



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 21, 2023 – 04:53 PM JST

PDB ID : 7W1R
Title : Crystal structure of human Suv3 monomer
Authors : Jain, M.; Yuan, H.S.
Deposited on : 2021-11-20
Resolution : 3.20 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

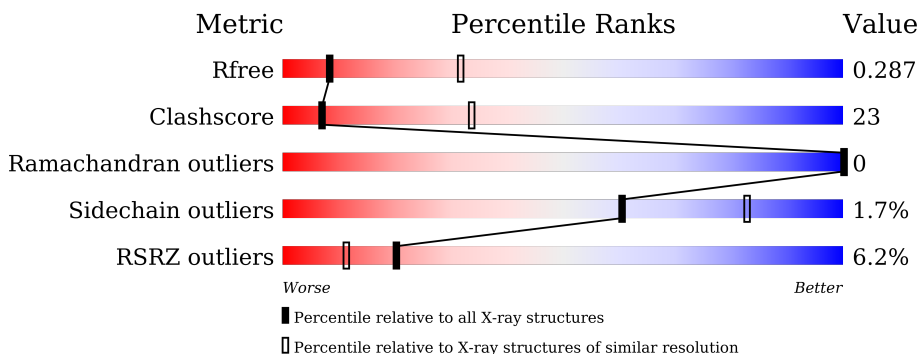
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	674	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4168 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 ATP-dependent RNA helicase SUPV3L1, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	519	4168	2692	702	752	22	0	0	0

4 Data and refinement statistics i

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	92.41Å 92.41Å 88.06Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.43 – 3.20 40.01 – 3.20	Depositor EDS
% Data completeness (in resolution range)	95.8 (36.43-3.20) 90.7 (40.01-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 3.18Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.240 , 0.286 0.240 , 0.287	Depositor DCC
R_{free} test set	1345 reflections (10.09%)	wwPDB-VP
Wilson B-factor (Å ²)	108.2	Xtriage
Anisotropy	0.354	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 72.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.025 for -h,-k,l 0.047 for h,-h-k,-l 0.037 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4168	wwPDB-VP
Average B, all atoms (Å ²)	124.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.39% 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	0.41	1/4251 (0.0%)	0.78	8/5738 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	615	PRO	N-CD	11.05	1.63	1.47

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	482	GLU	N-CA-CB	20.86	148.14	110.60
1	A	482	GLU	N-CA-C	-12.56	77.09	111.00
1	A	500	ARG	N-CA-CB	-7.89	96.40	110.60
1	A	616	LEU	N-CA-CB	7.38	125.16	110.40
1	A	615	PRO	N-CA-CB	5.63	110.06	103.30
1	A	616	LEU	N-CA-C	-5.51	96.14	111.00
1	A	498	LEU	CB-CA-C	5.42	120.50	110.20
1	A	615	PRO	CA-N-CD	-5.41	103.93	111.50

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	4168	0	4171	191	0
All	All	4168	0	4171	191	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 23.

