A:426:VAL:HG21	1:A:460:CYS:SG	2.50	0.52
1:A:226:PHE:CD2	1:A:297:LEU:HD12	2.45	0.51
1:A:5:TYR:OH	1:A:1091:GLY:HA2	2.11	0.51
1:A:472:THR:HG23	1:A:474:ALA:H	1.74	0.51
1:A:110:ASP:HB2	1:A:136:TYR:HE1	1.73	0.51
1:A:18:CYS:N	1:A:313:CYS:SG	2.84	0.51
1:A:1006:VAL:O	1:A:1030:PHE:HA	2.11	0.51
1:A:727:GLN:HE21	1:A:730:SER:HB2	1.75	0.51
1:A:824:ASP:OD2	1:A:828:TYR:OH	2.23	0.51
1:A:864:LYS:CE	1:A:899:VAL:O	2.56	0.51
1:A:543:ILE:HG21	1:A:571:LEU:HD11	1.92	0.51
1:A:928:ARG:HE	1:A:928:ARG:HA	1.76	0.51
1:A:928:ARG:HD3	1:A:953:TRP:HA	1.92	0.50
1:A:18:CYS:HA	1:A:32:LEU:O	2.11	0.50
1:A:881:LEU:HD21	1:A:922:LEU:HD21	1.93	0.50
1:A:923:VAL:HG21	1:A:959:ILE:HG13	1.92	0.50
1:A:482:GLU:CB	1:A:483:PRO:HD3	2.39	0.50
1:A:104:ALA:O	1:A:105:HIS:HB3	2.11	0.50
1:A:93:GLN:HG3	1:A:98:ILE:HG22	1.94	0.50
1:A:83:LYS:HZ1	1:A:1077:HIS:HB3	1.77	0.50
1:A:163:HIS:CD2	1:A:183:GLN:HB3	2.47	0.50
1:A:1102:ARG:NH2	1:A:1126:ALA:CB	2.75	0.50
1:A:199:GLU:HG3	1:A:201:GLU:HG3	1.94	0.50
1:A:4:ASN:ND2	1:A:976:VAL:HG21	2.27	0.50
1:A:501:ALA:O	1:A:502:SER:HB2	2.11	0.50
1:A:936:LYS:HG3	1:A:943:GLU:HB2	1.92	0.50
1:A:706:GLU:HG3	1:A:707:ILE:N	2.27	0.50
1:A:1097:PHE:HE2	1:A:1130:ILE:HA	1.77	0.49
1:A:340:SER:HB3	1:A:346:TYR:CZ	2.47	0.49
1:A:942:PHE:CD1	1:A:942:PHE:O	2.64	0.49
1:A:536:HIS:HB2	1:A:560:LEU:HD13	1.93	0.49
1:A:984:THR:O	1:A:986:ASP:N	2.45	0.49
1:A:1054:MET:O	1:A:1058:LEU:HB2	2.12	0.49
1:A:564:ILE:CD1	1:A:585:GLU:HA	2.41	0.49
1:A:679:MET:HA	1:A:692:ALA:O	2.12	0.49
1:A:304:LEU:HD12	1:A:306:GLY:H	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:294:THR:HG22	1:A:295:VAL:H	1.78	0.49
1:A:656:PRO:HB2	1:A:671:VAL:HB	1.94	0.49
1:A:811:GLU:OE2	1:A:847:ARG:NH1	2.41	0.49
1:A:10:GLN:O	1:A:1036:MET:O	2.30	0.49
1:A:452:VAL:HG13	1:A:477:ARG:CZ	2.43	0.49
1:A:270:ARG:HB3	1:A:282:MET:HE1	1.94	0.49
1:A:741:GLU:CB	1:A:749:THR:HB	2.43	0.49
1:A:49:LEU:HD13	1:A:333:LEU:HD21	1.95	0.49
1:A:1080:ARG:HG2	1:A:1081:LYS:HG2	1.93	0.49
1:A:213:GLU:OE1	1:A:234:GLN:O	2.31	0.48
1:A:753:ARG:CG	1:A:754:PRO:CD	2.86	0.48
1:A:985:THR:HA	1:A:989:ARG:HB2	1.95	0.48
1:A:893:TRP:CE3	1:A:899:VAL:HG13	2.47	0.48
