Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 05:23 am BST

PDB ID	:	5X2H
Title	:	Crystal structure of Campylobacter jejuni Cas9 in complex with sgRNA and target DNA (AGAAACA PAM)
Authors	:	Yamada, M.; Watanabe, Y.; Hirano, H.; Nakane, T.; Ishitani, R.; Nishimasu, H.; Nureki, O.
Deposited on	:	2017-01-31
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 ⓘ symbol.

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

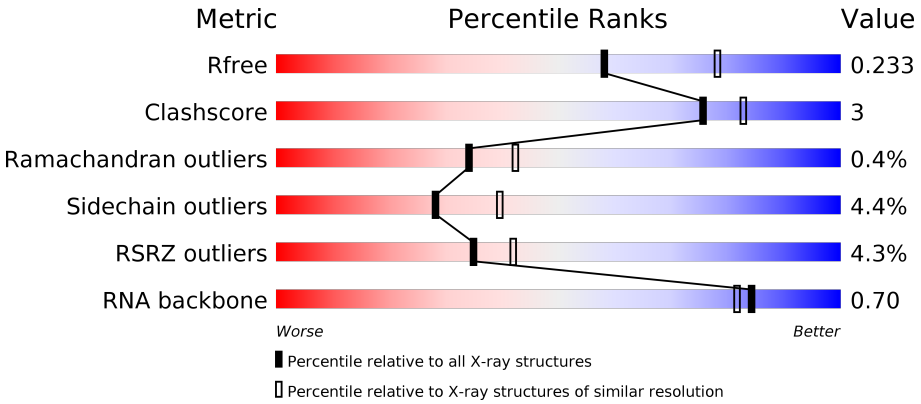
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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)
RNA backbone	3102	1090 (2.70-1.90)

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 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	835	5%, 78%, 11%, ·, 11%
2	B	93	83%, 16%, ·
3	C	28	86%, 14%
4	D	8	100%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8919 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 CRISPR-associated endonuclease Cas9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	746	Total	C	N	O	S	0	0	0
			5925	3824	1006	1084	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	SER	-	expression tag	UNP Q0P897
A	-4	SER	-	expression tag	UNP Q0P897
A	-3	GLY	-	expression tag	UNP Q0P897
A	-2	SER	-	expression tag	UNP Q0P897
A	-1	GLY	-	expression tag	UNP Q0P897
A	0	HIS	-	expression tag	UNP Q0P897
A	636	GLY	-	linker	UNP Q0P897
A	637	GLY	-	linker	UNP Q0P897
A	638	GLY	-	linker	UNP Q0P897
A	639	SER	-	linker	UNP Q0P897
A	640	GLY	-	linker	UNP Q0P897
A	641	GLY	-	linker	UNP Q0P897

- Molecule 2 is a RNA chain called sgRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	93	Total	C	N	O	P	0	0	0
			1990	889	361	647	93			

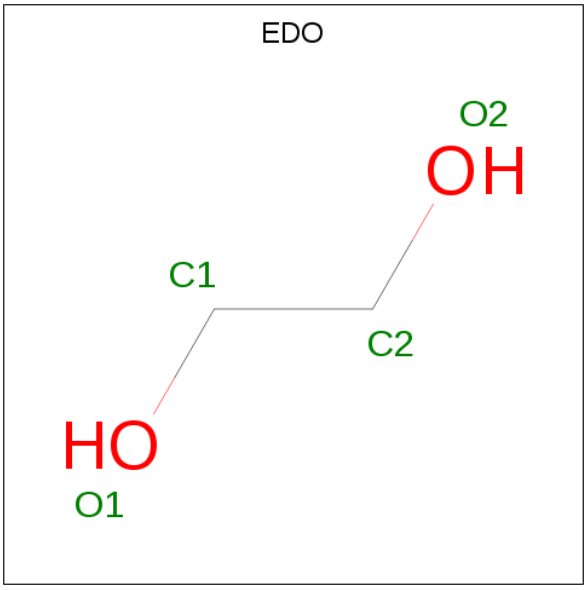
- Molecule 3 is a DNA chain called Target DNA strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	28	Total	C	N	O	P	0	0	0
			560	270	93	170	27			

- Molecule 4 is a DNA chain called Non-target DNA strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	8	Total	C	N	O	P	0	0	0
			165	79	38	41	7			

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is water.

