



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 3, 2023 – 02:40 am GMT

PDB ID : 2UXT
Title : SufI Protein from Escherichia Coli
Authors : Tarry, M.J.; Roversi, P.; Sargent, F.; Berks, B.C.; Lea, S.M.
Deposited on : 2007-03-29
Resolution : 1.90 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

<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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

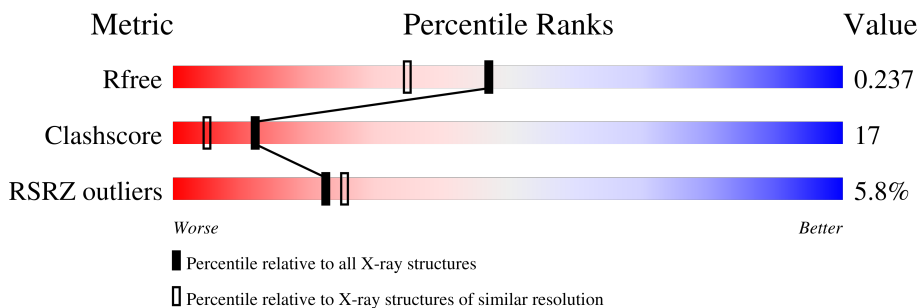
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 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	451	 5% 71% 22% 6%
1	B	451	 6% 70% 23% 7%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7014 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 PROTEIN SUFI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	422	3313	2103	589	607	14	0	0	0
1	B	420	3295	2095	580	606	14	0	0	0

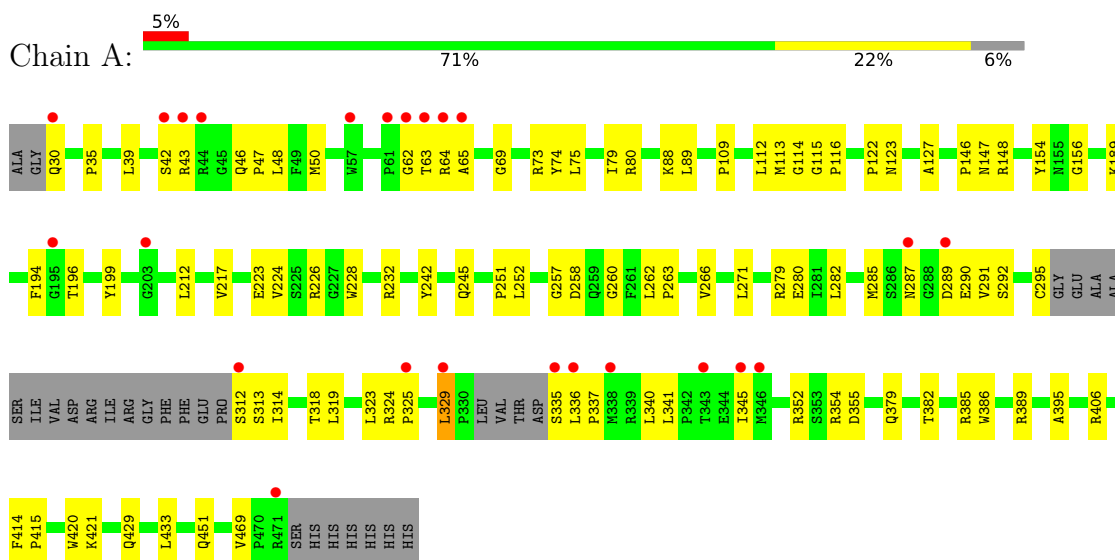
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	229	229	229	0	0
2	B	177	177	177	0	0

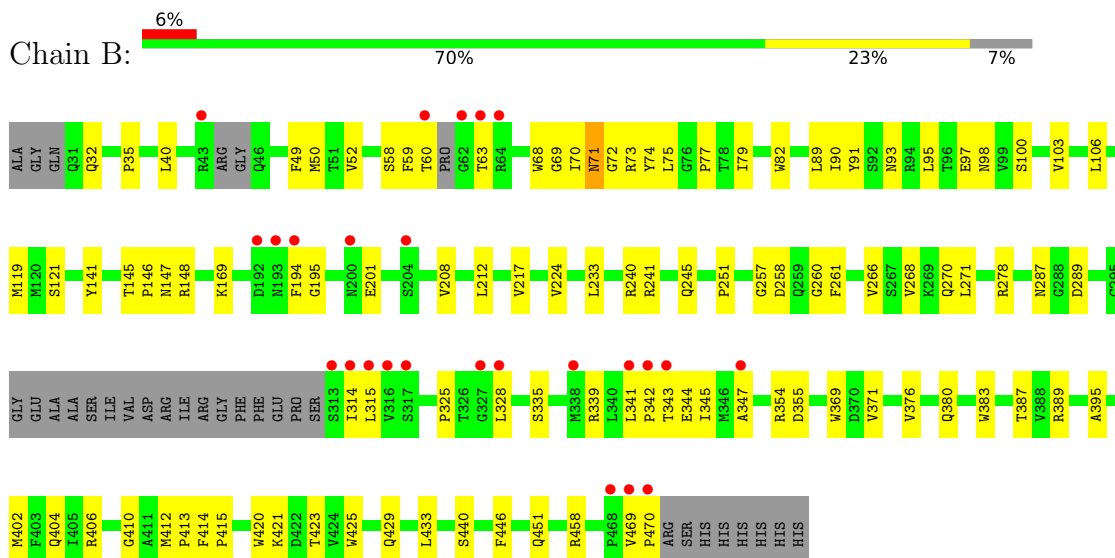
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: PROTEIN SUFI



• Molecule 1: PROTEIN SUFI



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	54.47Å 89.55Å 153.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.84 – 1.90 39.80 – 1.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (39.84-1.90) 98.0 (39.80-1.90)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 1.89Å)	Xtrriage
Refinement program	TNT 5.13.1.0	Depositor
R, R_{free}	0.191 , (Not available) 0.198 , 0.237	Depositor DCC
R_{free} test set	2976 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	24.8	Xtrriage
Anisotropy	0.338	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 49.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7014	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.69% 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 [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.32	0/3402	0.63	1/4645 (0.0%)
