Full wwPDB X-ray Structure Validation Report (i)

May 15, 2020 – 04:56 pm BST

PDB ID	:	3H1T
Title	:	The fragment structure of a putative HsdR subunit of a type I restriction enzyme from Vibrio vulnificus YJ016
Authors	:	Park, S.Y.; Lee, H.J.; Kim, J.S.
Deposited on	:	2009-04-13
Resolution	:	2.30 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

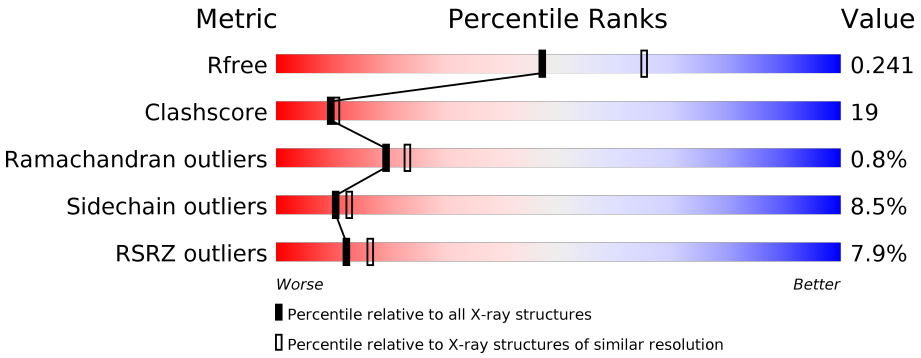
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 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 <=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	590	7%, 56%, 27%, ·, 13%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4519 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 Type I site-specific restriction-modification system, R (Restriction) subunit.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	515	4176	2652	717	795	5	7	0	0	0

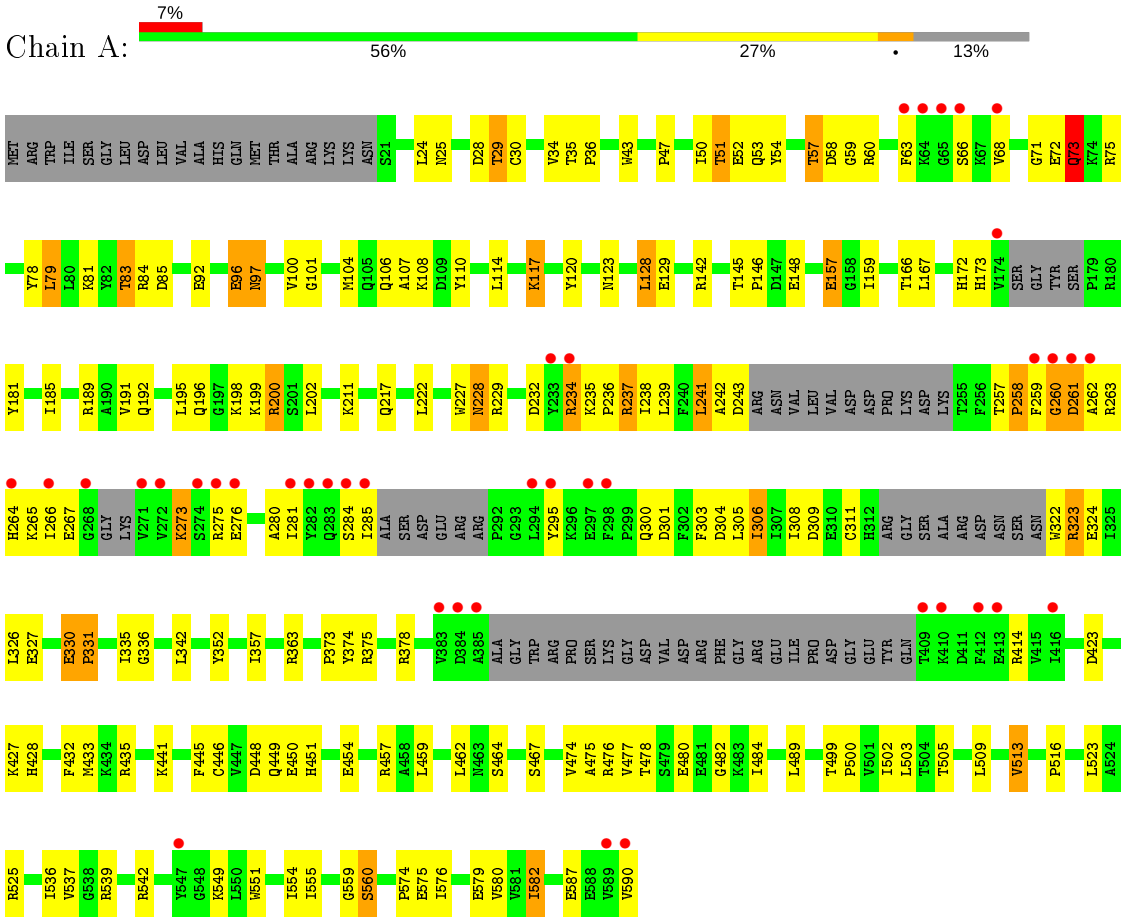
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	343	343	343	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: Type I site-specific restriction-modification system, R (Restriction) subunit