1:A:226:PHE:CZ	1:A:287:LYS:HG2	2.47	0.48
1:A:288:GLU:HG3	1:A:298:LYS:HD3	1.95	0.48
1:A:743:GLN:HB3	1:A:783:GLY:N	2.28	0.48
1:A:312:GLU:CG	1:A:327:ARG:HD3	2.44	0.48
1:A:1002:GLU:HB3	1:A:1032:THR:HG23	1.95	0.48
1:A:731:GLN:HA	1:A:796:GLN:NE2	2.24	0.47
1:A:949:PHE:O	1:A:950:ASN:HB3	2.14	0.47
1:A:83:LYS:NZ	1:A:1077:HIS:CB	2.76	0.47
1:A:518:TYR:HB3	1:A:530:SER:HB2	1.96	0.47
1:A:87:CYS:SG	1:A:89:LEU:HD21	2.55	0.47
1:A:660:TYR:CG	1:A:707:ILE:HG23	2.50	0.47
1:A:830:ILE:HG22	1:A:873:MET:HE1	1.96	0.47
1:A:923:VAL:CG2	1:A:959:ILE:HG13	2.45	0.47
1:A:1047:TRP:CZ3	1:A:1132:VAL:HG13	2.50	0.47
1:A:288:GLU:CG	1:A:298:LYS:HB2	2.45	0.47
2:B:93:ASN:O	2:B:97:GLY:O	2.33	0.47
1:A:440:GLY:O	1:A:686:GLY:HA3	2.14	0.47
1:A:864:LYS:HB2	1:A:899:VAL:HG23	1.97	0.47
1:A:679:MET:O	1:A:679:MET:SD	2.72	0.47
1:A:131:ILE:HG22	1:A:133:LEU:CD1	2.45	0.46
1:A:926:LEU:CB	1:A:931:LEU:HD11	2.45	0.46
1:A:1125:THR:CG2	1:A:1126:ALA:N	2.79	0.46
1:A:502:SER:OG	1:A:543:ILE:HG13	2.15	0.46
1:A:817:VAL:HG12	1:A:830:ILE:HB	1.98	0.46
1:A:518:TYR:HB2	1:A:574:PHE:CZ	2.51	0.46
1:A:1030:PHE:CE2	1:A:1038:GLY:HA3	2.50	0.46
1:A:69:PRO:HD2	1:A:72:GLU:HG3	1.98	0.46
1:A:143:ILE:HG12	1:A:154:ALA:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:GLN:HA	1:A:234:GLN:OE1	2.16	0.46
1:A:36:ASN:HD21	1:A:60:LYS:HG2	1.79	0.46
1:A:455:GLN:HA	1:A:455:GLN:HE21	1.80	0.46
1:A:616:LEU:HD12	1:A:622:LEU:O	2.16	0.46
1:A:910:MET:O	1:A:925:ASP:O	2.33	0.46
1:A:750:THR:CG2	1:A:751:ALA:N	2.45	0.46
1:A:919:ASP:HB3	1:A:921:ILE:HG13	1.98	0.46
1:A:1000:LEU:HD13	1:A:1002:GLU:HB2	1.98	0.45
1:A:679:MET:HB2	1:A:693:LEU:HG	1.98	0.45
1:A:359:ILE:HG13	1:A:1035:GLY:HA2	1.98	0.45
1:A:662:SER:HB3	1:A:665:LYS:HB3	1.97	0.45
1:A:288:GLU:HG3	1:A:298:LYS:HB2	1.99	0.45
1:A:690:SER:OG	1:A:691:LEU:N	2.50	0.45
1:A:424:THR:HG23	1:A:436:LEU:O	2.17	0.45
1:A:1045:GLU:CG	1:A:1046:SER:N	2.79	0.45
1:A:183:GLN:HG3	1:A:188:ARG:HG2	1.98	0.45
1:A:857:LYS:HB2	1:A:857:LYS:NZ	2.32	0.45
1:A:553:SER:HA	1:A:554:PRO:HD3	1.80	0.45
1:A:81:THR:HG22	1:A:83:LYS:H	1.81	0.44
1:A:1032:THR:HG22	1:A:1033:VAL:N	2.31	0.44
1:A:383:LYS:CB	1:A:753:ARG:HH21	2.30	0.44
2:B:94:ARG:CA	2:B:97:GLY:O	2.63	0.44
