Full wwPDB X-ray Structure Validation Report ⓘ

Aug 29, 2020 – 03:55 PM BST

PDB ID	:	6F3H
Title	:	Crystal structure of Dss1 exoribonuclease active site mutant D477N from Candida glabrata
Authors	:	Razew, M.; Nowak, E.; Nowotny, M.
Deposited on	:	2017-11-28
Resolution	:	2.70 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 following versions of software and data (see references ①) were used in the production of this report:

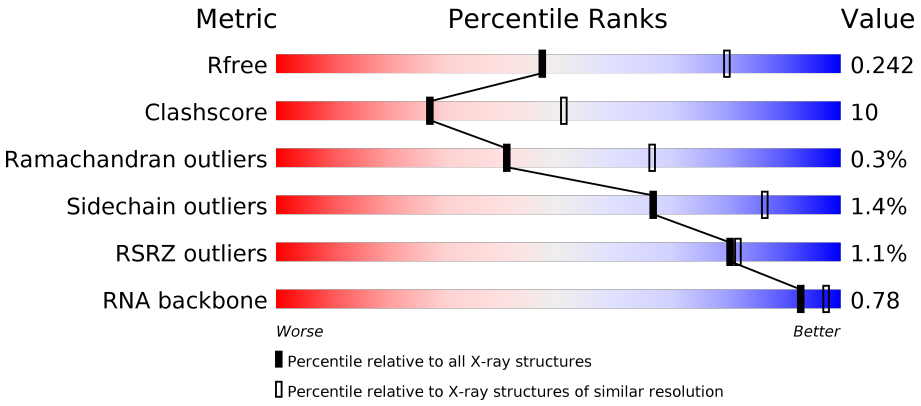
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13

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 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)
RNA backbone	3102	1159 (3.00-2.40)

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	832	% 73% 18% 8%
1	B	832	% 71% 24% 5%
2	C	6	17% 67% 17%
3	D	6	17% 67% 17%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12284 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 Exoribonuclease II, mitochondrial.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	762	Total	C	N	O	S	Se	0	0	0
			5802	3720	984	1076	10	12			
1	B	790	Total	C	N	O	S	Se	0	0	0
			6080	3899	1040	1119	10	12			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	69	MSE	-	initiating methionine	UNP Q6FJE0
A	477	ASN	ASP	engineered mutation	UNP Q6FJE0
B	69	MSE	-	initiating methionine	UNP Q6FJE0
B	477	ASN	ASP	engineered mutation	UNP Q6FJE0

- Molecule 2 is a RNA chain called RNA (5'-R(P*AP*GP*AP*UP*AP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	6	Total	C	N	O	P	0	0	0
			129	58	25	40	6			

- Molecule 3 is a RNA chain called RNA (5'-R(P*CP*AP*CP*UP*GP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	6	Total	C	N	O	P	0	0	0
			127	57	23	41	6			

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	A	1	Total	Mg	0	0
			1	1		

- Molecule 5 is water.

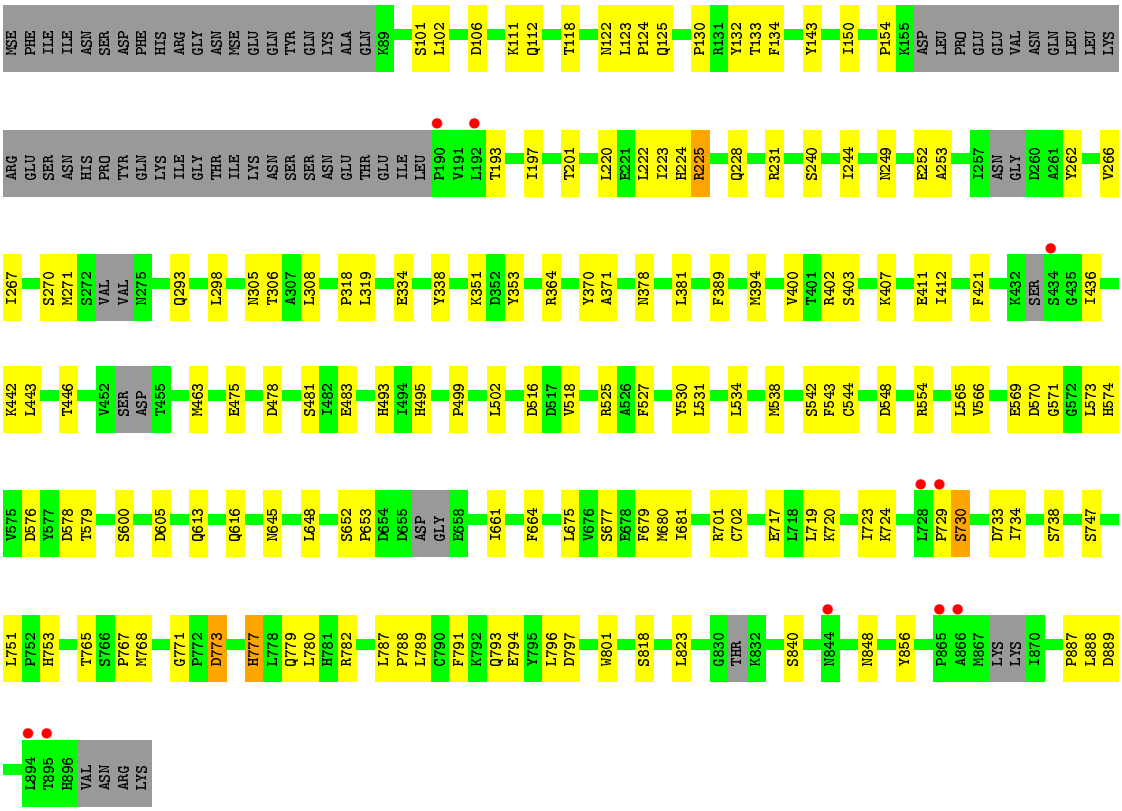
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	73	Total O 73 73	0	0
5	B	70	Total O 70 70	0	0
5	D	1	Total O 1 1	0	0