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	71.24Å 88.78Å 114.23Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.39 – 2.30 37.68 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.1 (44.39-2.30) 96.1 (37.68-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	2.20 (at 2.29Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.218 , 0.242 0.218 , 0.241	Depositor DCC
R_{free} test set	3168 reflections (9.99%)	wwPDB-VP
Wilson B-factor (Å^2)	34.8	Xtriage
Anisotropy	0.370	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 53.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4519	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.40% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	A	0.43	0/4259	0.74	4/5741 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	71	GLY	N-CA-C	-6.20	97.59	113.10
1	A	241	LEU	CA-CB-CG	6.05	129.22	115.30
1	A	330	GLU	N-CA-C	-5.90	95.06	111.00
1	A	262	ALA	N-CA-C	-5.25	96.84	111.00

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	4176	0	4064	160	0
2	A	343	0	0	11	0
All	All	4519	0	4064	160	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 19.

All (160) 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:59:GLY:HA2	1:A:72:GLU:HB3	1.48	0.95
1:A:25:ASN:O	1:A:29:THR:HG23	1.67	0.94
1:A:285:ILE:HD11	1:A:295:TYR:HB3	1.52	0.92
1:A:238:ILE:HD12	1:A:305:LEU:HB3	1.54	0.88
1:A:305:LEU:HD11	1:A:335:ILE:HD13	1.55	0.87
1:A:29:THR:HG21	1:A:96:GLU:H	1.40	0.86
1:A:260:GLY:HA2	1:A:263:ARG:HE	1.42	0.82
1:A:97:ASN:ND2	1:A:97:ASN:H	1.75	0.82
1:A:264:HIS:HB2	1:A:275:ARG:HG3	1.65	0.79
1:A:239:LEU:HB3	1:A:306:ILE:HD13	1.67	0.76
1:A:211:LYS:HG3	2:A:845:HOH:O	1.84	0.76
1:A:509:LEU:HB3	1:A:513:VAL:CG2	2.17	0.74
1:A:374:TYR:CE1	1:A:574:PRO:HB3	2.22	0.74
1:A:57:THR:O	1:A:73:GLN:NE2	2.21	0.74
1:A:322:TRP:N	1:A:324:GLU:OE2	2.22	0.72
1:A:509:LEU:HB3	1:A:513:VAL:HG22	1.72	0.72
1:A:239:LEU:HB2	1:A:303:PHE:CE2	2.28	0.68
1:A:117:LYS:HE3	2:A:696:HOH:O	1.94	0.68
1:A:172:HIS:H	1:A:217:GLN:HE22	1.40	0.67
1:A:323:ARG:O	1:A:327:GLU:HG2	1.95	0.67
1:A:375:ARG:HG3	1:A:576:ILE:HD13	1.76	0.66
1:A:576:ILE:HD12	1:A:576:ILE:N	2.11	0.65
1:A:84:ARG:NH1	1:A:173:HIS:HD2	1.95	0.64
1:A:375:ARG:HD3	1:A:551:TRP:CZ3	2.32	0.63
1:A:378:ARG:NH1	1:A:579:GLU:OE1	2.29	0.62
1:A:72:GLU:O	1:A:73:GLN:HB2	2.00	0.62
1:A:145:THR:OG1	1:A:148:GLU:HG3	2.00	0.61
1:A:24:LEU:HB2	1:A:96:GLU:HG2	1.83	0.61
1:A:191:VAL:O	1:A:195:LEU:HG	2.00	0.61
1:A:73:GLN:HA	1:A:73:GLN:HE21	1.66	0.60
1:A:450:GLU:O	1:A:454:GLU:HG3	2.01	0.59
1:A:97:ASN:HD22	1:A:97:ASN:H	1.50	0.59
1:A:575:GLU:HB2	1:A:576:ILE:HD12	1.85	0.59
1:A:52:GLU:HG2	1:A:78:TYR:CE2	2.37	0.59
1:A:263:ARG:O	1:A:275:ARG:HD2	2.03	0.59
1:A:84:ARG:NH1	1:A:173:HIS:CD2	2.72	0.58