1:A:275:ASP:HB3	1:A:277:GLU:H	1.82	0.44
1:A:1127:ASP:O	1:A:1130:ILE:HG22	2.18	0.44
1:A:23:PHE:H	1:A:30:ASN:HD22	1.64	0.44
1:A:358:PRO:HA	1:A:1033:VAL:O	2.17	0.44
1:A:1107:GLU:C	1:A:1109:VAL:N	2.71	0.44
1:A:921:ILE:CG2	1:A:932:LEU:HD11	2.47	0.43
1:A:692:ALA:HA	1:A:700:THR:O	2.17	0.43
1:A:598:SER:HB2	1:A:664:HIS:NE2	2.33	0.43
1:A:383:LYS:HB3	1:A:753:ARG:HH21	1.82	0.43
1:A:811:GLU:CD	1:A:847:ARG:HH11	2.22	0.43
1:A:888:VAL:HB	1:A:907:ASN:CG	2.38	0.43
1:A:69:PRO:O	1:A:72:GLU:HB2	2.19	0.43
1:A:811:GLU:CD	1:A:847:ARG:NH1	2.72	0.43
1:A:695:ASN:OD1	1:A:698:THR:N	2.51	0.43
1:A:920:PHE:O	1:A:934:ALA:HA	2.18	0.43
1:A:81:THR:HG22	1:A:83:LYS:N	2.33	0.43
1:A:694:ALA:HA	1:A:698:THR:O	2.19	0.43
1:A:255:GLN:O	1:A:256:SER:C	2.57	0.43
1:A:997:LEU:O	1:A:998:PHE:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:925:ASP:OD1	1:A:926:LEU:N	2.52	0.42
1:A:270:ARG:HB3	1:A:282:MET:HE2	2.01	0.42
1:A:660:TYR:HB3	1:A:661:SER:H	1.56	0.42
1:A:123:ILE:HD12	1:A:169:PHE:CD1	2.54	0.42
1:A:173:CYS:C	1:A:175:ALA:H	2.23	0.42
1:A:414:ARG:HB2	1:A:422:TYR:HA	2.00	0.42
1:A:893:TRP:HE3	1:A:899:VAL:HG13	1.84	0.42
1:A:639:ARG:HG3	1:A:640:THR:N	2.34	0.42
1:A:864:LYS:HB2	1:A:899:VAL:CG2	2.50	0.42
1:A:269:SER:HB3	1:A:287:LYS:HE2	2.01	0.42
1:A:276:MET:O	1:A:310:ILE:HD13	2.19	0.42
1:A:1057:ARG:O	1:A:1061:VAL:HG23	2.18	0.42
1:A:690:SER:O	1:A:691:LEU:HD23	2.20	0.42
1:A:411:TRP:HB2	1:A:460:CYS:HB3	2.01	0.42
1:A:38:ARG:NH1	1:A:54:GLU:OE2	2.52	0.42
1:A:869:ALA:H	1:A:885:ASN:HB2	1.85	0.42
1:A:194:GLU:O	1:A:202:PHE:O	2.38	0.42
1:A:162:LEU:HD12	1:A:162:LEU:N	2.34	0.42
1:A:368:GLU:O	1:A:370:GLN:HG3	2.20	0.42
1:A:222:VAL:HA	1:A:223:PRO:HD3	1.85	0.42
1:A:926:LEU:HG	1:A:927:MET:H	1.84	0.41
1:A:332:GLN:HB2	1:A:351:GLU:O	2.20	0.41
1:A:389:ILE:HD13	1:A:713:ARG:HB3	2.02	0.41
1:A:828:TYR:HB3	1:A:850:VAL:HG13	2.02	0.41
1:A:93:GLN:HG3	1:A:98:ILE:CG2	2.50	0.41
1:A:40:GLU:HG2	1:A:54:GLU:HG2	2.02	0.41
1:A:294:THR:HG22	1:A:295:VAL:HG22	2.02	0.41
1:A:648:ASN:HB3	1:A:649:VAL:H	1.74	0.41
1:A:887:THR:HA	1:A:907:ASN:O	2.20	0.41
1:A:516:LEU:HB3	1:A:574:PHE:HE1	1.83	0.41
1:A:367:LEU:HA	1:A:367:LEU:HD23	1.81	0.41
