



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:10 AM GMT

PDB ID : 2ZUB
Title : Left handed RadA
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Deposited on : 2008-10-15
Resolution : 2.90 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

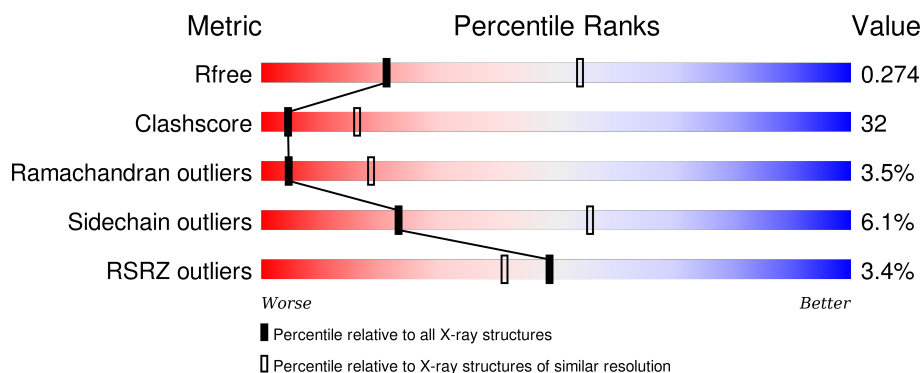
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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	324	<div> <div>3%</div> <div>40%</div> <div>46%</div> <div>•</div> <div>10%</div> </div>
1	B	324	<div> <div>3%</div> <div>44%</div> <div>40%</div> <div>5%</div> <div>10%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4619 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 repair and recombination protein radA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	290	Total	C	N	O	S	0	0	0
			2252	1417	401	428	6			
1	B	290	Total	C	N	O	S	0	0	0
			2252	1417	401	428	6			

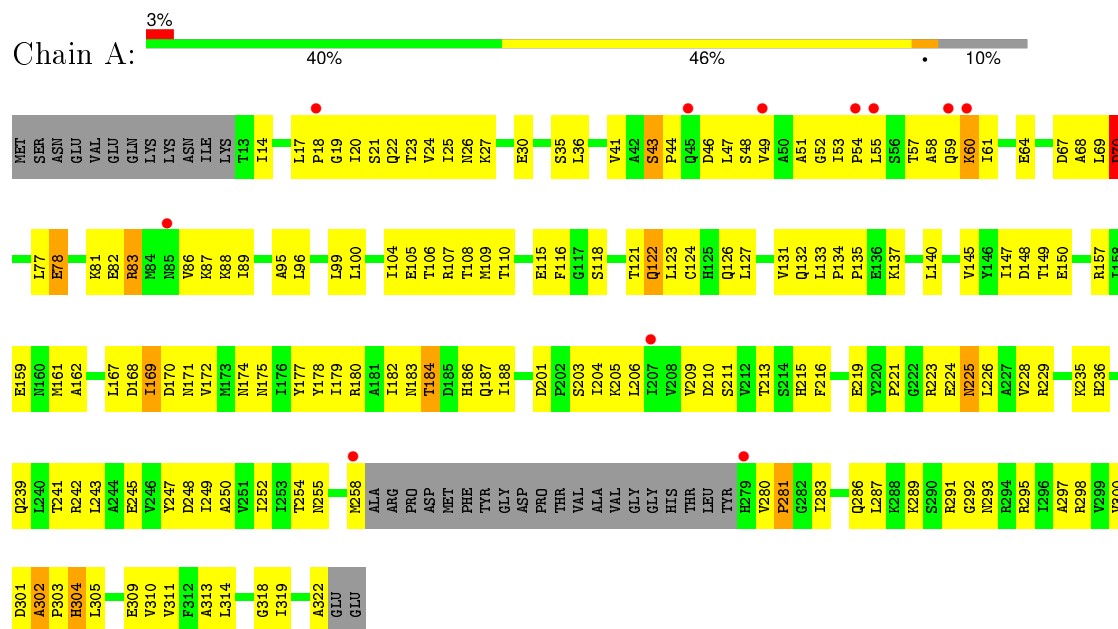
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	58	Total	O	0	0
			58	58		
2	B	57	Total	O	0	0
			57	57		