All (191) 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:439:ILE:HG23	1:A:484:THR:HG22	1.22	1.17
1:A:383:ARG:HA	1:A:386:GLU:OE2	1.53	1.08
1:A:408:ALA:HB1	1:A:433:LEU:HD21	1.43	1.00
1:A:154:HIS:HE1	1:A:156:ASP:OD1	1.42	0.99
1:A:215:TYR:HA	1:A:218:ILE:HD12	1.44	0.99
1:A:348:LEU:HD12	1:A:349:THR:OG1	1.62	0.98
1:A:432:ASN:O	1:A:433:LEU:HD23	1.66	0.94
1:A:439:ILE:HG23	1:A:484:THR:CG2	1.99	0.92
1:A:617:LEU:HD23	1:A:617:LEU:H	1.34	0.91
1:A:215:TYR:CG	1:A:218:ILE:HD12	2.10	0.87
1:A:154:HIS:CE1	1:A:156:ASP:OD1	2.28	0.85
1:A:572:TYR:O	1:A:576:THR:HG23	1.75	0.84
1:A:215:TYR:HA	1:A:218:ILE:CD1	2.08	0.82
1:A:71:PRO:HB3	1:A:134:SER:HB2	1.63	0.80
1:A:244:SER:OG	1:A:249:VAL:HG13	1.81	0.80
1:A:439:ILE:CG2	1:A:484:THR:HG22	2.09	0.78
1:A:550:ASN:ND2	1:A:552:ASP:OD1	2.16	0.77
1:A:518:GLU:OE2	1:A:569:ARG:HD3	1.85	0.77
1:A:520:PHE:HB3	1:A:532:LEU:HD22	1.65	0.77
1:A:666:ILE:O	1:A:670:VAL:HG23	1.87	0.73
1:A:347:ARG:HA	1:A:347:ARG:HE	1.52	0.73
1:A:328:LEU:O	1:A:331:GLU:OE1	2.08	0.71
1:A:334:TYR:HE1	1:A:336:THR:HG1	1.39	0.70
1:A:215:TYR:CA	1:A:218:ILE:HD12	2.20	0.70
1:A:383:ARG:CA	1:A:386:GLU:OE2	2.36	0.70
1:A:385:ILE:HG21	1:A:392:SER:HB3	1.74	0.70
1:A:218:ILE:HA	1:A:221:TYR:CE2	2.27	0.70
1:A:215:TYR:CD1	1:A:218:ILE:HD12	2.27	0.70
1:A:334:TYR:HE1	1:A:336:THR:OG1	1.73	0.69
1:A:673:ILE:HA	1:A:676:LEU:N	2.06	0.69
1:A:622:ILE:HG22	1:A:622:ILE:O	1.91	0.69
1:A:383:ARG:HD2	1:A:678:LYS:HE3	1.74	0.68
1:A:154:HIS:CE1	1:A:156:ASP:CG	2.67	0.68
1:A:228:VAL:HG23	1:A:272:VAL:HG13	1.74	0.68
1:A:382:SER:O	1:A:386:GLU:HG3	1.94	0.67
1:A:347:ARG:HA	1:A:347:ARG:NE	2.10	0.67
1:A:369:CYS:O	1:A:439:ILE:N	2.28	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:385:ILE:O	1:A:390:LEU:HD23	1.95	0.66
1:A:154:HIS:HE1	1:A:156:ASP:CG	1.99	0.66
1:A:557:SER:HB3	1:A:575:CYS:HB3	1.78	0.66
1:A:383:ARG:HD2	1:A:678:LYS:CE	2.27	0.65
1:A:325:ALA:HA	1:A:505:ILE:HG12	1.79	0.64
1:A:221:TYR:OH	1:A:240:ILE:CG2	2.45	0.64
1:A:379:TYR:CE1	1:A:622:ILE:HD12	2.34	0.63
1:A:244:SER:OG	1:A:249:VAL:CG1	2.46	0.63
1:A:394:VAL:O	1:A:407:GLN:HG2	2.00	0.62
1:A:215:TYR:HA	1:A:218:ILE:CG1	2.29	0.62
1:A:497:ILE:HD12	1:A:498:LEU:N	2.15	0.62
1:A:498:LEU:O	1:A:498:LEU:HD23	2.00	0.61
1:A:331:GLU:OE1	1:A:331:GLU:N	2.25	0.61
1:A:608:LEU:HD22	1:A:655:ILE:HD12	1.82	0.61
1:A:221:TYR:OH	1:A:240:ILE:HG21	2.01	0.60
1:A:121:HIS:NE2	1:A:125:ILE:HG13	2.16	0.60
1:A:214:THR:O	1:A:218:ILE:HG13	2.02	0.59
1:A:497:ILE:HG13	1:A:498:LEU:H	1.67	0.59
1:A:218:ILE:HA	1:A:221:TYR:HE2	1.66	0.59
1:A:638:TYR:CE1	1:A:649:PHE:HD1	2.19	0.59
1:A:617:LEU:H	1:A:617:LEU:CD2	2.14	0.59
1:A:678:LYS:NZ	1:A:681:GLU:HG2	2.18	0.58
1:A:383:ARG:CD	1:A:678:LYS:HE3	2.33	0.58
1:A:368:ASP:N	1:A:435:ILE:HD11	2.19	0.58
1:A:378:ILE:HG23	1:A:422:VAL:HG12	1.86	0.58
1:A:403:THR:HG21	1:A:670:VAL:HG21	1.85	0.58