1:A:559:GLY:O	1:A:560:SER:HB3	2.04	0.58
1:A:239:LEU:HD23	1:A:306:ILE:HD13	1.85	0.58
1:A:324:GLU:HA	1:A:327:GLU:HG2	1.84	0.57
1:A:227:TRP:O	1:A:236:PRO:HB3	2.04	0.57
1:A:375:ARG:HD3	1:A:551:TRP:CE3	2.40	0.57
1:A:114:LEU:O	1:A:185:ILE:HD11	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:MSE:HE3	1:A:104:MSE:HA	1.85	0.57
1:A:374:TYR:HE1	1:A:574:PRO:HB3	1.69	0.57
1:A:53:GLN:OE1	1:A:75:ARG:HD2	2.04	0.57
1:A:29:THR:HG21	1:A:96:GLU:N	2.15	0.56
1:A:229:ARG:HH22	1:A:301:ASP:HB2	1.69	0.56
1:A:330:GLU:HG3	1:A:331:PRO:HA	1.86	0.56
1:A:25:ASN:HB3	1:A:28:ASP:H	1.70	0.56
1:A:239:LEU:HD23	1:A:306:ILE:CD1	2.35	0.56
1:A:92:GLU:HB2	1:A:107:ALA:HB2	1.88	0.56
1:A:51:THR:HG23	1:A:79:LEU:HB3	1.86	0.56
1:A:192:GLN:O	1:A:196:GLN:HG3	2.06	0.56
1:A:489:LEU:HD11	1:A:513:VAL:HG13	1.88	0.55
1:A:237:ARG:O	1:A:238:ILE:HD13	2.06	0.55
1:A:446:CYS:HB3	1:A:451:HIS:ND1	2.21	0.55
1:A:363:ARG:HD2	2:A:814:HOH:O	2.07	0.55
1:A:476:ARG:HG2	1:A:478:THR:HG22	1.87	0.55
1:A:97:ASN:ND2	1:A:97:ASN:N	2.49	0.55
1:A:265:LYS:HD2	1:A:267:GLU:HG3	1.89	0.55
1:A:311:CYS:O	1:A:322:TRP:CH2	2.60	0.55
1:A:449:GLN:OE1	1:A:480:GLU:HG3	2.06	0.55
1:A:285:ILE:HD11	1:A:295:TYR:CB	2.31	0.55
1:A:199:LYS:HE2	2:A:879:HOH:O	2.06	0.54
1:A:228:ASN:HB2	1:A:304:ASP:OD2	2.07	0.54
1:A:474:VAL:HG13	1:A:502:ILE:HB	1.88	0.54
1:A:477:VAL:HG11	1:A:509:LEU:HD21	1.90	0.53
1:A:63:PHE:CE2	1:A:375:ARG:NH2	2.76	0.53
1:A:238:ILE:CD1	1:A:305:LEU:HB3	2.32	0.53
1:A:108:LYS:HE2	2:A:714:HOH:O	2.06	0.53
1:A:81:LYS:HB3	1:A:83:THR:O	2.09	0.52
1:A:196:GLN:OE1	1:A:198:LYS:HE2	2.09	0.52
1:A:375:ARG:CG	1:A:576:ILE:HD13	2.38	0.52
1:A:324:GLU:CD	1:A:324:GLU:H	2.13	0.52
1:A:423:ASP:OD1	2:A:752:HOH:O	2.19	0.52
1:A:484:ILE:HG12	2:A:780:HOH:O	2.10	0.52
1:A:159:ILE:HD13	1:A:167:LEU:HD13	1.92	0.51
1:A:35:THR:HB	1:A:36:PRO:HD3	1.93	0.51
1:A:464:SER:HA	1:A:467:SER:HB2	1.93	0.51
1:A:505:THR:HG21	1:A:509:LEU:HB2	1.92	0.51
1:A:575:GLU:CB	1:A:576:ILE:HD12	2.41	0.51
1:A:445:PHE:HB3	1:A:525:ARG:HD2	1.93	0.50
1:A:234:ARG:HA	1:A:234:ARG:NE	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:TYR:O	1:A:75:ARG:HA	2.11	0.50
1:A:264:HIS:HB2	1:A:275:ARG:CG	2.39	0.49
1:A:83:THR:CG2	1:A:84:ARG:N	2.75	0.49
1:A:202:LEU:HD12	1:A:336:GLY:O	2.12	0.49
1:A:222:LEU:HD22	1:A:227:TRP:CD2	2.47	0.49
1:A:60:ARG:H	1:A:72:GLU:CB	2.26	0.49
1:A:234:ARG:HE	1:A:234:ARG:CA	2.26	0.49
1:A:308:ILE:CD1	1:A:326:LEU:HD21	2.42	0.49
1:A:582:ILE:HD13	1:A:587:GLU:C	2.33	0.49
1:A:260:GLY:O	1:A:261:ASP:HB2	2.13	0.48
1:A:43:TRP:CE3	1:A:146:PRO:HG3	2.49	0.47
1:A:260:GLY:HA2	1:A:263:ARG:NE	2.21	0.47
1:A:52:GLU:HG2	1:A:78:TYR:CD2	2.50	0.47
1:A:97:ASN:HD22	1:A:97:ASN:N	2.12	0.47
1:A:157:GLU:CG	1:A:192:GLN:NE2	2.78	0.47
1:A:229:ARG:HH22	1:A:301:ASP:CB	2.28	0.47