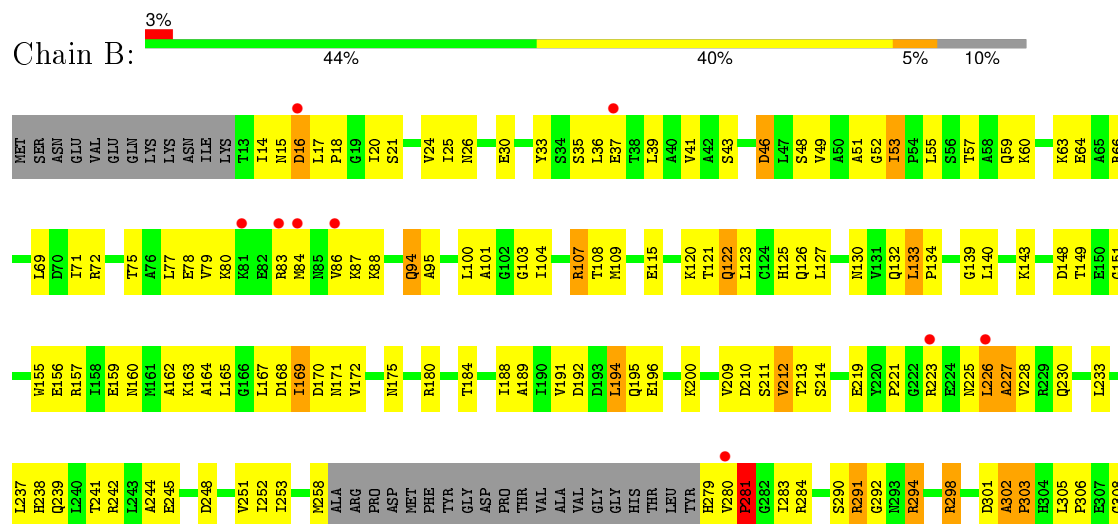
3 Residue-property plots

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 repair and recombination protein rada



- Molecule 1: DNA repair and recombination protein rada



F309	F310	F311	F312	A313	L314	F317	G318	L319	A322	GLU	GLU
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	50.78Å 103.47Å 130.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.90 28.53 – 2.90	Depositor EDS
% Data completeness (in resolution range)	95.2 (30.00-2.90) 95.2 (28.53-2.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 2.90Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.225 , 0.275 0.225 , 0.274	Depositor DCC
R_{free} test set	749 reflections (4.96%)	DCC
Wilson B-factor (Å ²)	49.9	Xtriage
Anisotropy	0.338	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 15107 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4619	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.08% 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	0.42	0/2282	0.65	0/3084
1	B	0.42	0/2282	0.65	0/3084
All	All	0.42	0/4564	0.65	0/6168

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2252	0	2314	161	0
1	B	2252	0	2314	142	0
2	A	58	0	0	0	0
2	B	57	0	0	1	0
All	All	4619	0	4628	296	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 32.