1:A:411:PHE:HZ	1:A:435:ILE:HD13	1.69	0.57
1:A:71:PRO:HG3	1:A:130:TYR:HA	1.86	0.57
1:A:141:ILE:HG12	1:A:145:LEU:HG	1.86	0.57
1:A:605:PHE:HD1	1:A:655:ILE:HD13	1.68	0.57
1:A:203:ILE:HD13	1:A:341:GLU:CD	2.24	0.57
1:A:378:ILE:HG23	1:A:422:VAL:CG1	2.35	0.57
1:A:520:PHE:HE2	1:A:535:ILE:HG22	1.70	0.56
1:A:214:THR:HG22	1:A:218:ILE:HD11	1.88	0.56
1:A:328:LEU:HD21	1:A:508:ALA:HB2	1.86	0.56
1:A:222:PHE:HE1	1:A:244:SER:HB2	1.71	0.55
1:A:408:ALA:HB1	1:A:433:LEU:CD2	2.29	0.55
1:A:608:LEU:HD21	1:A:635:LEU:CD2	2.37	0.54
1:A:245:ASN:HB3	1:A:251:CYS:H	1.73	0.54
1:A:497:ILE:HD12	1:A:498:LEU:HB2	1.89	0.54
1:A:515:GLU:H	1:A:515:GLU:CD	2.11	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:405:LEU:HD23	1:A:431:LEU:HD13	1.90	0.54
1:A:106:ILE:HG22	1:A:120:PHE:HZ	1.72	0.54
1:A:294:GLN:HA	1:A:296:ILE:HG22	1.89	0.53
1:A:365:ARG:O	1:A:368:ASP:HB2	2.07	0.53
1:A:554:PHE:CE2	1:A:576:THR:HG22	2.42	0.53
1:A:184:ASP:HA	1:A:541:GLN:HB2	1.90	0.53
1:A:198:MET:HE3	1:A:200:ARG:HG2	1.91	0.53
1:A:348:LEU:HD12	1:A:349:THR:N	2.23	0.53
1:A:221:TYR:OH	1:A:240:ILE:HG23	2.09	0.52
1:A:422:VAL:HG12	1:A:422:VAL:O	2.08	0.52
1:A:554:PHE:CD2	1:A:576:THR:HG22	2.44	0.52
1:A:330:MET:CE	1:A:340:VAL:HG11	2.38	0.52
1:A:189:PRO:HB3	1:A:336:THR:HG22	1.91	0.52
1:A:221:TYR:CE1	1:A:271:HIS:CE1	2.98	0.52
1:A:226:SER:O	1:A:286:GLU:HB3	2.10	0.52
1:A:215:TYR:O	1:A:219:GLN:HG2	2.11	0.51
1:A:484:THR:HG23	1:A:486:MET:H	1.74	0.51
1:A:373:PHE:CZ	1:A:459:ILE:HD11	2.45	0.51
1:A:554:PHE:HE2	1:A:576:THR:CG2	2.24	0.51
1:A:63:LEU:HD22	1:A:534:ASP:HB3	1.93	0.51
1:A:298:ASP:OD2	1:A:301:ARG:HB2	2.10	0.51
1:A:383:ARG:CD	1:A:678:LYS:CE	2.89	0.51
1:A:159:PHE:O	1:A:162:PHE:HB3	2.10	0.50
1:A:303:TRP:HA	1:A:509:GLY:O	2.12	0.50
1:A:424:THR:HG23	1:A:425:ASP:N	2.26	0.50
1:A:348:LEU:CD1	1:A:349:THR:OG1	2.48	0.50
1:A:66:PRO:HB3	1:A:170:PHE:CE1	2.47	0.50
1:A:424:THR:CG2	1:A:425:ASP:N	2.74	0.50
1:A:61:THR:OG1	1:A:118:ARG:HD3	2.13	0.49
1:A:287:VAL:HG22	1:A:316:GLU:HB2	1.94	0.49
1:A:383:ARG:O	1:A:386:GLU:OE2	2.30	0.49
1:A:497:ILE:C	1:A:499:LYS:H	2.15	0.49
1:A:497:ILE:CG1	1:A:498:LEU:H	2.26	0.49
1:A:550:ASN:OD1	1:A:552:ASP:CG	2.51	0.49
1:A:119:LEU:HD22	1:A:170:PHE:CE2	2.48	0.49
1:A:64:PHE:CD1	1:A:172:VAL:HG21	2.47	0.48
1:A:280:SER:OG	1:A:281:VAL:N	2.46	0.48
1:A:497:ILE:CG1	1:A:498:LEU:N	2.77	0.48
1:A:512:PRO:HD2	1:A:551:MET:SD	2.54	0.48
1:A:249:VAL:HG13	1:A:249:VAL:O	2.13	0.47
1:A:379:TYR:CZ	1:A:622:ILE:HG21	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:327:ASP:O	1:A:331:GLU:OE2	2.32	0.47
1:A:221:TYR:CD1	1:A:271:HIS:CE1	3.03	0.47
1:A:670:VAL:O	1:A:673:ILE:HG12	2.14	0.47
1:A:203:ILE:CD1	1:A:341:GLU:HB3	2.44	0.47
1:A:235:LEU:O	1:A:238:HIS:N	2.48	0.47
1:A:327:ASP:O	1:A:331:GLU:OE1	2.33	0.47
1:A:554:PHE:CE2	1:A:576:THR:CG2	2.99	0.46
1:A:154:HIS:CG	1:A:155:ALA:H	2.33	0.46
1:A:204:PHE:HE2	1:A:326:ILE:HA	1.81	0.46