1:A:312:GLU:CG	1:A:327:ARG:HB2	2.50	0.41
1:A:237:ILE:HD11	1:A:253:ILE:HD11	2.02	0.41
1:A:688:PRO:O	1:A:689:ASP:C	2.59	0.41
1:A:909:ILE:HA	1:A:926:LEU:HD13	2.01	0.41
1:A:1063:LYS:H	1:A:1063:LYS:HG2	1.69	0.41
1:A:1048:TYR:CE2	1:A:1052:LEU:HD12	2.55	0.41
1:A:361:ASP:OD2	1:A:723:LYS:HA	2.19	0.41
1:A:5:TYR:CE2	1:A:7:VAL:HG22	2.56	0.41
1:A:640:THR:O	1:A:681:PRO:HG3	2.21	0.41
1:A:1126:ALA:O	1:A:1130:ILE:HB	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:966:LEU:HD13	1:A:1007:PHE:CE2	2.56	0.41
1:A:977:CYS:HB3	1:A:992:LEU:HD13	2.03	0.41
1:A:1089:ILE:HG23	1:A:1094:ILE:HD12	2.03	0.41
1:A:920:PHE:HB3	1:A:935:TYR:HB3	2.02	0.41
1:A:571:LEU:HD23	1:A:574:PHE:CE2	2.55	0.41
1:A:706:GLU:HG3	1:A:707:ILE:H	1.86	0.41
1:A:5:TYR:OH	1:A:1091:GLY:CA	2.69	0.41
1:A:658:VAL:HG23	1:A:671:VAL:CG2	2.51	0.41
1:A:422:TYR:N	1:A:422:TYR:CD1	2.89	0.41
1:A:181:VAL:HA	1:A:189:HIS:O	2.21	0.41
1:A:63:VAL:HB	1:A:80:LEU:HB3	2.03	0.41
1:A:1032:THR:OG1	1:A:1036:MET:HB3	2.21	0.41
1:A:333:LEU:HA	1:A:333:LEU:HD12	1.82	0.41
1:A:273:LEU:HB2	1:A:281:PHE:HB2	2.03	0.41
1:A:700:THR:C	1:A:701:ILE:HD13	2.41	0.40
1:A:661:SER:HA	1:A:665:LYS:O	2.20	0.40
1:A:641:PHE:CE2	1:A:650:PHE:HB2	2.56	0.40
1:A:1089:ILE:CG2	1:A:1094:ILE:HD12	2.50	0.40
1:A:532:THR:CG2	1:A:533:GLU:N	2.84	0.40
1:A:842:GLU:HA	1:A:843:PRO:HD3	1.94	0.40
1:A:487:VAL:O	1:A:488:SER:HB3	2.21	0.40
1:A:544:THR:HA	1:A:545:PRO:HD2	1.91	0.40
1:A:411:TRP:HA	1:A:412:PRO:HD3	1.97	0.40
1:A:334:VAL:HG23	1:A:349:ALA:HA	2.04	0.40
1:A:545:PRO:HG3	1:A:551:GLY:H	1.86	0.40
1:A:632:GLY:HA3	1:A:654:ASP:OD1	2.22	0.40
1:A:558:ILE:HG23	1:A:567:ARG:CG	2.51	0.40
1:A:906:TYR:O	1:A:942:PHE:CZ	2.75	0.40
1:A:1104:LYS:O	1:A:1108:VAL:HG23	2.22	0.40
1:A:1101:SER:HB2	1:A:1103:PRO:HD2	2.03	0.40
1:A:111:ARG:HA	1:A:111:ARG:HD2	1.86	0.40
1:A:356:LEU:HD21	1:A:712:ILE:HD13	2.04	0.40
1:A:912:LEU:HD13	1:A:913:TYR:CZ	2.57	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	
1	A	1106/1143 (97%)	918 (83%)	145 (13%)	43 (4%)	4	12
2	B	12/14 (86%)	11 (92%)	1 (8%)	0	100	100
All	All	1118/1157 (97%)	929 (83%)	146 (13%)	43 (4%)	4	13