1	B	0.33	0/3382	0.61	1/4619 (0.0%)
All	All	0.32	0/6784	0.62	2/9264 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	329	LEU	C-N-CD	-13.22	91.52	120.60
1	B	71	ASN	N-CA-C	6.37	128.21	111.00

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	A	3313	0	3262	105	0
1	B	3295	0	3243	121	0
2	A	229	0	0	8	0
2	B	177	0	0	5	0
All	All	7014	0	6505	223	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 17.

All (223) 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:B:347:ALA:HB1	1:B:433:LEU:HD23	1.20	1.12
1:A:312:SER:HA	1:A:314:ILE:H	1.25	1.00
1:B:40:LEU:HD22	1:B:77:PRO:HB2	1.46	0.95
1:A:312:SER:N	1:A:313:SER:HB3	1.82	0.93
1:B:58:SER:HB2	1:B:60:THR:HG23	1.54	0.89
1:B:212:LEU:HD12	1:B:315:LEU:HD13	1.57	0.87
1:A:282:LEU:HD12	1:A:336:LEU:HD22	1.54	0.86
1:B:347:ALA:HB1	1:B:433:LEU:CD2	2.06	0.85
1:B:148:ARG:HG2	1:B:148:ARG:HH11	1.41	0.84
1:A:312:SER:HA	1:A:314:ILE:N	1.93	0.84
1:B:266:VAL:HG11	1:B:415:PRO:HB2	1.60	0.84
1:A:228:TRP:CZ3	1:A:336:LEU:HD21	2.12	0.84
1:A:282:LEU:CD1	1:A:336:LEU:HD22	2.08	0.82
1:A:287:ASN:HB3	2:A:2134:HOH:O	1.81	0.80
1:B:35:PRO:HD3	1:B:217:VAL:HG11	1.66	0.78
1:B:380:GLN:OE1	1:B:469:VAL:HG22	1.84	0.77
1:B:50:MET:HG3	1:B:70:ILE:HG21	1.68	0.76
1:A:257:GLY:HA2	2:A:2205:HOH:O	1.85	0.76
1:A:64:ARG:HD3	1:A:194:PHE:CD1	2.21	0.76
1:B:347:ALA:CB	1:B:433:LEU:HD23	2.09	0.74
1:A:65:ALA:HB3	1:A:196:THR:HG21	1.69	0.74
1:B:40:LEU:CD2	1:B:77:PRO:HB2	2.19	0.73
1:A:345:ILE:CD1	1:A:420:TRP:HE1	2.02	0.73
1:B:341:LEU:CD1	1:B:345:ILE:HD11	2.19	0.73
1:B:148:ARG:HG2	1:B:148:ARG:NH1	2.01	0.73
1:B:212:LEU:CD1	1:B:315:LEU:HD13	2.18	0.72
1:A:312:SER:HA	1:A:314:ILE:HD12	1.71	0.72
1:A:345:ILE:HD11	1:A:420:TRP:HE1	1.53	0.72
1:A:379:GLN:O	1:A:382:THR:HG22	1.89	0.71
1:A:35:PRO:HD3	1:A:217:VAL:HG11	1.73	0.71