1:A:431:LEU:HD23	1:A:431:LEU:N	2.30	0.46
1:A:678:LYS:HZ1	1:A:681:GLU:HG2	1.80	0.46
1:A:518:GLU:OE2	1:A:569:ARG:NH1	2.48	0.45
1:A:188:PRO:N	1:A:189:PRO:CD	2.80	0.45
1:A:200:ARG:O	1:A:338:GLU:HG2	2.17	0.45
1:A:221:TYR:CD2	1:A:289:VAL:HG21	2.52	0.45
1:A:179:LEU:HD11	1:A:524:LEU:HD11	1.99	0.45
1:A:230:CYS:HB2	1:A:290:ILE:HA	1.98	0.45
1:A:617:LEU:HD23	1:A:617:LEU:N	2.17	0.45
1:A:369:CYS:HB2	1:A:435:ILE:HG12	1.98	0.44
1:A:638:TYR:CD1	1:A:649:PHE:HD1	2.35	0.44
1:A:187:ILE:N	1:A:188:PRO:HD3	2.33	0.44
1:A:631:VAL:O	1:A:635:LEU:HG	2.18	0.44
1:A:411:PHE:CZ	1:A:435:ILE:HD13	2.49	0.44
1:A:202:ILE:HD11	1:A:319:LEU:HG	2.00	0.44
1:A:678:LYS:C	1:A:682:THR:HG22	2.38	0.44
1:A:330:MET:SD	1:A:340:VAL:HG21	2.58	0.44
1:A:59:PRO:HA	1:A:538:ASP:OD1	2.18	0.43
1:A:497:ILE:CD1	1:A:498:LEU:N	2.80	0.43
1:A:106:ILE:HG22	1:A:120:PHE:CZ	2.53	0.43
1:A:556:PHE:C	1:A:556:PHE:CD1	2.91	0.43
1:A:564:ILE:O	1:A:571:ARG:NH2	2.50	0.43
1:A:529:LEU:O	1:A:530:SER:C	2.57	0.43
1:A:203:ILE:HD13	1:A:341:GLU:HB3	2.00	0.43
1:A:334:TYR:CE1	1:A:336:THR:OG1	2.55	0.43
1:A:569:ARG:HA	1:A:569:ARG:HD2	1.67	0.43
1:A:68:THR:HG22	1:A:70:LYS:HG2	2.01	0.43
1:A:159:PHE:HB3	1:A:160:PRO:HD3	2.01	0.43
1:A:202:ILE:HG23	1:A:340:VAL:HA	2.01	0.43
1:A:346:LYS:HD2	1:A:346:LYS:HA	1.87	0.43
1:A:577:ALA:HA	1:A:578:PRO:HD3	1.86	0.43
1:A:187:ILE:C	1:A:189:PRO:HD2	2.39	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:293:ILE:HG21	1:A:319:LEU:HB3	2.01	0.42
1:A:459:ILE:HG13	1:A:463:GLN:OE1	2.19	0.42
1:A:557:SER:OG	1:A:575:CYS:HA	2.18	0.42
1:A:388:ARG:HG3	1:A:390:LEU:CD2	2.49	0.42
1:A:533:ILE:O	1:A:537:VAL:HG23	2.20	0.42
1:A:111:ALA:HA	1:A:115:LEU:O	2.18	0.42
1:A:550:ASN:HD21	1:A:552:ASP:CG	2.18	0.42
1:A:607:TRP:HA	1:A:610:ARG:HE	1.85	0.42
1:A:651:ASP:O	1:A:655:ILE:HG12	2.20	0.42
1:A:252:ASP:OD1	1:A:269:ALA:HB3	2.20	0.42
1:A:198:MET:HE1	1:A:313:CYS:HA	2.01	0.42
1:A:508:ALA:O	1:A:547:PHE:CD1	2.73	0.41
1:A:203:ILE:HD11	1:A:343:ARG:CD	2.50	0.41
1:A:518:GLU:HG3	1:A:568:LEU:HD12	2.03	0.41
1:A:189:PRO:CB	1:A:336:THR:HG22	2.50	0.41
1:A:529:LEU:HD22	1:A:571:ARG:HG2	2.03	0.41
1:A:331:GLU:N	1:A:331:GLU:CD	2.74	0.41
1:A:460:THR:O	1:A:461:THR:CG2	2.69	0.41
1:A:567:SER:O	1:A:568:LEU:C	2.58	0.41
1:A:263:GLN:HG3	1:A:269:ALA:HB2	2.03	0.41
1:A:290:ILE:HD11	1:A:312:LEU:HD12	2.03	0.41
1:A:325:ALA:HA	1:A:505:ILE:CG1	2.50	0.41
1:A:483:VAL:HG23	1:A:483:VAL:O	2.20	0.41
1:A:596:GLN:HB2	1:A:603:LEU:HD11	2.03	0.41
1:A:616:LEU:HD21	1:A:631:VAL:HG21	2.03	0.41
1:A:186:ARG:O	1:A:187:ILE:C	2.60	0.40
1:A:244:SER:HG	1:A:249:VAL:CG1	2.33	0.40
1:A:629:GLU:O	1:A:632:HIS:HB3	2.20	0.40
1:A:64:PHE:CG	1:A:172:VAL:HG21	2.57	0.40
1:A:215:TYR:HA	1:A:218:ILE:HG13	2.01	0.40
1:A:215:TYR:CD1	1:A:218:ILE:CD1	3.01	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	473/674 (70%)	425 (90%)	48 (10%)	0	100	100