All (43) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	208	LYS
1	A	235	GLU
1	A	256	SER
1	A	689	ASP
1	A	706	GLU
1	A	753	ARG
1	A	918	GLY
1	A	986	ASP
1	A	1045	GLU
1	A	186	GLN
1	A	371	GLY
1	A	463	VAL
1	A	502	SER
1	A	513	GLY
1	A	644	LEU
1	A	683	ASN
1	A	707	ILE
1	A	748	GLY
1	A	894	THR
1	A	970	ASN
1	A	985	THR
1	A	987	GLU
1	A	162	LEU
1	A	855	ASP
1	A	1103	PRO

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Mol	Chain	Res	Type
1	A	35	LYS
1	A	372	GLN
1	A	430	VAL
1	A	621	GLY
1	A	696	ASN
1	A	919	ASP
1	A	950	ASN
1	A	998	PHE
1	A	1124	ALA
1	A	343	GLN
1	A	366	ASP
1	A	523	PRO
1	A	1014	MET
1	A	1037	ILE
1	A	105	HIS
1	A	440	GLY
1	A	488	SER
1	A	1065	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	977/1001 (98%)	858 (88%)	119 (12%)	6	18
2	B	12/12 (100%)	12 (100%)	0	100	100
All	All	989/1013 (98%)	870 (88%)	119 (12%)	6	19

All (119) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	VAL
1	A	20	THR
1	A	24	THR
1	A	35	LYS
1	A	70	LYS

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Mol	Chain	Res	Type
1	A	98	ILE
1	A	116	SER
1	A	125	ASP
1	A	145	LEU
1	A	146	ASP
1	A	147	ARG
1	A	152	LEU
1	A	159	LEU
1	A	162	LEU
1	A	167	VAL
1	A	168	LYS
1	A	198	ARG
1	A	208	LYS
1	A	224	GLU
1	A	252	ILE
1	A	253	ILE
1	A	254	LYS
1	A	256	SER
1	A	269	SER
1	A	276	MET
1	A	277	GLU
1	A	292	ASP
1	A	294	THR
1	A	296	THR
1	A	299	ASP
1	A	309	SER
1	A	313	CYS
1	A	314	LEU
1	A	331	SER
1	A	333	LEU
1	A	334	VAL
1	A	354	THR
1	A	372	GLN
1	A	374	GLN
1	A	375	LEU
1	A	421	THR
1	A	422	TYR
1	A	447	GLU
1	A	449	MET
1	A	453	ASP
1	A	455	GLN
1	A	463	VAL

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Mol	Chain	Res	Type
1	A	468	LEU
1	A	472	THR
1	A	476	VAL
1	A	481	GLN
1	A	482	GLU
1	A	521	ILE
1	A	537	GLU
1	A	556	CYS
1	A	561	TRP
1	A	567	ARG
1	A	587	ILE
1	A	589	ARG
1	A	603	LEU
1	A	604	CYS
1	A	613	TYR
1	A	616	LEU
1	A	626	ARG
1	A	630	THR
1	A	638	LEU
1	A	640	THR
1	A	644	LEU
1	A	663	ASN
1	A	666	LEU
1	A	679	MET
1	A	682	LEU
1	A	695	ASN
1	A	701	ILE
1	A	704	ILE
1	A	705	ASP
1	A	708	GLN
1	A	713	ARG
1	A	752	LEU
1	A	763	SER
1	A	765	VAL
1	A	766	SER
1	A	768	SER
1	A	773	SER
1	A	847	ARG
1	A	857	LYS
1	A	858	LEU
1	A	866	VAL
1	A	898	ASP