All (296) 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:224:GLU:HG3	1:A:225:ASN:H	1.05	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:ILE:HD13	1:A:131:VAL:HG12	1.36	1.03
1:A:221:PRO:HG3	1:B:291:ARG:HH12	1.22	1.02
1:B:94:GLN:HA	1:B:94:GLN:HE21	1.21	0.99
1:A:127:LEU:O	1:A:131:VAL:HG13	1.69	0.92
1:A:224:GLU:HG3	1:A:225:ASN:N	1.84	0.91
1:A:126:GLN:HE21	1:A:319:ILE:H	1.03	0.91
1:A:126:GLN:NE2	1:A:319:ILE:H	1.70	0.90
1:B:107:ARG:HG3	1:B:107:ARG:HH11	1.39	0.86
1:A:21:SER:O	1:A:24:VAL:HG22	1.76	0.86
1:A:95:ALA:HB1	1:A:310:VAL:HG21	1.58	0.86
1:A:55:LEU:H	1:A:55:LEU:HD12	1.41	0.84
1:A:47:LEU:HD21	1:A:61:ILE:HD11	1.58	0.84
1:A:109:MET:HE3	1:A:281:PRO:HA	1.59	0.84
1:A:132:GLN:NE2	1:A:175:ASN:HD22	1.76	0.83
1:B:148:ASP:HB3	1:B:180:ARG:HD2	1.60	0.83
1:A:122:GLN:H	1:A:122:GLN:NE2	1.79	0.81
1:B:200:LYS:O	1:B:200:LYS:HD3	1.80	0.81
1:B:94:GLN:NE2	1:B:94:GLN:HA	1.96	0.80
1:B:213:THR:HG22	1:B:233:LEU:HD21	1.66	0.78
1:B:107:ARG:HA	1:B:244:ALA:O	1.85	0.77
1:A:58:ALA:O	1:A:61:ILE:HG12	1.85	0.76
1:A:224:GLU:CG	1:A:225:ASN:H	1.90	0.76
1:A:221:PRO:HB2	1:B:291:ARG:HH22	1.50	0.75
1:A:221:PRO:HG3	1:B:291:ARG:NH1	2.01	0.75
1:B:55:LEU:O	1:B:59:GLN:HG2	1.87	0.74
1:B:209:VAL:HG11	1:B:212:VAL:HG13	1.70	0.73
1:A:110:THR:HG23	1:A:283:ILE:HB	1.70	0.73
1:A:149:THR:HB	1:A:210:ASP:O	1.89	0.73
1:A:105:GLU:HB2	1:A:108:THR:HG21	1.71	0.72
1:B:126:GLN:HG3	1:B:130:ASN:ND2	2.05	0.72
1:A:283:ILE:HG23	1:A:302:ALA:HB2	1.72	0.72
1:A:221:PRO:CB	1:B:291:ARG:HH22	2.03	0.72
1:A:291:ARG:HH11	1:A:291:ARG:HG3	1.55	0.71
1:B:242:ARG:HH11	1:B:242:ARG:HG2	1.55	0.71
1:B:200:LYS:C	1:B:200:LYS:HD3	2.11	0.71
1:A:57:THR:O	1:A:61:ILE:HG23	1.91	0.71
1:A:35:SER:HB3	1:A:298:ARG:HH22	1.57	0.70
1:A:87:LYS:HE3	1:A:135:PRO:HB3	1.72	0.70
1:B:130:ASN:HA	1:B:133:LEU:HD22	1.74	0.70
1:B:283:ILE:HD12	1:B:283:ILE:N	2.07	0.70
1:A:224:GLU:C	1:A:226:LEU:H	1.95	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:115:GLU:HG2	1:B:258:MET:HA	1.74	0.69
1:A:17:LEU:HD21	1:A:36:LEU:HD21	1.73	0.69
1:B:95:ALA:HB1	1:B:310:VAL:HG21	1.74	0.69
1:A:88:LYS:HE2	1:A:105:GLU:HG2	1.74	0.69
1:A:53:ILE:HD12	1:A:54:PRO:HD2	1.74	0.69
1:B:80:LYS:O	1:B:84:MET:HG2	1.93	0.68
1:A:49:VAL:HG12	1:A:49:VAL:O	1.94	0.67
1:B:104:ILE:HG12	1:B:252:ILE:HD11	1.76	0.67
1:B:127:LEU:HD13	1:B:252:ILE:CD1	2.25	0.67
1:B:107:ARG:HG3	1:B:107:ARG:NH1	2.07	0.66
1:B:233:LEU:O	1:B:237:LEU:HG	1.96	0.66
1:A:21:SER:HB2	1:A:23:THR:HG22	1.78	0.66
1:A:57:THR:HA	1:A:60:LYS:NZ	2.11	0.65
1:B:95:ALA:HB1	1:B:310:VAL:CG2	2.26	0.65
1:A:162:ALA:HA	1:A:167:LEU:HD12	1.79	0.65
1:B:17:LEU:O	1:B:20:ILE:HG22	1.97	0.65