1:B:50:MET:CE	1:B:79:ILE:HD11	2.21	0.70
1:B:89:LEU:HD23	1:B:91:TYR:CE1	2.27	0.70
1:A:42:SER:O	1:A:43:ARG:HB2	1.90	0.70
1:A:345:ILE:HD11	1:A:420:TRP:NE1	2.07	0.70
1:B:40:LEU:HD22	1:B:77:PRO:CB	2.21	0.69
1:A:287:ASN:O	1:A:287:ASN:ND2	2.26	0.69
1:A:312:SER:CA	1:A:314:ILE:H	2.04	0.68
1:B:245:GLN:HG2	1:B:270:GLN:HG3	1.75	0.68
1:A:226:ARG:HD3	1:A:329:LEU:CD2	2.24	0.67
1:A:257:GLY:HA3	1:A:260:GLY:O	1.95	0.66
1:B:257:GLY:HA2	2:B:2160:HOH:O	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:58:SER:HB2	1:B:60:THR:CG2	2.24	0.66
1:A:289:ASP:HB2	2:A:2134:HOH:O	1.94	0.65
1:B:50:MET:HE3	1:B:70:ILE:HG21	1.79	0.64
1:B:341:LEU:HD23	1:B:342:PRO:HD2	1.78	0.64
1:B:339:ARG:HG2	1:B:339:ARG:HH11	1.63	0.64
1:B:32:GLN:HB2	1:B:217:VAL:HG21	1.80	0.62
1:A:228:TRP:CE3	1:A:336:LEU:HD21	2.34	0.62
1:A:414:PHE:CE2	1:B:251:PRO:HB3	2.34	0.62
1:A:258:ASP:HB2	1:A:421:LYS:HA	1.81	0.62
1:A:312:SER:CA	1:A:313:SER:HB3	2.29	0.62
1:B:395:ALA:HB3	1:B:451:GLN:HB2	1.81	0.62
1:B:50:MET:HG3	1:B:70:ILE:CG2	2.30	0.62
1:B:148:ARG:HA	2:B:2176:HOH:O	1.98	0.62
1:A:63:THR:HG21	2:A:2022:HOH:O	1.98	0.61
1:B:406:ARG:HD3	1:B:433:LEU:CD2	2.30	0.61
1:A:226:ARG:HD3	1:A:329:LEU:HD21	1.81	0.61
1:B:49:PHE:CZ	1:B:90:ILE:HD12	2.36	0.61
1:B:380:GLN:CD	1:B:469:VAL:HG22	2.20	0.61
1:A:336:LEU:HB3	1:A:337:PRO:CD	2.32	0.60
1:A:406:ARG:HD2	1:A:433:LEU:HB2	1.84	0.60
1:A:289:ASP:O	1:A:325:PRO:HG2	2.02	0.60
1:A:30:GLN:HG3	2:A:2140:HOH:O	2.01	0.59
1:B:406:ARG:HH11	1:B:433:LEU:CD2	2.15	0.59
1:B:212:LEU:HD12	1:B:315:LEU:CD1	2.31	0.59
1:A:355:ASP:OD2	1:A:389:ARG:NH1	2.35	0.59
1:A:287:ASN:OD1	1:B:410:GLY:HA3	2.02	0.58
1:B:406:ARG:HD3	1:B:433:LEU:HD22	1.84	0.58
1:A:406:ARG:CD	1:A:433:LEU:HB2	2.33	0.58
1:B:146:PRO:O	1:B:147:ASN:HB2	2.03	0.58
1:B:268:VAL:HG21	1:B:271:LEU:HD13	1.86	0.58
1:A:266:VAL:HG11	1:A:415:PRO:HB2	1.85	0.58
1:B:68:TRP:CE3	1:B:95:LEU:HD13	2.38	0.58
1:B:406:ARG:NH1	2:B:2149:HOH:O	2.29	0.57