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Mol	Chain	Res	Type
1	A	903	CYS
1	A	912	LEU
1	A	923	VAL
1	A	931	LEU
1	A	936	LYS
1	A	944	GLU
1	A	957	VAL
1	A	966	LEU
1	A	969	GLU
1	A	970	ASN
1	A	972	PHE
1	A	981	SER
1	A	984	THR
1	A	986	ASP
1	A	990	GLN
1	A	992	LEU
1	A	994	GLU
1	A	1000	LEU
1	A	1036	MET
1	A	1041	THR
1	A	1042	SER
1	A	1045	GLU
1	A	1050	LEU
1	A	1052	LEU
1	A	1069	GLU
1	A	1081	LYS
1	A	1093	LEU
1	A	1102	ARG
1	A	1111	ASN
1	A	1139	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	ASN
1	A	22	HIS
1	A	30	ASN
1	A	36	ASN
1	A	105	HIS
1	A	156	ASN
1	A	163	HIS
1	A	262	ASN

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Mol	Chain	Res	Type
1	A	374	GLN
1	A	439	ASN
1	A	455	GLN
1	A	462	ASN
1	A	467	GLN
1	A	507	GLN
1	A	648	ASN
1	A	708	GLN
1	A	727	GLN
1	A	743	GLN
1	A	796	GLN
1	A	852	GLN
1	A	885	ASN
1	A	970	ASN
1	A	1034	ASN
1	A	1055	GLN
1	A	1070	HIS
1	A	1111	ASN
2	B	91	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	1114/1143 (97%)	-0.01	51 (4%)	36 25	11, 61, 144, 192	0
2	B	14/14 (100%)	0.05	1 (7%)	19 10	24, 35, 65, 68	0
All	All	1128/1157 (97%)	-0.01	52 (4%)	36 25	11, 61, 142, 192	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	569	LEU	7.0
1	A	483	PRO	6.6
1	A	571	LEU	4.8
1	A	519	LEU	4.7
1	A	294	THR	4.4
1	A	616	LEU	4.4
1	A	751	ALA	4.2
1	A	508	VAL	4.1
1	A	660	TYR	4.1
1	A	556	CYS	3.9
1	A	907	ASN	3.9
1	A	577	LEU	3.9
1	A	613	TYR	3.7
1	A	661	SER	3.6
1	A	404	LEU	3.5
1	A	439	ASN	3.5
2	B	97	GLY	3.3
1	A	292	ASP	3.2
1	A	295	VAL	3.1
1	A	406	GLY	3.1
1	A	503	CYS	3.0
1	A	628	LYS	3.0
1	A	745	THR	2.8
1	A	1015	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	621	GLY	2.7
1	A	918	GLY	2.6
1	A	462	ASN	2.6
1	A	622	LEU	2.6
1	A	555	LEU	2.6
1	A	460	CYS	2.6
1	A	293	GLY	2.5
1	A	599	SER	2.5
1	A	468	LEU	2.4
1	A	744	ASP	2.4
1	A	546	LEU	2.3
1	A	752	LEU	2.3
1	A	419	ARG	2.3
1	A	526	LEU	2.3
1	A	1108	VAL	2.3
1	A	982	ALA	2.3
1	A	2	SER	2.2
1	A	568	ILE	2.2
1	A	663	ASN	2.2
1	A	478	LEU	2.2
1	A	620	THR	2.2
1	A	518	TYR	2.2
1	A	291	MET	2.1
1	A	595	THR	2.1
1	A	416	ASP	2.1
1	A	1122	ARG	2.1
1	A	985	THR	2.0
1	A	547	GLY	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.