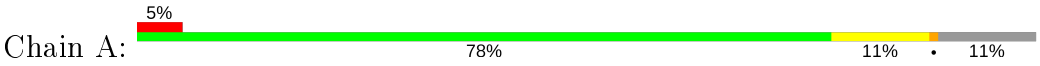
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	145	Total	O	0	0
			145	145		
6	B	99	Total	O	0	0
			99	99		
6	C	18	Total	O	0	0
			18	18		
6	D	13	Total	O	0	0
			13	13		

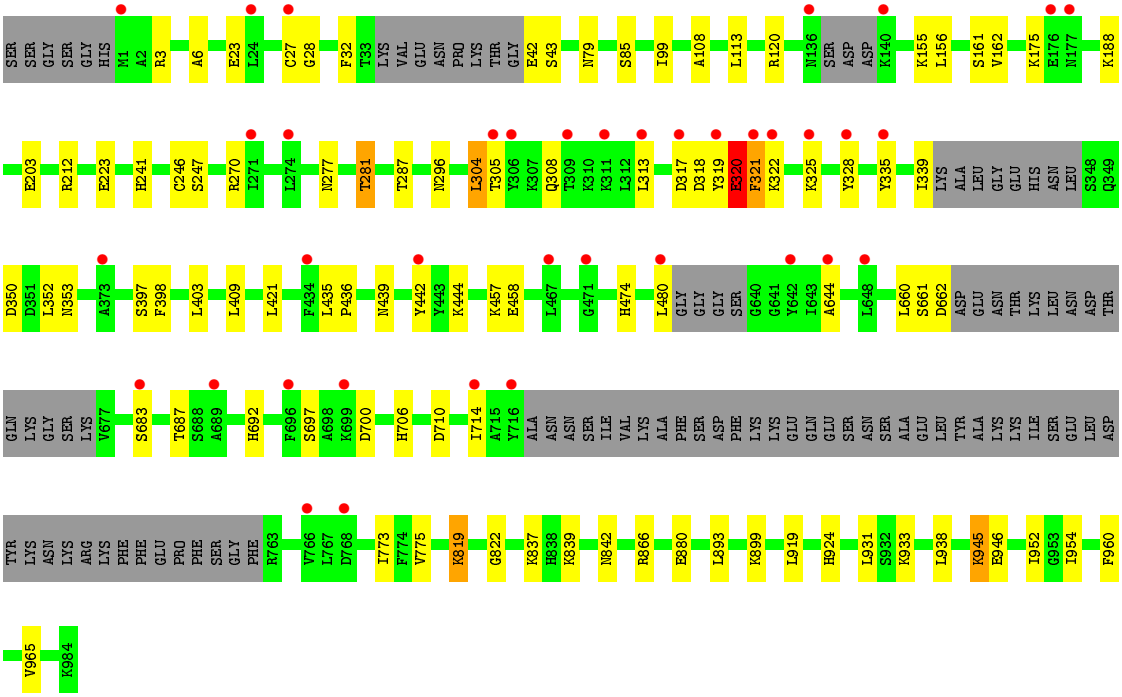
3 Residue-property plots (i)

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: CRISPR-associated endonuclease Cas9

Chain A:



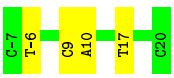


- Molecule 2: sgRNA

Chain B:

- Molecule 3: Target DNA strand

Chain C:



- Molecule 4: Non-target DNA strand

Chain D: 

There are no outlier residues recorded for this chain.