1:B:339:ARG:HH11	1:B:339:ARG:CG	2.18	0.57
1:B:458:ARG:HD3	2:B:2070:HOH:O	2.05	0.57
1:A:312:SER:CB	1:A:314:ILE:HD13	2.35	0.56
1:A:395:ALA:HB3	1:A:451:GLN:HB2	1.85	0.56
1:A:285:MET:CE	1:A:325:PRO:HG3	2.35	0.56
1:A:62:GLY:N	1:A:196:THR:OG1	2.38	0.56
1:A:323:LEU:O	1:A:325:PRO:HD3	2.06	0.56
1:B:59:PHE:O	1:B:60:THR:O	2.24	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:ARG:NH1	1:A:148:ARG:HG2	2.19	0.56
1:A:325:PRO:HB2	2:A:2142:HOH:O	2.07	0.55
1:B:35:PRO:HD3	1:B:217:VAL:CG1	2.36	0.55
1:B:369:TRP:CZ2	1:B:371:VAL:HG12	2.42	0.55
1:A:39:LEU:HD21	1:A:80:ARG:CZ	2.37	0.55
1:A:46:GLN:HB3	1:A:47:PRO:HD2	1.88	0.55
1:A:212:LEU:HD21	1:A:242:TYR:HE2	1.72	0.55
1:B:50:MET:HE1	1:B:77:PRO:HG2	1.88	0.55
1:B:224:VAL:O	1:B:325:PRO:HA	2.07	0.55
1:A:382:THR:HG21	2:A:2180:HOH:O	2.07	0.53
1:A:385:ARG:HH11	1:A:406:ARG:HH22	1.56	0.53
1:B:68:TRP:CZ3	1:B:95:LEU:HD13	2.43	0.53
1:B:341:LEU:HD13	1:B:345:ILE:HD11	1.90	0.53
1:A:312:SER:HB2	1:A:314:ILE:HD13	1.91	0.52
1:A:312:SER:CA	1:A:314:ILE:HD12	2.37	0.52
1:B:258:ASP:HB2	1:B:421:LYS:HA	1.92	0.52
1:B:241:ARG:HD2	1:B:425:TRP:CE2	2.44	0.52
1:B:50:MET:HE1	1:B:79:ILE:HD11	1.91	0.52
1:A:148:ARG:HG2	1:A:148:ARG:HH11	1.74	0.52
1:A:154:TYR:O	1:A:189:LYS:NZ	2.43	0.52
1:A:245:GLN:HA	1:A:252:LEU:HD11	1.92	0.52
1:B:63:THR:HG21	1:B:195:GLY:HA3	1.91	0.52
1:B:257:GLY:HA3	1:B:260:GLY:O	2.10	0.52
1:A:35:PRO:CD	1:A:217:VAL:HG11	2.40	0.51
1:B:341:LEU:HD23	1:B:342:PRO:CD	2.40	0.51
1:A:352:ARG:HD3	1:A:354:ARG:NH2	2.26	0.51
1:B:49:PHE:CE2	1:B:90:ILE:HD12	2.46	0.51
1:B:69:GLY:HA3	1:B:73:ARG:O	2.11	0.51
1:A:352:ARG:HD3	1:A:354:ARG:CZ	2.40	0.51
1:B:402:MET:HE3	1:B:420:TRP:CE2	2.45	0.51
1:A:146:PRO:O	1:A:147:ASN:HB2	2.09	0.51
1:A:336:LEU:HB3	1:A:337:PRO:HD2	1.93	0.50
1:B:74:TYR:O	1:B:75:LEU:HB2	2.10	0.50
1:B:383:TRP:CH2	1:B:420:TRP:HH2	2.30	0.50
1:A:64:ARG:HD3	1:A:194:PHE:CE1	2.47	0.50
1:B:68:TRP:CD2	1:B:95:LEU:HD13	2.46	0.50