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.

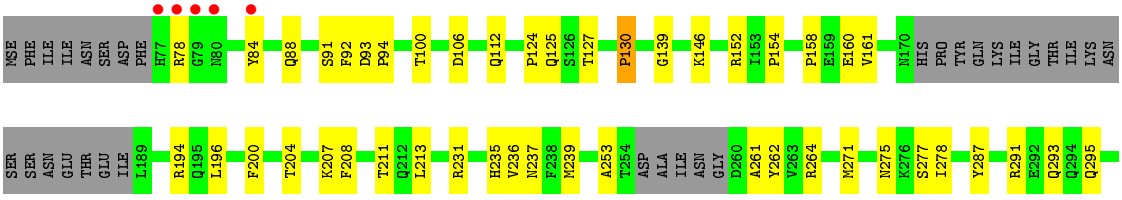
- Molecule 1: Exoribonuclease II, mitochondrial

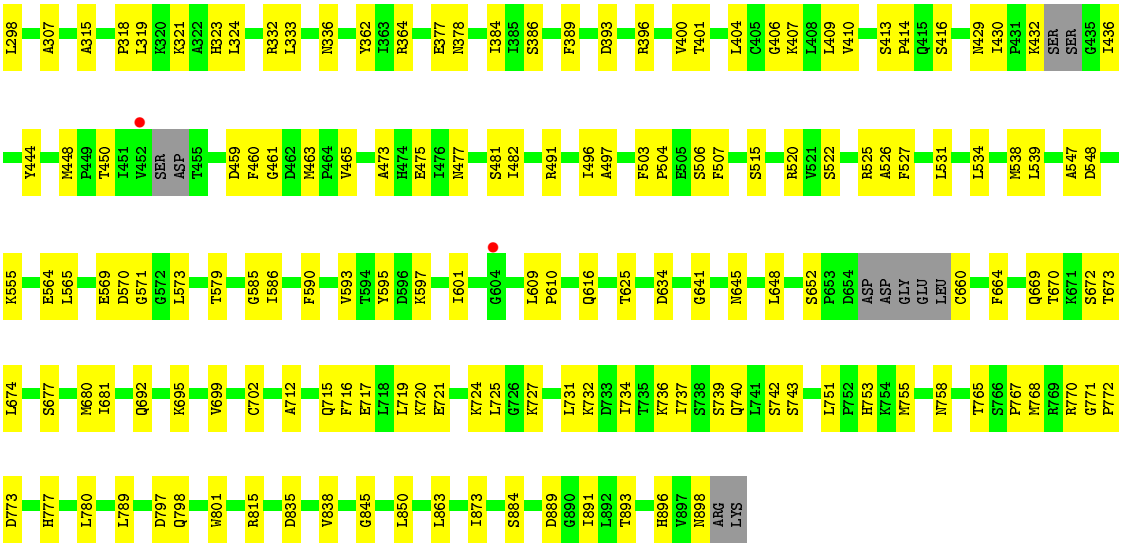
Chain A:



- Molecule 1: Exoribonuclease II, mitochondrial

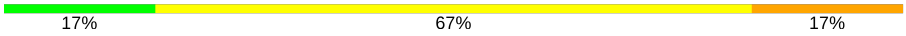
Chain B:





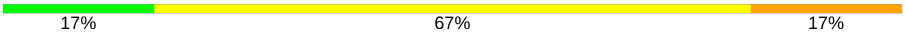
- Molecule 2: RNA (5'-R(P*AP*GP*AP*UP*AP*C)-3')

Chain C:



- Molecule 3: RNA (5'-R(P*CP*AP*CP*UP*GP*A)-3')

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	73.37Å 83.23Å 110.37Å 106.21° 106.56° 90.93°	Depositor
Resolution (Å)	29.21 – 2.70 29.21 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (29.21-2.70) 95.6 (29.21-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.38 (at 2.72Å)	Xtriage
Refinement program	PHENIX (dev_2733: ???)	Depositor
R, R_{free}	0.196 , 0.240 0.196 , 0.242	Depositor DCC
R_{free} test set	3252 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	57.4	Xtriage
Anisotropy	0.650	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 60.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.022 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	12284	wwPDB-VP
Average B, all atoms (Å^2)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% 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

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	0.55	0/5909	0.73	3/8026 (0.0%)
1	B	0.55	0/6195	0.72	1/8412 (0.0%)
2	C	1.32	2/144 (1.4%)	2.35	14/222 (6.3%)
3	D	1.02	0/141	1.73	4/217 (1.8%)
All	All	0.57	2/12389 (0.0%)	0.79	22/16877 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	2	A	N9-C4	-6.63	1.33	1.37
2	C	4	A	N9-C4	-6.13	1.34	1.37

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	554	ARG	NE-CZ-NH1	13.27	126.94	120.30
2	C	1	G	N9-C4-C5	-10.90	101.04	105.40
2	C	1	G	C8-N9-C4	10.22	110.49	106.40
1	A	554	ARG	NE-CZ-NH2	-8.77	115.92	120.30
1	A	554	ARG	CD-NE-CZ	8.20	135.09	123.60
2	C	1	G	C4-C5-N7	6.92	113.57	110.80
2	C	5	C	N3-C2-O2	-6.87	117.09	121.90
2	C	1	G	C5-C6-O6	-6.78	124.53	128.60
2	C	2	A	C2-N3-C4	-6.37	107.41	110.60
1	B	850	LEU	CB-CG-CD2	-6.12	100.59	111.00
2	C	2	A	C8-N9-C4	6.11	108.24	105.80
2	C	2	A	N3-C4-C5	5.85	130.90	126.80
2	C	5	C	C6-N1-C2	-5.84	117.96	120.30
2	C	5	C	N1-C2-N3	5.76	123.23	119.20
2	C	4	A	C2-N3-C4	-5.69	107.76	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	4	G	C5-N7-C8	-5.68	101.46	104.30
2	C	1	G	N1-C6-O6	5.66	123.30	119.90
3	D	4	G	C4-C5-N7	5.47	112.99	110.80
3	D	4	G	C2-N3-C4	-5.40	109.20	111.90
2	C	5	C	C4-C5-C6	5.36	120.08	117.40
3	D	4	G	N3-C4-C5	5.27	131.24	128.60
2	C	2	A	N9-C4-C5	-5.22	103.71	105.80

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	5802	0	5579	108	0
1	B	6080	0	5918	132	0
2	C	129	0	66	3	0
3	D	127	0	66	6	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	73	0	0	1	0
5	B	70	0	0	0	0
5	D	1	0	0	0	0
All	All	12284	0	11629	241	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 10.

