



Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 12:02 pm BST

PDB ID : 6IMD
Title : Crystal structure of PDE4D complexed with a novel inhibitor
Authors : Zhang, X.; Su, H.; Xu, Y.
Deposited on : 2018-10-22
Resolution : 1.50 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

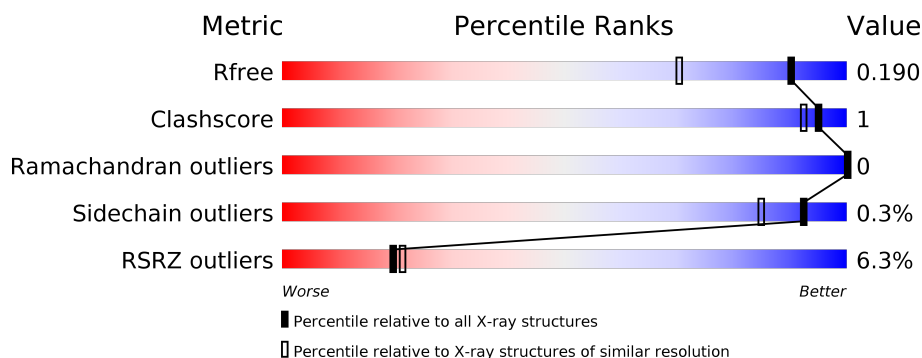
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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 $\leq 5\%$. 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	349	<div> <div>3%</div> <div> <div></div> <div>88%</div> <div>5%</div> <div>7%</div> </div> </div>
1	B	349	<div> <div>8%</div> <div> <div></div> <div>89%</div> <div>•</div> <div>7%</div> </div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 5730 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 cAMP-specific 3',5'-cyclic phosphodiesterase 4D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	325	Total	C	N	O	S	0	2	0
			2639	1671	447	506	15			
1	B	323	Total	C	N	O	S	0	0	0
			2555	1622	434	485	14			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	65	MET	-	expression tag	UNP Q08499
A	66	GLY	-	expression tag	UNP Q08499
A	67	SER	-	expression tag	UNP Q08499
A	68	SER	-	expression tag	UNP Q08499
A	69	HIS	-	expression tag	UNP Q08499
A	70	HIS	-	expression tag	UNP Q08499
A	71	HIS	-	expression tag	UNP Q08499
A	72	HIS	-	expression tag	UNP Q08499
A	73	HIS	-	expression tag	UNP Q08499
A	74	HIS	-	expression tag	UNP Q08499
A	75	SER	-	expression tag	UNP Q08499
A	76	SER	-	expression tag	UNP Q08499
A	77	GLY	-	expression tag	UNP Q08499
A	78	LEU	-	expression tag	UNP Q08499
A	79	VAL	-	expression tag	UNP Q08499
A	80	PRO	-	expression tag	UNP Q08499
A	81	ARG	-	expression tag	UNP Q08499
A	82	GLY	-	expression tag	UNP Q08499
A	83	SER	-	expression tag	UNP Q08499
A	84	HIS	-	expression tag	UNP Q08499
A	85	MET	-	expression tag	UNP Q08499
B	65	MET	-	expression tag	UNP Q08499
B	66	GLY	-	expression tag	UNP Q08499
B	67	SER	-	expression tag	UNP Q08499
B	68	SER	-	expression tag	UNP Q08499

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Chain	Residue	Modelled	Actual	Comment	Reference
B	69	HIS	-	expression tag	UNP Q08499
B	70	HIS	-	expression tag	UNP Q08499
B	71	HIS	-	expression tag	UNP Q08499
B	72	HIS	-	expression tag	UNP Q08499
B	73	HIS	-	expression tag	UNP Q08499
B	74	HIS	-	expression tag	UNP Q08499
B	75	SER	-	expression tag	UNP Q08499
B	76	SER	-	expression tag	UNP Q08499
B	77	GLY	-	expression tag	UNP Q08499
B	78	LEU	-	expression tag	UNP Q08499
B	79	VAL	-	expression tag	UNP Q08499
B	80	PRO	-	expression tag	UNP Q08499
B	81	ARG	-	expression tag	UNP Q08499
B	82	GLY	-	expression tag	UNP Q08499
B	83	SER	-	expression tag	UNP Q08499
B	84	HIS	-	expression tag	UNP Q08499
B	85	MET	-	expression tag	UNP Q08499