1:A:282:LEU:HD13	1:A:336:LEU:HD22	1.93	0.50
1:A:226:ARG:NH2	1:A:329:LEU:HD21	2.26	0.50
1:A:74:TYR:O	1:A:75:LEU:HB2	2.12	0.49
1:A:212:LEU:HD21	1:A:242:TYR:CE2	2.47	0.49
1:A:148:ARG:HH11	1:A:148:ARG:CG	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:245:GLN:NE2	1:B:270:GLN:HE21	2.11	0.49
1:B:52:VAL:HG22	1:B:93:ASN:HA	1.96	0.48
1:A:224:VAL:HG21	1:A:285:MET:HG3	1.94	0.48
1:B:354:ARG:O	1:B:387:THR:HG22	2.14	0.47
1:B:421:LYS:HE3	1:B:423:THR:O	2.13	0.47
1:A:379:GLN:HE21	1:A:469:VAL:CG2	2.28	0.47
1:B:208:VAL:CG1	1:B:240:ARG:NH2	2.77	0.47
1:B:355:ASP:OD1	1:B:389:ARG:NH2	2.35	0.47
1:B:50:MET:HE2	1:B:141:TYR:CZ	2.50	0.47
1:B:404:GLN:HG2	1:B:406:ARG:HD2	1.97	0.47
1:A:69:GLY:HA3	1:A:73:ARG:O	2.14	0.46
1:A:226:ARG:HD3	1:A:329:LEU:HD22	1.96	0.46
1:A:354:ARG:HG3	1:A:386:TRP:NE1	2.29	0.46
1:A:389:ARG:HD3	1:A:429:GLN:OE1	2.15	0.46
1:B:35:PRO:CD	1:B:217:VAL:CG1	2.93	0.46
1:B:98:ASN:HB3	1:B:119:MET:HG2	1.97	0.46
1:A:263:PRO:HA	1:A:341:LEU:HB2	1.97	0.46
1:B:82:TRP:CH2	1:B:169:LYS:HD2	2.51	0.46
1:B:354:ARG:CZ	1:B:376:VAL:HG13	2.46	0.46
1:B:355:ASP:HA	1:B:387:THR:HG23	1.98	0.45
1:A:335:SER:N	1:A:336:LEU:CA	2.80	0.45
1:B:98:ASN:HB2	1:B:119:MET:CE	2.46	0.45
1:A:385:ARG:NH1	1:A:406:ARG:HH22	2.13	0.45
1:A:389:ARG:HG2	1:A:429:GLN:HG3	1.97	0.45
1:B:119:MET:CE	1:B:145:THR:HG23	2.46	0.45
1:B:402:MET:CE	1:B:420:TRP:CE2	2.99	0.45
1:B:63:THR:OG1	1:B:194:PHE:O	2.26	0.45
1:B:194:PHE:CD1	1:B:194:PHE:N	2.84	0.45
1:B:328:LEU:N	1:B:328:LEU:HD13	2.31	0.45
1:B:339:ARG:CG	1:B:339:ARG:NH1	2.78	0.45
1:B:389:ARG:HG2	1:B:429:GLN:HB2	1.98	0.45
1:A:385:ARG:HH11	1:A:406:ARG:NH2	2.13	0.45
1:B:50:MET:CE	1:B:141:TYR:CZ	3.00	0.45
1:B:98:ASN:CB	1:B:119:MET:HE3	2.47	0.44
1:A:226:ARG:HH21	1:A:329:LEU:HD21	1.81	0.44
1:B:98:ASN:CB	1:B:119:MET:CE	2.95	0.44
1:B:50:MET:O	1:B:91:TYR:HA	2.18	0.44
1:B:369:TRP:CZ2	1:B:371:VAL:CG1	3.00	0.44
1:A:223:GLU:HA	1:A:324:ARG:O	2.18	0.44