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	102.04Å 103.91Å 134.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	72.81 – 2.30 82.22 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.6 (72.81-2.30) 99.7 (82.22-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.47 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.200 , 0.231 0.201 , 0.233	Depositor DCC
R_{free} test set	3145 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å^2)	44.1	Xtriage
Anisotropy	0.814	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 39.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.013 for k,h,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	8919	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.58% 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: EDO

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	0.25	0/6030	0.41	0/8109
2	B	0.20	0/2227	0.73	0/3470
3	C	0.52	0/624	0.96	0/959
4	D	0.62	0/187	0.88	0/287
All	All	0.28	0/9068	0.58	0/12825

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	5925	0	5871	44	0
2	B	1990	0	1002	4	0
3	C	560	0	319	4	0
4	D	165	0	90	0	0
5	B	4	0	6	0	0
6	A	145	0	0	1	0
6	B	99	0	0	0	0
6	C	18	0	0	0	0
6	D	13	0	0	0	0
All	All	8919	0	7288	49	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 3.

All (49) 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:320:GLU:HG3	3:C:17:DT:H5'	1.70	0.72
1:A:305:THR:HA	1:A:325:LYS:HA	1.75	0.68
1:A:480:LEU:HG	1:A:644:ALA:HB2	1.74	0.67
1:A:893:LEU:HD22	1:A:965:VAL:HG22	1.76	0.66
1:A:212:ARG:NH2	1:A:223:GLU:OE2	2.27	0.66
1:A:866:ARG:NH2	3:C:-6:DT:O4	2.30	0.64
1:A:775:VAL:H	1:A:924:HIS:HD2	1.47	0.62
1:A:277:ASN:O	1:A:281:THR:OG1	2.18	0.61
1:A:247:SER:OG	2:B:4:A:OP1	2.16	0.59
1:A:839:LYS:NZ	1:A:880:GLU:O	2.36	0.58
1:A:661:SER:OG	1:A:662:ASP:N	2.37	0.58
1:A:317:ASP:OD1	1:A:318:ASP:N	2.36	0.57
1:A:27:CYS:HB3	1:A:773:ILE:HD11	1.85	0.56
1:A:99:ILE:O	1:A:120:ARG:NH2	2.28	0.56
1:A:305:THR:HG22	1:A:308:GLN:HG3	1.87	0.56
1:A:710:ASP:O	1:A:714:ILE:HG12	2.07	0.55
1:A:819:LYS:HD3	1:A:822:GLY:HA2	1.90	0.54
1:A:85:SER:OG	6:A:1001:HOH:O	2.18	0.54
1:A:3:ARG:H	1:A:474:HIS:HD2	1.56	0.53
1:A:6:ALA:HB1	1:A:714:ILE:HB	1.92	0.52
1:A:775:VAL:H	1:A:924:HIS:CD2	2.28	0.50
1:A:246:CYS:HB2	1:A:397:SER:HB3	1.95	0.48
1:A:108:ALA:HB2	1:A:113:LEU:HD11	1.96	0.47
1:A:42:GLU:HG2	1:A:43:SER:H	1.80	0.47
1:A:353:ASN:HB3	1:A:398:PHE:CZ	2.50	0.47
1:A:919:LEU:HG	1:A:954:ILE:HG22	1.97	0.47
1:A:318:ASP:HA	1:A:321:PHE:CE2	2.49	0.47
2:B:36:A:H5'	2:B:37:A:OP2	2.15	0.46
1:A:161:SER:HB2	1:A:203:GLU:HG3	1.97	0.46
1:A:32:PHE:CG	1:A:458:GLU:HG3	2.52	0.45
1:A:700:ASP:O	1:A:706:HIS:HB3	2.17	0.45
2:B:40:G:H2'	2:B:41:A:C8	2.51	0.45
2:B:34:A:H2'	2:B:35:A:O4'	2.16	0.45
1:A:403:LEU:HB3	1:A:421:LEU:HD13	2.00	0.44
1:A:692:HIS:HA	1:A:697:SER:HB2	2.00	0.44
1:A:945:LYS:HG3	1:A:946:GLU:HG2	2.01	0.43
3:C:9:DC:H2'	3:C:10:DA:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:439:ASN:HA	1:A:444:LYS:HD3	1.99	0.43
1:A:320:GLU:H	1:A:320:GLU:CD	2.22	0.43
1:A:304:LEU:HD23	1:A:304:LEU:HA	1.90	0.43
1:A:938:LEU:HD11	1:A:952:ILE:HD13	2.01	0.43
1:A:435:LEU:HD12	1:A:436:PRO:HD2	2.01	0.42
1:A:683:SER:O	1:A:687:THR:HG23	2.20	0.41
3:C:9:DC:H2'	3:C:10:DA:H8	1.86	0.41
1:A:321:PHE:HA	1:A:321:PHE:HD1	1.70	0.41
1:A:335:TYR:O	1:A:339:ILE:HG13	2.20	0.41
1:A:28:GLY:HA2	1:A:773:ILE:HG23	2.02	0.41
1:A:837:LYS:NZ	1:A:842:ASN:OD1	2.42	0.40
1:A:156:LEU:HD21	1:A:162:VAL:HG22	2.03	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	732/835 (88%)	707 (97%)	22 (3%)	3 (0%)	34 42