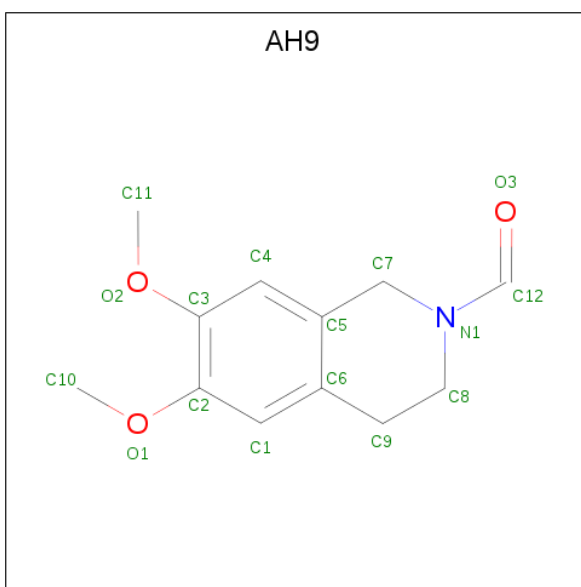
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

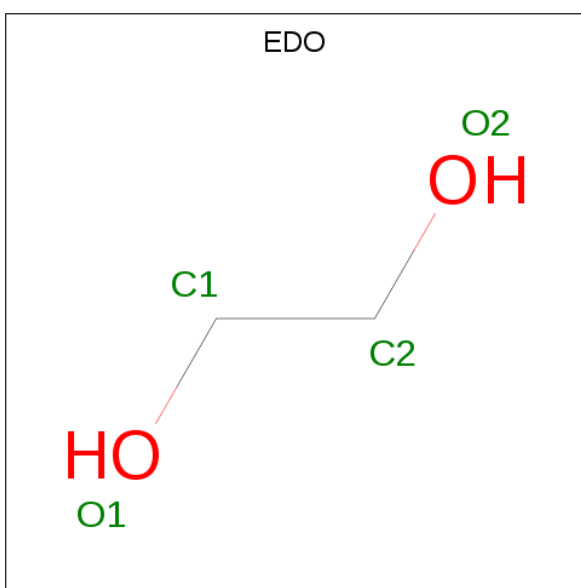
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	A	3	Total Mg 3 3	0	0

- Molecule 4 is 6,7-dimethoxy-3,4-dihydroisoquinoline-2(1H)-carbaldehyde (three-letter code: AH9) (formula: C₁₂H₁₅NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			16	12	1	3		
4	B	1	Total	C	N	O	0	0
			16	12	1	3		

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

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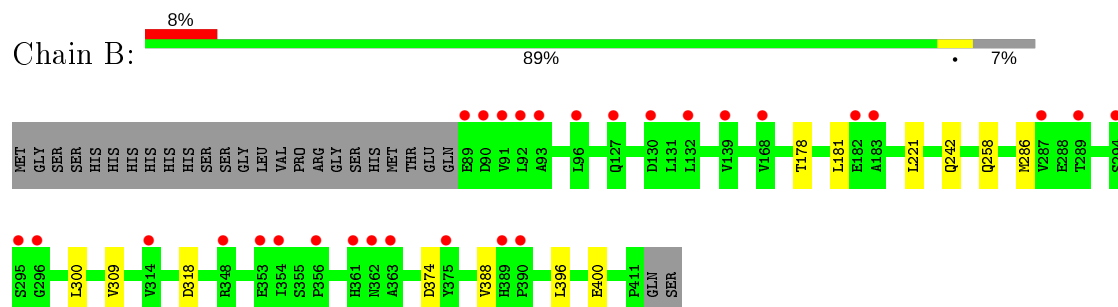
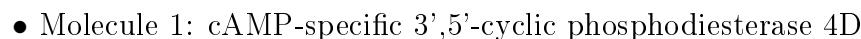
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	269	Total O 269 269	0	0
6	B	185	Total O 185 185	0	0

- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.40 Å 80.36 Å 163.44 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.02 – 1.50 39.02 – 1.50	Depositor EDS
% Data completeness (in resolution range)	92.7 (39.02-1.50) 92.7 (39.02-1.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 1.50 Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.168 , 0.190 0.168 , 0.190	Depositor DCC
R_{free} test set	5684 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	12.9	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 56.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5730	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.55% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, AH9, MG, 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	0.76	1/2693 (0.0%)	0.86	5/3660 (0.1%)
1	B	0.66	0/2609	0.77	2/3557 (0.1%)
All	All	0.71	1/5302 (0.0%)	0.82	7/7217 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	247	ASP	CB-CG	6.00	1.64	1.51

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	247	ASP	CB-CG-OD1	8.49	125.94	118.30
1	A	261	ARG	NE-CZ-NH2	-6.29	117.15	120.30
1	B	374	ASP	CB-CG-OD1	6.29	123.96	118.30
1	A	335	ARG	NE-CZ-NH2	-5.90	117.35	120.30
1	A	391	ASP	CB-CG-OD1	5.54	123.28	118.30
1	B	318	ASP	CB-CG-OD2	-5.26	113.56	118.30
1	A	364	SER	N-CA-CB	5.13	118.19	110.50

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	2639	0	2584	8	0
1	B	2555	0	2466	6	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	3	0	0	0	0
3	B	1	0	0	0	0
4	A	16	0	0	0	0
4	B	16	0	0	0	0
5	A	36	0	54	1	0
5	B	8	0	12	0	0
6	A	269	0	0	0	0
6	B	185	0	0	0	0
All	All	5730	0	5116	12	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 1.

All (12) 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:282:ASP:HB3	1:A:308:GLN:NE2	2.11	0.65
1:A:239:LYS:HD3	1:B:221:LEU:HD21	1.96	0.48
1:A:221:LEU:HD11	1:B:242:GLN:OE1	2.13	0.47
1:B:300:LEU:HD11	1:B:309:VAL:HG21	1.97	0.46
1:B:178:THR:HG21	1:B:388:VAL:HB	1.99	0.43
1:A:354:ILE:HG21	1:A:359:ASP:HB2	2.01	0.43
1:A:290:LYS:HA	5:A:512:EDO:H22	2.00	0.43
1:A:373:ILE:HA	1:A:377:VAL:HB	2.01	0.42
1:B:181:LEU:HD23	1:B:181:LEU:HA	1.80	0.42
1:B:396:LEU:O	1:B:400:GLU:HG3	2.18	0.42
1:A:298:LEU:HD21	1:A:387:LEU:HD11	2.02	0.41
1:A:291:LYS:HE2	1:A:291:LYS:HB2	1.86	0.41

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	325/349 (93%)	319 (98%)	6 (2%)	0	100	100
1	B	321/349 (92%)	318 (99%)	3 (1%)	0	100	100
All	All	646/698 (93%)	637 (99%)	9 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	297/318 (93%)	297 (100%)	0	100	100
1	B	280/318 (88%)	278 (99%)	2 (1%)	84	69
All	All	577/636 (91%)	575 (100%)	2 (0%)	92	85

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	258	GLN
1	B	286	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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

Of 19 ligands modelled in this entry, 6 are monoatomic - leaving 13 for Mogul analysis.

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	A	511	-	3,3,3	0.53	0	2,2,2	0.68	0
5	EDO	A	509	-	3,3,3	0.56	0	2,2,2	1.47	0
5	EDO	A	510	-	3,3,3	0.46	0	2,2,2	0.45	0
5	EDO	A	508	-	3,3,3	0.51	0	2,2,2	0.24	0
5	EDO	A	512	-	3,3,3	0.48	0	2,2,2	0.59	0
4	AH9	A	505	-	17,17,17	0.28	0	21,23,23	0.53	0
5	EDO	A	513	-	3,3,3	0.43	0	2,2,2	0.72	0
5	EDO	A	506	-	3,3,3	0.33	0	2,2,2	1.08	0
4	AH9	B	504	-	17,17,17	0.24	0	21,23,23	0.49	0
5	EDO	A	507	-	3,3,3	0.45	0	2,2,2	0.69	0
5	EDO	B	505	-	3,3,3	0.41	0	2,2,2	0.70	0
5	EDO	A	514	-	3,3,3	0.45	0	2,2,2	0.55	0
5	EDO	B	501	-	3,3,3	0.43	0	2,2,2	0.33	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	A	511	-	-	1/1/1/1	-
5	EDO	A	509	-	-	0/1/1/1	-
5	EDO	A	510	-	-	0/1/1/1	-
5	EDO	A	508	-	-	0/1/1/1	-
5	EDO	A	512	-	-	0/1/1/1	-
4	AH9	A	505	-	-	0/6/15/15	0/2/2/2
5	EDO	A	513	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	A	506	-	-	0/1/1/1	-
4	AH9	B	504	-	-	0/6/15/15	0/2/2/2
5	EDO	A	507	-	-	1/1/1/1	-
5	EDO	B	505	-	-	0/1/1/1	-
5	EDO	A	514	-	-	1/1/1/1	-
5	EDO	B	501	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	514	EDO	O1-C1-C2-O2
5	A	511	EDO	O1-C1-C2-O2
5	A	513	EDO	O1-C1-C2-O2
5	A	507	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	512	EDO	1	0