1:A:555:ILE:HD12	1:A:555:ILE:N	2.30	0.47
1:A:273:LYS:NZ	2:A:831:HOH:O	2.48	0.46
1:A:24:LEU:HB2	1:A:29:THR:HG22	1.96	0.46
1:A:489:LEU:CD1	1:A:513:VAL:HG13	2.45	0.46
1:A:266:ILE:HD12	1:A:280:ALA:HB2	1.98	0.46
1:A:257:THR:N	1:A:258:PRO:CD	2.78	0.46
1:A:259:PHE:O	1:A:260:GLY:O	2.33	0.46
1:A:237:ARG:HB3	1:A:303:PHE:HA	1.98	0.45
1:A:30:CYS:HB3	1:A:78:TYR:OH	2.17	0.45
1:A:305:LEU:HD11	1:A:335:ILE:CD1	2.37	0.45
1:A:308:ILE:HD11	1:A:326:LEU:HD11	1.97	0.45
1:A:513:VAL:O	1:A:539:ARG:NH1	2.47	0.45
1:A:516:PRO:O	1:A:549:LYS:HG2	2.17	0.45
1:A:537:VAL:HG13	1:A:554:ILE:HD11	1.98	0.45
1:A:499:THR:HA	1:A:500:PRO:C	2.37	0.45
1:A:234:ARG:HA	1:A:234:ARG:HE	1.82	0.44
1:A:57:THR:CG2	1:A:59:GLY:H	2.30	0.44
1:A:308:ILE:HD11	1:A:326:LEU:HD21	1.99	0.44
1:A:57:THR:CG2	1:A:58:ASP:N	2.80	0.44
1:A:428:HIS:HD2	1:A:582:ILE:HD11	1.83	0.44
1:A:523:LEU:HD21	1:A:536:ILE:HG21	2.00	0.44
1:A:120:TYR:CE1	1:A:129:GLU:HG3	2.53	0.44
1:A:200:ARG:HD2	1:A:352:TYR:CE1	2.53	0.44
1:A:575:GLU:C	1:A:576:ILE:HD12	2.37	0.44
1:A:378:ARG:O	1:A:579:GLU:HA	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:GLU:HA	1:A:123:ASN:O	2.18	0.44
1:A:229:ARG:NH2	1:A:301:ASP:HB2	2.31	0.44
1:A:189:ARG:HB2	1:A:357:ILE:HD13	2.00	0.44
1:A:166:THR:HG21	1:A:222:LEU:HD23	2.00	0.43
1:A:229:ARG:NH1	1:A:303:PHE:O	2.50	0.43
1:A:114:LEU:O	1:A:185:ILE:CD1	2.65	0.43
1:A:243:ASP:HA	1:A:281:ILE:HG13	2.00	0.43
1:A:234:ARG:N	1:A:234:ARG:HE	2.17	0.43
1:A:239:LEU:HD21	1:A:241:LEU:HD21	2.01	0.43
1:A:228:ASN:HD22	1:A:228:ASN:N	2.17	0.43
1:A:84:ARG:HH11	1:A:173:HIS:CD2	2.37	0.42
1:A:237:ARG:C	1:A:238:ILE:HD13	2.39	0.42
1:A:580:VAL:HG22	2:A:675:HOH:O	2.19	0.42
1:A:30:CYS:HA	1:A:34:VAL:HB	2.01	0.42
1:A:433:MSE:HE1	1:A:502:ILE:HD11	2.01	0.42
1:A:43:TRP:O	1:A:50:ILE:HD12	2.20	0.42
1:A:106:GLN:NE2	1:A:110:TYR:CE2	2.88	0.42
1:A:84:ARG:HH12	1:A:173:HIS:HD2	1.66	0.42
1:A:172:HIS:N	1:A:217:GLN:HE22	2.14	0.42
1:A:234:ARG:NE	1:A:234:ARG:CA	2.83	0.42
1:A:457:ARG:NH1	2:A:808:HOH:O	2.51	0.42
1:A:43:TRP:CD2	1:A:146:PRO:HG3	2.55	0.41
1:A:227:TRP:CG	1:A:228:ASN:N	2.88	0.41
1:A:83:THR:HG22	1:A:85:ASP:H	1.85	0.41
1:A:229:ARG:HG3	1:A:304:ASP:HA	2.02	0.41
1:A:260:GLY:CA	1:A:263:ARG:HE	2.23	0.41
1:A:432:PHE:HA	1:A:435:ARG:NH1	2.35	0.41
1:A:235:LYS:HB2	1:A:276:GLU:OE1	2.20	0.41
1:A:242:ALA:HB2	1:A:309:ASP:HB2	2.03	0.41
1:A:441:LYS:HE2	2:A:626:HOH:O	2.20	0.41
1:A:373:PRO:HG2	1:A:551:TRP:HB3	2.04	0.40
1:A:181:TYR:O	1:A:185:ILE:HG12	2.22	0.40
1:A:475:ALA:O	1:A:503:LEU:HA	2.22	0.40
1:A:427:LYS:HE3	1:A:587:GLU:OE2	2.21	0.40
1:A:101:GLY:HA2	1:A:128:LEU:HD12	2.04	0.40
1:A:375:ARG:NE	1:A:576:ILE:HD13	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	501/590 (85%)	474 (95%)	23 (5%)	4 (1%)	19 23