1:B:130:ASN:HA	1:B:133:LEU:CD2	2.27	0.65
1:A:149:THR:HG22	1:A:150:GLU:HG3	1.79	0.65
1:B:126:GLN:HE21	1:B:319:ILE:H	1.46	0.64
1:B:226:LEU:C	1:B:226:LEU:HD23	2.18	0.64
1:B:196:GLU:OE2	1:B:196:GLU:N	2.31	0.64
1:A:57:THR:HA	1:A:60:LYS:HZ3	1.62	0.64
1:B:75:THR:HG22	1:B:78:GLU:HG3	1.79	0.64
1:A:126:GLN:HE21	1:A:319:ILE:N	1.86	0.63
1:A:27:LYS:HB3	1:A:27:LYS:NZ	2.13	0.63
1:A:132:GLN:HE22	1:A:172:VAL:HA	1.64	0.63
1:A:148:ASP:HB3	1:A:180:ARG:HG3	1.81	0.62
1:B:125:HIS:CG	1:B:157:ARG:HD2	2.33	0.62
1:A:127:LEU:HD12	1:A:252:ILE:CD1	2.30	0.62
1:A:68:ALA:C	1:A:70:ASP:H	2.01	0.62
1:B:212:VAL:HG21	1:B:253:ILE:HB	1.81	0.61
1:A:133:LEU:HD13	1:A:137:LYS:HB3	1.81	0.61
1:A:283:ILE:HG23	1:A:302:ALA:CB	2.31	0.61
1:A:51:ALA:C	1:A:53:ILE:H	2.03	0.61
1:B:132:GLN:HE22	1:B:172:VAL:HA	1.65	0.60
1:B:211:SER:HB3	1:B:214:SER:HB2	1.83	0.60
1:A:174:ASN:HB2	1:B:77:LEU:HD12	1.84	0.60
1:A:291:ARG:O	1:A:293:ASN:N	2.31	0.60
1:A:99:LEU:HD22	1:A:310:VAL:HG12	1.83	0.59
1:A:51:ALA:O	1:A:53:ILE:N	2.33	0.59
1:A:221:PRO:CG	1:B:291:ARG:HH22	2.15	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:GLN:H	1:A:122:GLN:CD	2.02	0.58
1:A:95:ALA:HB1	1:A:310:VAL:CG2	2.33	0.58
1:A:107:ARG:NH1	1:A:248:ASP:HB2	2.17	0.58
1:A:310:VAL:HG22	1:A:311:VAL:H	1.67	0.58
1:A:147:ILE:HD12	1:A:209:VAL:HG22	1.84	0.58
1:B:148:ASP:OD1	1:B:151:GLY:N	2.37	0.58
1:B:94:GLN:CA	1:B:94:GLN:HE21	2.06	0.58
1:A:301:ASP:O	1:A:302:ALA:HB2	2.04	0.57
1:A:106:THR:O	1:A:108:THR:HG22	2.04	0.57
1:A:289:LYS:HA	1:A:295:ARG:HD3	1.87	0.57
1:A:310:VAL:HG22	1:A:311:VAL:N	2.19	0.57
1:A:21:SER:OG	1:A:24:VAL:HG13	2.05	0.57
1:A:41:VAL:HG23	1:A:41:VAL:O	2.05	0.57
1:B:159:GLU:HA	1:B:169:ILE:HD12	1.86	0.57
1:A:121:THR:O	1:A:124:CYS:HB2	2.04	0.56
1:B:133:LEU:HB3	1:B:134:PRO:HD2	1.87	0.56
1:B:17:LEU:HD21	1:B:36:LEU:HD21	1.87	0.56
1:A:55:LEU:HD12	1:A:55:LEU:N	2.14	0.56
1:B:60:LYS:O	1:B:64:GLU:HG3	2.05	0.56
1:B:75:THR:CG2	1:B:78:GLU:HG3	2.36	0.56
1:B:162:ALA:HB3	1:B:169:ILE:HD13	1.86	0.56
1:A:60:LYS:HG2	1:A:60:LYS:O	2.04	0.56
1:A:184:THR:OG1	1:A:219:GLU:OE1	2.24	0.56
1:A:304:HIS:CG	1:A:305:LEU:H	2.24	0.55
1:B:148:ASP:OD1	1:B:151:GLY:CA	2.54	0.55
1:B:24:VAL:HG23	1:B:25:ILE:N	2.21	0.55
1:B:16:ASP:HB2	1:B:303:PRO:HB3	1.88	0.55
1:A:87:LYS:HB3	1:A:140:LEU:CD2	2.37	0.55
1:B:283:ILE:HD12	1:B:283:ILE:H	1.71	0.55
1:B:284:ARG:HG3	1:B:301:ASP:HB2	1.88	0.55
1:A:107:ARG:HG3	1:A:248:ASP:HA	1.90	0.54
1:B:298:ARG:NH2	1:B:308:GLY:H	2.06	0.54
1:A:55:LEU:CD1	1:A:55:LEU:H	2.17	0.54
1:A:184:THR:HG22	1:A:216:PHE:CZ	2.42	0.54
1:B:86:VAL:HG12	1:B:87:LYS:H	1.72	0.54
1:A:145:VAL:HG22	1:A:177:TYR:HB2	1.90	0.54