All (241) 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:478:ASP:OD2	5:A:1102:HOH:O	1.61	1.14
1:B:680:MSE:HE3	1:B:765:THR:HB	1.32	1.09
1:A:228:GLN:HE21	1:A:319:LEU:H	1.23	0.85
1:A:538:MSE:HE1	1:A:771:GLY:N	1.93	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:460:PHE:HB3	1:B:463:MSE:HE2	1.60	0.84
1:B:680:MSE:CE	1:B:765:THR:HB	2.11	0.81
1:B:401:THR:HG22	1:B:404:LEU:HB2	1.64	0.79
1:A:112:GLN:OE1	1:A:112:GLN:N	2.14	0.79
1:B:680:MSE:HE3	1:B:765:THR:CB	2.11	0.78
1:A:782:ARG:NH2	1:A:788:PRO:O	2.15	0.78
1:B:112:GLN:OE1	1:B:112:GLN:N	2.13	0.78
1:B:538:MSE:HE1	1:B:771:GLY:N	1.99	0.78
1:B:527:PHE:HA	1:B:538:MSE:HE3	1.70	0.73
1:B:336:ASN:ND2	1:B:336:ASN:O	2.22	0.72
1:A:305:ASN:HD22	1:A:308:LEU:HG	1.54	0.72
1:A:193:THR:O	1:A:197:ILE:HG13	1.88	0.72
1:B:200:PHE:O	1:B:204:THR:OG1	2.08	0.70
1:B:670:THR:H	1:B:673:THR:HB	1.57	0.70
1:B:753:HIS:CE1	1:B:755:MSE:HB2	2.26	0.70
1:B:731:LEU:HA	1:B:734:ILE:HD12	1.73	0.69
1:A:478:ASP:HB3	1:A:680:MSE:HE1	1.74	0.68
1:A:565:LEU:HB3	1:A:573:LEU:HD11	1.75	0.68
1:B:295:GLN:O	1:B:378:ASN:ND2	2.27	0.67
1:B:477:ASN:OD1	1:B:768:MSE:HG2	1.96	0.65
1:A:305:ASN:ND2	1:A:308:LEU:HG	2.11	0.64
1:B:465:VAL:HG12	1:B:481:SER:OG	1.97	0.64
1:A:734:ILE:O	1:A:738:SER:N	2.26	0.64
1:A:222:LEU:CD1	1:A:225:ARG:NH1	2.60	0.63
1:B:204:THR:HG22	1:B:208:PHE:CE2	2.34	0.63
1:A:228:GLN:HE21	1:A:319:LEU:N	1.94	0.62
1:A:228:GLN:NE2	1:A:319:LEU:H	1.95	0.62
1:A:797:ASP:O	1:A:801:TRP:HD1	1.83	0.61
1:B:652:SER:O	1:B:660:CYS:N	2.33	0.61
1:B:364:ARG:NH2	1:B:413:SER:OG	2.34	0.61
1:B:845:GLY:O	1:B:863:LEU:HD12	2.01	0.61
1:B:261:ALA:HA	1:B:264:ARG:HH11	1.66	0.61
1:B:465:VAL:HG23	1:B:590:PHE:CD1	2.37	0.60
1:B:100:THR:OG1	1:B:152:ARG:NH2	2.35	0.59
1:B:595:TYR:HD1	1:B:672:SER:HG	1.50	0.59
1:B:838:VAL:HG23	1:B:873:ILE:HA	1.82	0.59
1:B:389:PHE:HD2	1:B:400:VAL:HG22	1.68	0.59
1:A:527:PHE:HA	1:A:538:MSE:HE3	1.85	0.59
1:A:389:PHE:HD2	1:A:400:VAL:HG22	1.67	0.58
1:A:293:GLN:HB3	1:A:298:LEU:HD12	1.85	0.58
1:B:609:LEU:HD22	1:B:610:PRO:HD2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:459:ASP:OD1	1:B:461:GLY:N	2.28	0.57
1:B:496:ILE:HG22	1:B:497:ALA:O	2.04	0.57
1:B:527:PHE:HA	1:B:538:MSE:CE	2.34	0.57
1:B:593:VAL:HA	1:B:597:LYS:HE3	1.87	0.57
1:A:249:ASN:OD1	1:A:252:GLU:N	2.31	0.56
1:B:645:ASN:HB3	1:B:648:LEU:HD11	1.87	0.56
1:B:401:THR:HG23	1:B:404:LEU:H	1.71	0.55
1:B:448:MSE:HB3	1:B:450:THR:HG23	1.88	0.55
1:A:823:LEU:HD12	1:A:887:PRO:HA	1.87	0.55
1:A:305:ASN:ND2	1:A:308:LEU:H	2.05	0.55
1:A:701:ARG:HG2	1:A:753:HIS:HD2	1.72	0.54
1:B:127:THR:HG23	1:B:715:GLN:OE1	2.07	0.54
1:B:475:GLU:O	3:D:5:A:H5"	2.07	0.54
1:B:531:LEU:HB2	1:B:534:LEU:HD23	1.88	0.54
1:A:443:LEU:HD21	1:A:518:VAL:HG22	1.90	0.54