There are no Ramachandran outliers to report.

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	463/588 (79%)	455 (98%)	8 (2%)	60	83

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	204	PHE
1	A	305	TRP
1	A	364	LEU
1	A	431	LEU
1	A	545	GLN
1	A	613	LYS
1	A	646	MET
1	A	678	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	511	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 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	519/674 (77%)	0.20	32 (6%) 20 11	59, 123, 176, 208	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	497	ILE	6.6
1	A	422	VAL	5.5
1	A	443	LEU	4.4
1	A	140	ASP	4.1
1	A	155	ALA	3.4
1	A	221	TYR	3.4
1	A	261	THR	3.0
1	A	371	VAL	3.0
1	A	482	GLU	3.0
1	A	351	ILE	2.9
1	A	101	TYR	2.9
1	A	441	TYR	2.9
1	A	97	LEU	2.9
1	A	394	VAL	2.8
1	A	444	ILE	2.7
1	A	363	ASN	2.6
1	A	440	PHE	2.6
1	A	131	ILE	2.6
1	A	145	LEU	2.5
1	A	263	GLN	2.4
1	A	96	VAL	2.4
1	A	393	ALA	2.2
1	A	100	PHE	2.2
1	A	154	HIS	2.2
1	A	150	PHE	2.1
1	A	373	PHE	2.1
1	A	352	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	421	LEU	2.1
1	A	372	CYS	2.1
1	A	159	PHE	2.1
1	A	146	ASN	2.0
1	A	676	LEU	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 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.