1:B:164:ALA:CB	1:B:317:GLU:HB3	2.38	0.54
1:B:53:ILE:HG23	1:B:57:THR:HB	1.89	0.54
1:A:224:GLU:O	1:A:226:LEU:N	2.40	0.53
1:B:126:GLN:HG2	1:B:319:ILE:HB	1.90	0.53
1:B:192:ASP:OD2	1:B:239:GLN:NE2	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:SER:HB3	1:A:287:LEU:HB2	1.90	0.53
1:A:289:LYS:HG2	1:A:295:ARG:NE	2.24	0.53
1:A:126:GLN:NE2	1:A:319:ILE:N	2.51	0.52
1:B:156:GLU:O	1:B:160:ASN:ND2	2.42	0.52
1:B:66:ARG:HH11	1:B:66:ARG:HG2	1.74	0.52
1:B:126:GLN:HG3	1:B:130:ASN:HD21	1.75	0.52
1:A:213:THR:OG1	1:A:255:ASN:ND2	2.42	0.52
1:A:22:GLN:NE2	1:A:25:ILE:HB	2.24	0.52
1:B:123:LEU:HD12	1:B:319:ILE:HG13	1.91	0.52
1:A:133:LEU:HB3	1:A:134:PRO:HD2	1.90	0.52
1:B:244:ALA:HB2	1:B:251:VAL:HG23	1.92	0.52
1:B:121:THR:HG22	1:B:125:HIS:CE1	2.45	0.52
1:A:177:TYR:CE1	1:A:204:ILE:HD11	2.45	0.52
1:B:52:GLY:O	1:B:53:ILE:O	2.28	0.52
1:B:33:TYR:CD2	1:B:39:LEU:HD23	2.45	0.51
1:A:77:LEU:O	1:A:81:LYS:HG2	2.09	0.51
1:B:123:LEU:CD1	1:B:319:ILE:HG13	2.39	0.51
1:B:37:GLU:O	1:B:41:VAL:HG22	2.09	0.51
1:A:297:ALA:O	1:A:309:GLU:HB2	2.10	0.51
1:B:195:GLN:HB2	1:B:196:GLU:OE2	2.11	0.51
1:B:191:VAL:HA	1:B:194:LEU:HD22	1.91	0.51
1:A:291:ARG:HG3	1:A:291:ARG:NH1	2.25	0.51
1:B:298:ARG:NH2	1:B:308:GLY:N	2.59	0.51
1:A:24:VAL:HG23	1:A:25:ILE:N	2.25	0.50
1:A:14:ILE:HG22	1:A:36:LEU:CD2	2.41	0.50
1:A:100:LEU:HD13	1:A:104:ILE:HD12	1.93	0.50
1:A:26:ASN:O	1:A:30:GLU:HB2	2.12	0.50
1:B:290:SER:HB2	1:B:294:ARG:HB2	1.92	0.50
1:A:126:GLN:HE22	1:A:318:GLY:HA3	1.77	0.50
1:A:57:THR:HG22	1:A:60:LYS:NZ	2.27	0.50
1:B:132:GLN:NE2	1:B:175:ASN:HD22	2.09	0.50
1:A:241:THR:O	1:A:245:GLU:HG3	2.11	0.50
1:A:82:GLU:O	1:A:86:VAL:HG12	2.12	0.50
1:B:242:ARG:NH1	1:B:242:ARG:HG2	2.25	0.50
1:A:27:LYS:HB3	1:A:27:LYS:HZ2	1.77	0.49
1:A:235:LYS:O	1:A:239:GLN:HB2	2.12	0.49
1:A:221:PRO:CG	1:B:291:ARG:HH12	2.09	0.49
1:A:115:GLU:O	1:A:116:PHE:C	2.51	0.49
1:A:99:LEU:O	1:A:305:LEU:HD22	2.12	0.49
1:B:148:ASP:OD1	1:B:151:GLY:HA2	2.13	0.49
1:B:301:ASP:O	1:B:302:ALA:HB2	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:GLU:HG2	1:A:258:MET:HA	1.95	0.49
1:A:47:LEU:HD23	1:A:58:ALA:HB1	1.95	0.49
1:A:53:ILE:HD12	1:A:54:PRO:CD	2.42	0.49
1:B:184:THR:HG23	1:B:219:GLU:OE2	2.13	0.49
1:B:104:ILE:HD12	1:B:104:ILE:N	2.28	0.48
1:A:188:ILE:HG12	1:A:236:HIS:HD2	1.77	0.48
1:A:64:GLU:HA	1:A:64:GLU:OE1	2.13	0.48
1:B:14:ILE:HG22	1:B:36:LEU:HG	1.95	0.48
1:A:184:THR:OG1	1:A:219:GLU:CD	2.52	0.48
1:B:189:ALA:O	1:B:192:ASP:HB2	2.13	0.48
1:A:57:THR:HG22	1:A:60:LYS:HZ3	1.79	0.48
1:B:127:LEU:HD13	1:B:252:ILE:HD13	1.96	0.48
1:B:17:LEU:HD21	1:B:36:LEU:CD2	2.43	0.48
1:A:247:TYR:O	1:A:249:ILE:HG13	2.13	0.48