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	320	GLU
1	A	322	LYS
1	A	188	LYS

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	610/740 (82%)	583 (96%)	27 (4%)	28 39

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	GLU
1	A	79	ASN
1	A	155	LYS
1	A	175	LYS
1	A	241	HIS
1	A	270	ARG
1	A	281	THR
1	A	287	THR
1	A	296	ASN
1	A	304	LEU
1	A	313	LEU
1	A	319	TYR
1	A	320	GLU
1	A	321	PHE
1	A	328	TYR
1	A	350	ASP
1	A	352	LEU
1	A	409	LEU
1	A	442	TYR
1	A	457	LYS
1	A	660	LEU
1	A	819	LYS
1	A	899	LYS
1	A	931	LEU
1	A	933	LYS
1	A	945	LYS
1	A	960	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	HIS
1	A	474	HIS

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Mol	Chain	Res	Type
1	A	764	GLN
1	A	924	HIS
1	A	955	GLN
1	A	978	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	92/93 (98%)	9 (9%)	1 (1%)

All (9) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	37	A
2	B	38	G
2	B	49	A
2	B	51	A
2	B	55	U
2	B	58	G
2	B	64	C
2	B	77	C
2	B	86	A

All (1) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	63	A

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

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	EDO	B	101	-	3,3,3	0.46	0	2,2,2	0.32	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	B	101	-	-	0/1/1/1	-

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 (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, 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	746/835 (89%)	0.24	38 (5%) 28 35	29, 62, 108, 132	0
2	B	93/93 (100%)	-0.28	0 100 100	35, 51, 80, 140	0
3	C	28/28 (100%)	-0.34	0 100 100	41, 48, 73, 77	0
4	D	8/8 (100%)	-0.16	0 100 100	33, 40, 55, 64	0
All	All	875/964 (90%)	0.16	38 (4%) 35 42	29, 60, 108, 140	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	321	PHE	5.4
1	A	27	CYS	4.8
1	A	319	TYR	4.7
1	A	696	PHE	4.7
1	A	24	LEU	4.2
1	A	328	TYR	3.9
1	A	317	ASP	3.7
1	A	480	LEU	3.7
1	A	305	THR	3.5
1	A	306	TYR	3.4
1	A	311	LYS	3.4
1	A	313	LEU	3.4
1	A	176	GLU	3.1
1	A	699	LYS	3.1
1	A	766	VAL	3.0
1	A	644	ALA	3.0
1	A	373	ALA	2.9
1	A	274	LEU	2.9
1	A	714	ILE	2.8
1	A	322	LYS	2.7
1	A	434	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	642	TYR	2.5
1	A	471	GLY	2.5
1	A	1	MET	2.4
1	A	136	ASN	2.3
1	A	648	LEU	2.3
1	A	325	LYS	2.3
1	A	177	ASN	2.2
1	A	467	LEU	2.2
1	A	768	ASP	2.2
1	A	442	TYR	2.2
1	A	140	LYS	2.2
1	A	309	THR	2.1
1	A	335	TYR	2.1
1	A	683	SER	2.1
1	A	271	ILE	2.0
1	A	689	ALA	2.0
1	A	716	TYR	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)

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
5	EDO	B	101	4/4	0.97	0.17	28,30,32,33	0

6.5 Other polymers (i)

There are no such residues in this entry.