1:B:100:SER:OG	1:B:145:THR:HA	2.17	0.44
1:A:75:LEU:HA	1:A:156:GLY:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:40:LEU:H	1:B:40:LEU:HD23	1.82	0.44
1:A:35:PRO:CD	1:A:217:VAL:CG1	2.95	0.44
1:B:412:MET:HB3	1:B:412:MET:HE2	1.85	0.44
1:A:89:LEU:O	1:A:127:ALA:HA	2.18	0.44
1:B:71:ASN:N	1:B:72:GLY:HA2	2.33	0.44
1:B:383:TRP:HH2	1:B:420:TRP:HH2	1.65	0.44
1:B:469:VAL:O	1:B:470:PRO:O	2.36	0.44
1:A:122:PRO:O	1:A:123:ASN:HB2	2.17	0.44
1:B:68:TRP:CE3	1:B:95:LEU:CD1	3.01	0.43
1:B:103:VAL:HG12	1:B:106:LEU:HB2	2.00	0.43
1:A:312:SER:OG	1:A:314:ILE:HB	2.18	0.43
1:B:97:GLU:CD	1:B:148:ARG:HE	2.21	0.43
1:B:261:PHE:O	1:B:341:LEU:HD12	2.19	0.43
1:B:201:GLU:CG	1:B:458:ARG:HH21	2.31	0.43
1:B:89:LEU:HD21	1:B:91:TYR:CZ	2.54	0.43
1:B:287:ASN:OD1	1:B:289:ASP:HB2	2.19	0.43
1:A:212:LEU:HD11	1:A:295:CYS:SG	2.58	0.43
1:A:271:LEU:HD21	1:A:279:ARG:HD2	2.01	0.43
1:B:339:ARG:NH2	1:B:344:GLU:OE2	2.51	0.43
1:A:251:PRO:HB3	1:B:414:PHE:CE2	2.53	0.43
1:B:343:THR:OG1	1:B:344:GLU:N	2.51	0.43
1:A:232:ARG:HG2	1:A:280:GLU:HG2	2.01	0.42
1:A:285:MET:HE2	1:A:325:PRO:HG3	2.01	0.42
1:A:292:SER:HB3	1:A:319:LEU:CD1	2.50	0.42
1:B:406:ARG:HD3	1:B:433:LEU:HD23	2.01	0.42
1:B:208:VAL:HG13	1:B:240:ARG:NH2	2.34	0.42
1:B:241:ARG:HD2	1:B:425:TRP:CZ2	2.55	0.42
1:A:312:SER:CB	1:A:314:ILE:CD1	2.98	0.42
1:B:89:LEU:CD2	1:B:91:TYR:CE1	2.99	0.42
1:B:148:ARG:HH11	1:B:148:ARG:CG	2.17	0.42
1:A:113:MET:HB2	1:A:114:GLY:HA2	2.01	0.42
1:A:290:GLU:HG2	1:A:291:VAL:N	2.35	0.42
1:A:42:SER:OG	1:A:43:ARG:N	2.53	0.42
1:B:89:LEU:CD2	1:B:91:TYR:CZ	3.03	0.42
1:B:50:MET:CE	1:B:79:ILE:CD1	2.95	0.42
1:A:65:ALA:HB3	1:A:196:THR:CG2	2.45	0.41
1:B:63:THR:CG2	1:B:195:GLY:HA3	2.50	0.41
1:A:285:MET:HE3	1:A:325:PRO:HG3	2.02	0.41
1:A:345:ILE:HD11	1:A:420:TRP:CE2	2.54	0.41
1:A:47:PRO:HB3	1:A:88:LYS:CG	2.50	0.41
1:A:48:LEU:HB2	1:A:89:LEU:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:PRO:HD2	1:A:112:LEU:HD12	2.03	0.41