1:B:149:THR:HB	1:B:210:ASP:O	2.13	0.48
1:A:131:VAL:HG11	1:A:206:LEU:HD22	1.95	0.48
1:A:20:ILE:HG23	1:A:25:ILE:HD11	1.95	0.48
1:B:35:SER:OG	1:B:37:GLU:HG2	2.14	0.48
1:B:122:GLN:H	1:B:122:GLN:HE21	1.60	0.48
1:A:69:LEU:O	1:A:70:ASP:C	2.52	0.48
1:B:212:VAL:CG2	1:B:253:ILE:HB	2.42	0.48
1:A:83:ARG:HG2	1:A:83:ARG:NH1	2.29	0.47
1:B:298:ARG:HB2	1:B:309:GLU:HB3	1.96	0.47
1:B:60:LYS:HA	1:B:63:LYS:HE2	1.96	0.47
1:A:14:ILE:HG22	1:A:36:LEU:HD23	1.96	0.47
1:B:86:VAL:HG12	1:B:87:LYS:N	2.29	0.47
1:A:83:ARG:HH11	1:A:83:ARG:HG2	1.78	0.47
1:B:298:ARG:HH21	1:B:308:GLY:HA2	1.79	0.47
1:A:123:LEU:HD12	1:A:319:ILE:HG13	1.97	0.47
1:B:155:TRP:HZ3	1:B:159:GLU:OE1	1.98	0.47
1:B:284:ARG:HD3	1:B:301:ASP:OD2	2.14	0.47
1:B:184:THR:O	1:B:188:ILE:HG12	2.14	0.47
1:A:205:LYS:HA	1:A:249:ILE:HG12	1.95	0.47
1:B:305:LEU:HA	1:B:306:PRO:HD3	1.64	0.47
1:B:17:LEU:HB2	1:B:20:ILE:HG21	1.96	0.47
1:B:241:THR:O	1:B:245:GLU:HG3	2.15	0.47
1:B:75:THR:HG23	1:B:78:GLU:H	1.80	0.46
1:A:157:ARG:C	1:A:159:GLU:N	2.69	0.46
1:B:21:SER:O	1:B:24:VAL:HG22	2.16	0.46
1:B:223:ARG:C	1:B:225:ASN:N	2.68	0.46
1:B:225:ASN:O	1:B:227:ALA:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:49:VAL:O	1:B:49:VAL:HG12	2.15	0.46
1:A:44:PRO:O	1:A:48:SER:HB2	2.15	0.46
1:A:178:TYR:CD2	1:A:179:ILE:N	2.84	0.46
1:A:127:LEU:HD12	1:A:252:ILE:HD12	1.98	0.46
1:B:107:ARG:HG2	1:B:248:ASP:HA	1.97	0.46
1:B:209:VAL:HG12	1:B:212:VAL:HG22	1.98	0.46
1:B:283:ILE:CD1	1:B:283:ILE:N	2.76	0.46
1:A:157:ARG:O	1:A:161:MET:HG3	2.16	0.46
1:B:165:LEU:O	1:B:167:LEU:HG	2.16	0.46
1:A:68:ALA:C	1:A:70:ASP:N	2.70	0.46
1:A:224:GLU:CG	1:A:225:ASN:N	2.58	0.45
1:A:304:HIS:CD2	1:A:305:LEU:H	2.34	0.45
1:A:20:ILE:CG2	1:A:25:ILE:HD11	2.47	0.45
1:B:48:SER:O	1:B:52:GLY:O	2.34	0.45
1:A:286:GLN:HB2	1:A:300:VAL:HG21	1.98	0.45
1:A:43:SER:CB	1:A:46:ASP:HB2	2.47	0.45
1:B:43:SER:HB3	1:B:46:ASP:OD1	2.17	0.45
1:A:24:VAL:CG2	1:A:25:ILE:N	2.79	0.45
1:B:122:GLN:OE1	1:B:314:LEU:HD13	2.16	0.45
1:B:238:HIS:HE1	1:B:280:VAL:HG22	1.81	0.45
1:B:164:ALA:HB1	1:B:317:GLU:HB3	1.99	0.45
1:A:87:LYS:HB3	1:A:140:LEU:HD22	1.99	0.45
1:A:206:LEU:HD12	1:A:250:ALA:O	2.16	0.44
1:A:20:ILE:HG13	1:A:24:VAL:CG2	2.46	0.44
1:A:122:GLN:HG3	1:A:314:LEU:HD13	2.00	0.44
1:B:168:ASP:HB3	1:B:171:ASN:HB2	1.99	0.44
1:A:188:ILE:HG12	1:A:236:HIS:CD2	2.53	0.44
1:A:168:ASP:O	1:A:171:ASN:N	2.50	0.44
1:A:178:TYR:CD2	1:A:178:TYR:C	2.91	0.44
1:A:67:ASP:O	1:A:70:ASP:HB2	2.18	0.44
1:B:133:LEU:HB3	1:B:134:PRO:CD	2.48	0.44
1:A:24:VAL:C	1:A:26:ASN:N	2.70	0.44
1:A:132:GLN:HE22	1:A:175:ASN:HD22	1.59	0.43
1:A:44:PRO:HB3	1:A:59:GLN:HG2	1.99	0.43