1:B:261:ALA:HA	1:B:264:ARG:NH1	2.22	0.54
1:B:207:LYS:O	1:B:211:THR:HG23	2.08	0.53
1:A:730:SER:HB3	1:A:733:ASP:OD2	2.09	0.53
1:A:463:MSE:HE1	1:A:493:HIS:CD2	2.43	0.53
1:B:271:MSE:HE2	1:B:798:GLN:HG3	1.89	0.53
1:B:84:TYR:O	1:B:88:GLN:NE2	2.41	0.53
1:B:231:ARG:HE	1:B:436:ILE:HD13	1.73	0.53
1:B:702:CYS:SG	1:B:751:LEU:HB2	2.49	0.52
1:B:565:LEU:HD13	1:B:573:LEU:HD21	1.90	0.52
1:A:463:MSE:HE2	1:A:481:SER:HB3	1.91	0.52
1:B:160:GLU:H	1:B:160:GLU:CD	2.12	0.52
1:B:503:PHE:O	1:B:506:SER:OG	2.24	0.52
1:B:406:GLY:O	1:B:410:VAL:HG13	2.10	0.52
1:B:547:ALA:CB	1:B:768:MSE:HE1	2.40	0.52
1:B:332:ARG:HD3	1:B:362:TYR:CZ	2.45	0.52
1:A:779:GLN:HE22	1:A:791:PHE:H	1.58	0.51
1:B:231:ARG:HB2	1:B:436:ILE:HD13	1.91	0.51
1:B:742:SER:O	3:D:0:C:H4'	2.10	0.51
1:A:111:LYS:HA	1:A:150:ILE:HD11	1.93	0.51
1:B:753:HIS:HE1	1:B:755:MSE:HB2	1.72	0.51
1:A:118:THR:HG22	1:A:134:PHE:HB3	1.93	0.51
1:B:106:ASP:OD1	1:B:154:PRO:HA	2.10	0.51
1:B:139:GLY:O	1:B:194:ARG:NH1	2.44	0.51
1:A:578:ASP:OD1	1:B:78:ARG:N	2.41	0.50
1:A:231:ARG:HB2	1:A:436:ILE:HG12	1.94	0.50
1:A:394:MSE:HE1	1:A:411:GLU:OE2	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:515:SER:O	1:B:520:ARG:NH2	2.44	0.50
1:B:625:THR:HG22	1:B:674:LEU:HD21	1.94	0.49
1:B:525:ARG:O	1:B:538:MSE:HG3	2.12	0.49
1:B:699:VAL:HG21	1:B:772:PRO:HA	1.94	0.49
1:A:569:GLU:C	1:A:571:GLY:H	2.16	0.49
1:A:702:CYS:SG	1:A:747:SER:HB3	2.51	0.49
1:B:287:TYR:CZ	1:B:291:ARG:HD3	2.48	0.49
1:B:235:HIS:HA	1:B:315:ALA:HA	1.94	0.49
1:B:564:GLU:HB2	1:B:579:THR:HG21	1.94	0.49
1:B:407:LYS:O	1:B:410:VAL:HG22	2.13	0.49
1:A:478:ASP:CB	1:A:680:MSE:HE1	2.41	0.49
1:B:569:GLU:C	1:B:571:GLY:H	2.16	0.49
1:B:677:SER:O	1:B:681:ILE:HG13	2.12	0.49
1:A:719:LEU:HD11	1:A:729:PRO:HB3	1.95	0.49
1:B:732:LYS:O	1:B:736:LYS:HG3	2.12	0.49
1:A:262:TYR:O	1:A:266:VAL:HG23	2.12	0.48
1:A:652:SER:N	1:A:661:ILE:O	2.34	0.48
1:A:767:PRO:HG3	1:A:777:HIS:NE2	2.28	0.48
1:A:720:LYS:O	1:A:723:ILE:HG12	2.13	0.48
1:B:526:ALA:C	1:B:538:MSE:HE2	2.33	0.48
1:A:240:SER:O	1:A:244:ILE:HG13	2.14	0.48
1:A:499:PRO:HA	1:A:502:LEU:CD1	2.44	0.48
1:B:527:PHE:CA	1:B:538:MSE:HE3	2.42	0.48
1:A:197:ILE:O	1:A:201:THR:OG1	2.22	0.47
1:B:538:MSE:HE1	1:B:771:GLY:H	1.76	0.47
1:A:600:SER:HB2	1:A:605:ASP:HB2	1.95	0.47
1:B:539:LEU:HD12	1:B:768:MSE:HB2	1.95	0.47
1:A:370:TYR:O	1:A:402:ARG:HD2	2.13	0.47
1:A:544:CYS:HA	1:A:768:MSE:HE3	1.95	0.47
1:A:481:SER:HB2	1:A:493:HIS:HB2	1.97	0.47
1:B:307:ALA:HB2	1:B:743:SER:OG	2.15	0.47
1:A:442:LYS:O	1:A:446:THR:HG22	2.15	0.47
1:B:460:PHE:HE2	1:B:585:GLY:HA3	1.80	0.46
1:A:421:PHE:HD2	1:A:888:LEU:HD11	1.80	0.46
1:B:555:LYS:HG2	1:B:586:ILE:HG21	1.98	0.46
1:B:716:PHE:HD1	1:B:740:GLN:NE2	2.14	0.46
1:B:680:MSE:HE3	1:B:765:THR:CG2	2.45	0.46