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	260	GLY
1	A	560	SER
1	A	73	GLN
1	A	482	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
1	A	448/505 (89%)	410 (92%)	38 (8%)	10 13

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	THR
1	A	47	PRO
1	A	51	THR
1	A	57	THR
1	A	66	SER
1	A	68	VAL
1	A	73	GLN

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Mol	Chain	Res	Type
1	A	79	LEU
1	A	83	THR
1	A	96	GLU
1	A	97	ASN
1	A	100	VAL
1	A	117	LYS
1	A	128	LEU
1	A	142	ARG
1	A	157	GLU
1	A	200	ARG
1	A	228	ASN
1	A	232	ASP
1	A	234	ARG
1	A	237	ARG
1	A	258	PRO
1	A	261	ASP
1	A	273	LYS
1	A	284	SER
1	A	300	GLN
1	A	306	ILE
1	A	323	ARG
1	A	331	PRO
1	A	342	LEU
1	A	414	ARG
1	A	448	ASP
1	A	459	LEU
1	A	462	LEU
1	A	513	VAL
1	A	542	ARG
1	A	582	ILE
1	A	590	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	ASN
1	A	45	ASN
1	A	69	GLN
1	A	73	GLN
1	A	97	ASN
1	A	102	GLN
1	A	138	GLN

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Mol	Chain	Res	Type
1	A	183	GLN
1	A	192	GLN
1	A	217	GLN
1	A	228	ASN
1	A	312	HIS
1	A	535	GLN

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, 95^{th} 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	508/590 (86%)	0.20	40 (7%)	12	17	19, 38, 75, 98	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	65	GLY	6.7
1	A	385	ALA	6.3
1	A	64	LYS	5.8
1	A	271	VAL	5.7
1	A	275	ARG	5.0
1	A	233	TYR	4.9
1	A	266	ILE	4.8
1	A	272	VAL	4.8
1	A	409	THR	4.6
1	A	284	SER	4.6
1	A	384	ASP	4.5
1	A	383	VAL	4.3
1	A	285	ILE	4.2
1	A	66	SER	3.7
1	A	234	ARG	3.6
1	A	283	GLN	3.4
1	A	68	VAL	3.3
1	A	413	GLU	3.3
1	A	268	GLY	3.3
1	A	274	SER	3.2
1	A	412	PHE	3.1
1	A	410	LYS	3.1
1	A	276	GLU	3.0
1	A	294	LEU	3.0
1	A	260	GLY	3.0
1	A	264	HIS	2.9
1	A	295	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	547	TYR	2.7
1	A	282	TYR	2.6
1	A	589	VAL	2.6
1	A	259	PHE	2.4
1	A	261	ASP	2.3
1	A	297	GLU	2.3
1	A	262	ALA	2.3
1	A	174	VAL	2.2
1	A	298	PHE	2.2
1	A	281	ILE	2.1
1	A	416	ILE	2.0
1	A	590	VAL	2.0
1	A	63	PHE	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.