1:B:26:ASN:O	1:B:30:GLU:HG2	2.18	0.43
1:A:168:ASP:O	1:A:169:ILE:C	2.56	0.43
1:B:109:MET:HA	1:B:251:VAL:O	2.17	0.43
1:B:298:ARG:NH2	1:B:308:GLY:CA	2.81	0.43
1:A:224:GLU:C	1:A:226:LEU:N	2.63	0.43
1:A:283:ILE:HD11	1:A:304:HIS:CE1	2.54	0.43
1:B:242:ARG:NH1	1:B:242:ARG:CG	2.80	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:17:LEU:HA	1:B:18:PRO:HD3	1.91	0.43
1:A:43:SER:OG	1:A:46:ASP:HB2	2.18	0.43
1:B:143:LYS:HE2	1:B:175:ASN:OD1	2.18	0.43
1:B:223:ARG:C	1:B:225:ASN:H	2.22	0.43
1:B:21:SER:OG	1:B:24:VAL:HG13	2.19	0.43
1:A:20:ILE:HD11	1:A:24:VAL:HG21	2.00	0.43
1:A:107:ARG:CG	1:A:248:ASP:HA	2.48	0.42
1:A:215:HIS:HB3	1:A:219:GLU:OE2	2.18	0.42
1:A:127:LEU:HD23	1:A:127:LEU:HA	1.79	0.42
1:A:280:VAL:N	1:A:281:PRO:CD	2.83	0.42
1:A:27:LYS:NZ	1:A:51:ALA:O	2.52	0.42
1:B:75:THR:O	1:B:79:VAL:HG23	2.19	0.42
1:B:219:GLU:C	1:B:221:PRO:HD3	2.40	0.42
1:B:59:GLN:O	1:B:63:LYS:HG3	2.20	0.42
1:A:228:VAL:O	1:A:229:ARG:C	2.58	0.42
1:A:211:SER:N	1:A:254:THR:OG1	2.46	0.42
1:B:283:ILE:H	1:B:283:ILE:CD1	2.32	0.42
1:A:186:HIS:O	1:A:187:GLN:C	2.58	0.42
1:B:66:ARG:O	1:B:69:LEU:N	2.51	0.42
1:B:126:GLN:NE2	1:B:318:GLY:HA3	2.35	0.41
1:A:201:ASP:OD1	1:A:203:SER:HB3	2.19	0.41
1:A:301:ASP:O	1:A:302:ALA:CB	2.69	0.41
1:B:163:LYS:HZ3	1:B:169:ILE:HD11	1.85	0.41
1:A:88:LYS:CE	1:A:105:GLU:HG2	2.47	0.41
1:B:71:ILE:C	1:B:72:ARG:HD2	2.40	0.41
1:B:37:GLU:HA	1:B:69:LEU:HD11	2.02	0.41
1:B:280:VAL:O	1:B:281:PRO:O	2.38	0.41
1:A:313:ALA:HB2	1:A:322:ALA:HB2	2.02	0.41
1:A:304:HIS:ND1	1:A:304:HIS:N	2.68	0.41
1:A:304:HIS:CG	1:A:305:LEU:N	2.89	0.41
1:B:88:LYS:HD3	1:B:103:GLY:O	2.20	0.41
1:B:100:LEU:O	1:B:101:ALA:C	2.58	0.41
1:B:126:GLN:HE21	1:B:319:ILE:N	2.14	0.41
1:A:14:ILE:O	1:A:17:LEU:HG	2.20	0.41
1:B:139:GLY:O	1:B:140:LEU:HD23	2.20	0.41
1:A:182:ILE:HG13	1:A:183:ASN:N	2.36	0.41
1:B:24:VAL:CG2	1:B:25:ILE:N	2.83	0.41
1:B:311:VAL:HG22	1:B:312:PHE:N	2.36	0.41
1:B:120:LYS:HE3	1:B:120:LYS:HB2	1.86	0.41
1:A:51:ALA:C	1:A:53:ILE:N	2.69	0.41
1:B:314:LEU:HD23	1:B:319:ILE:HD13	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:143:LYS:HB3	1:B:175:ASN:O	2.22	0.40
1:A:18:PRO:HG3	1:A:64:GLU:HB3	2.03	0.40
1:B:302:ALA:HA	1:B:303:PRO:HD3	1.79	0.40
1:A:78:GLU:O	1:A:81:LYS:HB2	2.21	0.40
1:A:132:GLN:CD	1:A:175:ASN:HB2	2.42	0.40
1:B:115:GLU:HG3	2:B:357:HOH:O	2.21	0.40
1:A:49:VAL:O	1:A:49:VAL:CG1	2.65	0.40
1:B:298:ARG:NH2	1:B:308:GLY:HA2	2.36	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	286/324 (88%)	245 (86%)	31 (11%)	10 (4%)	4	18
1	B	286/324 (88%)	250 (87%)	26 (9%)	10 (4%)	4	18
All	All	572/648 (88%)	495 (86%)	57 (10%)	20 (4%)	4	18