1:B:724:LYS:NZ	1:B:727:LYS:HZ2	2.13	0.46
1:B:271:MSE:CE	1:B:798:GLN:HG3	2.46	0.46
1:A:306:THR:HG21	2:C:0:A:OP1	2.15	0.46
1:B:158:PRO:HG2	1:B:161:VAL:CG2	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:334:GLU:HG2	1:A:338:TYR:CE1	2.50	0.46
1:A:122:ASN:ND2	1:A:125:GLN:HE21	2.13	0.46
1:A:223:ILE:HD12	1:A:224:HIS:N	2.31	0.46
1:A:493:HIS:HB3	1:A:495:HIS:CE1	2.50	0.46
1:B:797:ASP:O	1:B:801:TRP:HD1	1.99	0.46
1:B:158:PRO:HG2	1:B:161:VAL:HG21	1.98	0.46
1:A:702:CYS:SG	1:A:751:LEU:HB2	2.56	0.45
1:B:91:SER:HA	1:B:278:ILE:O	2.15	0.45
1:A:818:SER:HB3	1:A:856:TYR:CD2	2.52	0.45
1:B:386:SER:HA	1:B:400:VAL:HG21	1.98	0.45
1:B:125:GLN:C	1:B:712:ALA:HB2	2.37	0.45
1:B:889:ASP:HB2	1:B:891:ILE:HD12	1.98	0.45
1:A:122:ASN:HB3	1:A:133:THR:HB	1.99	0.45
1:A:364:ARG:HG2	1:A:412:ILE:HD12	1.98	0.45
1:A:499:PRO:O	1:A:502:LEU:HD12	2.17	0.45
1:B:721:GLU:O	1:B:724:LYS:HG3	2.17	0.45
3:D:3:U:H2'	3:D:4:G:C8	2.52	0.45
1:B:253:ALA:HA	1:B:262:TYR:HD2	1.83	0.44
1:A:122:ASN:HB3	1:A:133:THR:OG1	2.18	0.44
1:A:443:LEU:C	1:A:443:LEU:HD23	2.37	0.44
1:A:793:GLN:HG3	1:A:793:GLN:O	2.17	0.44
1:A:222:LEU:HD13	1:A:225:ARG:NH1	2.32	0.44
1:B:393:ASP:HA	1:B:396:ARG:NH1	2.32	0.44
1:A:403:SER:O	1:A:407:LYS:HG3	2.18	0.44
1:A:576:ASP:HB3	1:A:579:THR:OG1	2.17	0.44
1:A:613:GLN:HA	1:A:616:GLN:OE1	2.18	0.44
1:B:430:ILE:HD13	1:B:534:LEU:HD11	1.99	0.44
1:B:547:ALA:HB1	1:B:768:MSE:HE1	1.99	0.44
1:A:680:MSE:HE3	2:C:4:A:OP1	2.17	0.44
1:B:124:PRO:HB3	1:B:130:PRO:C	2.37	0.44
1:A:789:LEU:HD23	1:A:789:LEU:HA	1.78	0.44
1:B:491:ARG:HB2	1:B:564:GLU:HG2	1.99	0.44
1:A:675:LEU:O	1:A:679:PHE:HD2	2.01	0.44
1:B:237:ASN:ND2	1:B:239:MSE:H	2.15	0.44
1:B:473:ALA:HB1	3:D:5:A:H4'	2.00	0.44
1:B:569:GLU:O	1:B:571:GLY:N	2.51	0.44
1:A:475:GLU:OE2	1:A:530:TYR:OH	2.27	0.43
1:B:231:ARG:HB2	1:B:436:ILE:CD1	2.48	0.43
1:B:758:ASN:N	1:B:758:ASN:OD1	2.51	0.43
1:A:723:ILE:HG13	1:A:724:LYS:N	2.33	0.43
1:B:669:GLN:HA	1:B:673:THR:HG21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:889:ASP:CB	1:B:891:ILE:HD12	2.48	0.43
1:A:544:CYS:HA	1:A:768:MSE:CE	2.49	0.43
1:A:463:MSE:HE3	1:A:483:GLU:HG3	2.01	0.43
1:A:645:ASN:HB3	1:A:648:LEU:HD11	1.99	0.43
1:B:767:PRO:HG3	1:B:777:HIS:CE1	2.54	0.43
1:B:295:GLN:NE2	1:B:377:GLU:O	2.47	0.43
1:B:460:PHE:CD1	1:B:463:MSE:HE1	2.54	0.43
1:B:333:LEU:HA	1:B:333:LEU:HD23	1.80	0.43
1:B:692:GLN:O	1:B:695:LYS:HD2	2.18	0.43
1:B:93:ASP:OD1	1:B:94:PRO:HD2	2.18	0.43
1:A:773:ASP:N	1:A:773:ASP:OD1	2.52	0.43
1:A:797:ASP:O	1:A:801:TRP:CD1	2.69	0.43
1:B:275:ASN:C	1:B:277:SER:N	2.72	0.43
1:A:122:ASN:HD21	1:A:125:GLN:HE21	1.67	0.42
1:A:780:LEU:HD23	1:A:780:LEU:HA	1.76	0.42
1:B:409:LEU:HD23	1:B:409:LEU:HA	1.75	0.42