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	325/349 (93%)	0.04	12 (3%) 41 46	6, 16, 35, 76	0
1	B	323/349 (92%)	0.53	29 (8%) 9 10	8, 24, 44, 61	0
All	All	648/698 (92%)	0.28	41 (6%) 20 21	6, 20, 41, 76	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	91	VAL	6.4
1	B	354	ILE	6.0
1	B	183	ALA	5.4
1	B	294	SER	5.0
1	A	294	SER	4.7
1	B	295	SER	4.6
1	B	296	GLY	4.6
1	B	139	VAL	4.1
1	B	92	LEU	4.1
1	B	375	TYR	4.1
1	B	362	ASN	4.1
1	B	90	ASP	4.0
1	B	361	HIS	3.9
1	B	93	ALA	3.8
1	A	295	SER	3.7
1	A	292	VAL	3.6
1	B	390	PRO	3.6
1	B	89	GLU	3.5
1	B	127	GLN	3.4
1	B	130	ASP	3.4
1	B	363	ALA	3.3
1	B	314	VAL	3.1
1	A	362	ASN	3.0
1	A	349	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	90	ASP	2.9
1	B	132	LEU	2.9
1	B	389	HIS	2.9
1	A	293	THR	2.7
1	B	353	GLU	2.7
1	B	182	GLU	2.6
1	B	356	PRO	2.6
1	B	287	VAL	2.6
1	A	411	PRO	2.6
1	A	361	HIS	2.4
1	A	363	ALA	2.3
1	A	348	ARG	2.3
1	A	296	GLY	2.2
1	B	96	LEU	2.2
1	B	168	VAL	2.2
1	B	348	ARG	2.0
1	B	289	THR	2.0

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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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, 95th 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	AH9	B	504	16/16	0.51	0.32	61,74,84,85	0
4	AH9	A	505	16/16	0.63	0.23	35,49,68,73	0
5	EDO	B	505	4/4	0.68	0.14	34,35,35,35	0
5	EDO	A	506	4/4	0.75	0.13	35,35,36,37	0
5	EDO	A	507	4/4	0.80	0.26	49,50,53,54	0
5	EDO	A	514	4/4	0.81	0.17	43,44,44,45	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	EDO	A	511	4/4	0.82	0.14	50,50,50,50	0
5	EDO	A	509	4/4	0.83	0.12	34,34,34,34	0
5	EDO	A	508	4/4	0.86	0.15	26,27,29,31	0
5	EDO	A	512	4/4	0.90	0.14	44,45,45,45	0
5	EDO	A	510	4/4	0.91	0.08	34,37,40,42	0
5	EDO	A	513	4/4	0.91	0.09	24,25,25,27	0
3	MG	A	504	1/1	0.92	0.13	23,23,23,23	0
5	EDO	B	501	4/4	0.93	0.09	25,28,30,30	0
3	MG	A	503	1/1	1.00	0.10	15,15,15,15	0
3	MG	B	503	1/1	1.00	0.10	8,8,8,8	0
2	ZN	A	501	1/1	1.00	0.04	12,12,12,12	0
3	MG	A	502	1/1	1.00	0.05	7,7,7,7	0
2	ZN	B	502	1/1	1.00	0.04	15,15,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.