1:A:262:LEU:O	1:A:340:LEU:HB2	2.21	0.41
1:A:50:MET:CE	1:A:79:ILE:HD11	2.49	0.41
1:B:68:TRP:CH2	1:B:95:LEU:HD13	2.56	0.41
1:B:98:ASN:OD1	1:B:121:SER:HA	2.21	0.41
1:B:440:SER:HB3	1:B:446:PHE:CE2	2.56	0.41
1:B:395:ALA:CB	1:B:451:GLN:HB2	2.49	0.41
1:A:154:TYR:CD2	1:A:199:TYR:HB2	2.57	0.40
1:A:292:SER:HB3	1:A:319:LEU:HD11	2.02	0.40
1:A:295:CYS:O	1:A:318:THR:OG1	2.28	0.40
1:B:233:LEU:O	1:B:278:ARG:HA	2.21	0.40
1:B:412:MET:HA	1:B:413:PRO:HD3	1.91	0.40
1:B:58:SER:CB	1:B:60:THR:HG23	2.39	0.40
1:B:314:ILE:H	1:B:314:ILE:HG12	1.60	0.40
1:B:335:SER:HA	2:B:2111:HOH:O	2.21	0.40
1:A:73:ARG:HD2	2:A:2026:HOH:O	2.20	0.40
1:B:341:LEU:CD2	1:B:343:THR:CG2	2.98	0.40
1:A:115:GLY:HA3	1:A:116:PRO:HD2	1.90	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	422/451 (93%)	0.16	24 (5%) 23 26	15, 26, 50, 72	0
1	B	420/451 (93%)	0.47	25 (5%) 21 24	18, 29, 52, 78	0
All	All	842/902 (93%)	0.32	49 (5%) 23 25	15, 27, 51, 78	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	469	VAL	8.1
1	B	314	ILE	7.3
1	A	57	TRP	6.1
1	A	43	ARG	6.0
1	B	328	LEU	5.9
1	B	315	LEU	5.6
1	A	345	ILE	5.5
1	A	63	THR	5.2
1	A	62	GLY	5.2
1	B	194	PHE	5.2
1	B	470	PRO	5.1
1	B	316	VAL	5.0
1	A	471	ARG	5.0
1	A	65	ALA	4.6
1	A	312	SER	4.6
1	A	61	PRO	4.5
1	B	200	ASN	4.4
1	B	60	THR	4.4
1	B	313	SER	4.1
1	A	336	LEU	4.0
1	B	64	ARG	3.9
1	A	64	ARG	3.6
1	A	287	ASN	3.6
1	A	343	THR	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	204	SER	3.4
1	B	62	GLY	3.4
1	B	63	THR	3.1
1	B	347	ALA	2.9
1	A	195	GLY	2.8
1	B	193	ASN	2.8
1	A	44	ARG	2.8
1	B	343	THR	2.7
1	A	289	ASP	2.7
1	A	338	MET	2.7
1	A	325	PRO	2.6
1	B	192	ASP	2.6
1	A	30	GLN	2.6
1	B	338	MET	2.6
1	A	346	MET	2.4
1	A	335	SER	2.3
1	B	317	SER	2.3
1	B	468	PRO	2.2
1	B	341	LEU	2.2
1	B	327	GLY	2.2
1	A	42	SER	2.2
1	B	43	ARG	2.2
1	A	329	LEU	2.1
1	B	342	PRO	2.1
1	A	203	GLY	2.1

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.