1:A:253:ALA:HA	1:A:262:TYR:HD2	1.84	0.42
1:A:566:VAL:CG2	1:A:574:HIS:HB3	2.49	0.42
1:B:504:PRO:HA	1:B:507:PHE:CE2	2.55	0.42
1:B:780:LEU:HA	1:B:780:LEU:HD23	1.76	0.42
1:B:538:MSE:HE1	1:B:770:ARG:C	2.39	0.42
1:A:319:LEU:HD12	1:A:319:LEU:HA	1.91	0.42
3:D:2:C:H2'	3:D:3:U:C6	2.54	0.42
1:A:267:ILE:O	1:A:270:SER:HB3	2.18	0.42
1:B:444:TYR:HH	1:B:522:SER:HG	1.66	0.42
1:B:482:ILE:CG2	1:B:616:GLN:HB3	2.50	0.42
1:B:797:ASP:N	1:B:797:ASP:OD1	2.52	0.42
1:A:680:MSE:HE2	2:C:4:A:H5"	2.01	0.42
1:B:236:VAL:HG12	1:B:237:ASN:O	2.20	0.42
1:A:220:LEU:HD23	1:A:220:LEU:HA	1.86	0.42
1:A:102:LEU:HD23	1:A:132:TYR:CE2	2.55	0.42
1:A:122:ASN:HB3	1:A:133:THR:CB	2.50	0.42
1:A:648:LEU:O	1:A:664:PHE:HA	2.20	0.42
1:A:680:MSE:HE3	1:A:765:THR:HB	2.02	0.42
1:B:597:LYS:HB2	1:B:597:LYS:HE2	1.49	0.42
1:A:101:SER:OG	1:A:102:LEU:N	2.53	0.41
1:A:228:GLN:CG	1:A:318:PRO:HA	2.50	0.41
1:A:677:SER:O	1:A:681:ILE:HG13	2.20	0.41
1:B:389:PHE:CE2	1:B:404:LEU:HD23	2.55	0.41
1:B:414:PRO:C	1:B:416:SER:H	2.22	0.41
1:B:648:LEU:O	1:B:664:PHE:HA	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:884:SER:HB3	1:B:893:THR:OG1	2.20	0.41
1:A:371:ALA:HA	1:A:402:ARG:HB3	2.02	0.41
1:A:118:THR:CG2	1:A:134:PHE:HB3	2.51	0.41
1:A:132:TYR:O	1:A:143:TYR:HA	2.20	0.41
1:A:106:ASP:OD1	1:A:154:PRO:HA	2.20	0.41
1:A:796:LEU:HA	1:A:796:LEU:HD12	1.89	0.41
1:B:719:LEU:HB3	1:B:737:ILE:HD12	2.02	0.41
1:A:150:ILE:HD13	1:A:150:ILE:HG21	1.81	0.41
1:A:516:ASP:OD1	1:A:518:VAL:N	2.54	0.41
1:A:378:ASN:HB3	1:A:381:LEU:HD12	2.03	0.41
1:A:351:LYS:HD3	1:A:353:TYR:OH	2.21	0.41
1:A:653:PRO:O	1:A:661:ILE:HD13	2.20	0.41
1:B:601:ILE:HD13	1:B:609:LEU:HD12	2.03	0.41
1:B:634:ASP:OD1	1:B:634:ASP:N	2.52	0.41
1:B:789:LEU:HD23	1:B:789:LEU:HA	1.82	0.41
1:A:402:ARG:N	1:A:889:ASP:OD2	2.49	0.41
1:B:92:PHE:O	1:B:278:ILE:N	2.48	0.41
1:A:123:LEU:HB3	1:A:124:PRO:HD2	2.03	0.41
1:B:641:GLY:HA2	1:B:725:LEU:HD12	2.03	0.40
1:A:525:ARG:O	1:A:527:PHE:N	2.55	0.40
1:A:787:LEU:HD23	1:A:787:LEU:HA	1.79	0.40
1:B:717:GLU:OE2	1:B:720:LYS:HD2	2.22	0.40
1:B:293:GLN:HB3	1:B:298:LEU:HD12	2.03	0.40
1:A:542:SER:OG	1:A:543:PHE:HD1	2.04	0.40
1:B:896:HIS:CE1	1:B:898:ASN:H	2.39	0.40
1:A:531:LEU:HB2	1:A:534:LEU:HD23	2.04	0.40
1:A:840:SER:HB3	1:A:848:ASN:HB2	2.04	0.40
1:B:213:LEU:O	1:B:213:LEU:HD12	2.21	0.40
1:B:318:PRO:HG2	1:B:321:LYS:HB2	2.02	0.40
1:B:323:HIS:CD2	1:B:324:LEU:HD23	2.56	0.40
1:B:384:ILE:HA	1:B:384:ILE:HD13	1.92	0.40
1:B:475:GLU:H	3:D:5:A:HO3'	1.64	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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	744/832 (89%)	715 (96%)	27 (4%)	2 (0%)	41 66
1	B	778/832 (94%)	749 (96%)	27 (4%)	2 (0%)	41 66
All	All	1522/1664 (92%)	1464 (96%)	54 (4%)	4 (0%)	41 66