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	292	GLY
1	A	302	ALA
1	A	303	PRO
1	B	51	ALA
1	B	53	ILE
1	B	281	PRO
1	A	169	ILE
1	A	225	ASN
1	B	226	LEU
1	B	227	ALA

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Mol	Chain	Res	Type
1	B	292	GLY
1	A	70	ASP
1	A	304	HIS
1	B	303	PRO
1	A	19	GLY
1	B	169	ILE
1	B	228	VAL
1	A	52	GLY
1	B	302	ALA
1	A	281	PRO

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	246/275 (90%)	234 (95%)	12 (5%)	31	67
1	B	246/275 (90%)	228 (93%)	18 (7%)	17	45
All	All	492/550 (90%)	462 (94%)	30 (6%)	23	56

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	SER
1	A	60	LYS
1	A	70	ASP
1	A	78	GLU
1	A	83	ARG
1	A	96	LEU
1	A	122	GLN
1	A	170	ASP
1	A	184	THR
1	A	223	ARG
1	A	242	ARG
1	A	243	LEU
1	B	15	ASN

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Mol	Chain	Res	Type
1	B	16	ASP
1	B	46	ASP
1	B	83	ARG
1	B	94	GLN
1	B	107	ARG
1	B	108	THR
1	B	122	GLN
1	B	133	LEU
1	B	170	ASP
1	B	194	LEU
1	B	212	VAL
1	B	230	GLN
1	B	279	HIS
1	B	281	PRO
1	B	291	ARG
1	B	294	ARG
1	B	298	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	45	GLN
1	A	122	GLN
1	A	126	GLN
1	A	132	GLN
1	A	186	HIS
1	A	236	HIS
1	A	239	GLN
1	A	255	ASN
1	B	94	GLN
1	B	126	GLN
1	B	130	ASN
1	B	132	GLN
1	B	160	ASN
1	B	230	GLN
1	B	234	ASN
1	B	236	HIS
1	B	238	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates 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

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	290/324 (89%)	0.22	11 (3%) 44 37	24, 48, 92, 106	0
1	B	290/324 (89%)	0.04	9 (3%) 52 45	21, 40, 86, 103	0
All	All	580/648 (89%)	0.13	20 (3%) 49 41	21, 44, 90, 106	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	279	HIS	4.3
1	A	85	ASN	3.7
1	A	55	LEU	3.5
1	A	258	MET	3.0
1	B	280	VAL	2.7
1	A	54	PRO	2.7
1	B	226	LEU	2.7
1	A	59	GLN	2.5
1	A	45	GLN	2.5
1	B	81	LYS	2.5
1	B	37	GLU	2.4
1	B	16	ASP	2.4
1	A	60	LYS	2.4
1	A	49	VAL	2.3
1	B	223	ARG	2.1
1	A	207	ILE	2.1
1	A	18	PRO	2.1
1	B	83	ARG	2.0
1	B	84	MET	2.0
1	B	86	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.