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	570	ASP
1	A	570	ASP
1	A	130	PRO
1	B	130	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	608/745 (82%)	600 (99%)	8 (1%)	69 87
1	B	645/745 (87%)	635 (98%)	10 (2%)	62 85
All	All	1253/1490 (84%)	1235 (99%)	18 (1%)	67 86

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	225	ARG
1	A	271	MSE
1	A	548	ASP
1	A	717	GLU
1	A	730	SER
1	A	773	ASP
1	A	777	HIS
1	A	794	GLU

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Mol	Chain	Res	Type
1	B	146	LYS
1	B	196	LEU
1	B	319	LEU
1	B	429	ASN
1	B	432	LYS
1	B	548	ASP
1	B	739	SER
1	B	773	ASP
1	B	815	ARG
1	B	835	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	125	GLN
1	A	228	GLN
1	A	305	ASN
1	A	574	HIS
1	A	779	GLN
1	B	237	ASN
1	B	294	GLN
1	B	429	ASN
1	B	707	ASN
1	B	711	GLN
1	B	740	GLN
1	B	879	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	5/6 (83%)	0	0
3	D	5/6 (83%)	0	0
All	All	10/12 (83%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	750/832 (90%)	-0.31	10 (1%) 77 78	40, 64, 104, 161	0
1	B	777/832 (93%)	-0.39	7 (0%) 84 85	40, 59, 103, 145	0
2	C	6/6 (100%)	-0.36	0 100 100	50, 54, 64, 135	0
3	D	6/6 (100%)	-0.53	0 100 100	49, 57, 65, 131	0
All	All	1539/1676 (91%)	-0.35	17 (1%) 80 82	40, 61, 104, 161	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	79	GLY	3.5
1	B	77	HIS	3.1
1	B	80	ASN	2.9
1	A	434	SER	2.8
1	B	604	GLY	2.7
1	B	84	TYR	2.7
1	A	190	PRO	2.5
1	A	866	ALA	2.5
1	A	865	PRO	2.4
1	A	895	THR	2.3
1	A	192	LEU	2.2
1	A	844	ASN	2.2
1	B	452	VAL	2.2
1	A	728	LEU	2.2
1	A	894	LEU	2.1
1	B	78	ARG	2.1
1	A	729	PRO	2.1

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 (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	MG	B	1001	1/1	0.94	0.15	101,101,101,101	0
4	MG	A	1001	1/1	0.95	0.23	126,126,126,126	0

6.5 Other polymers (i)

There are no such residues in this entry.