



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:03 PM GMT

PDB ID : 4NMF
Title : Crystal structure of proline utilization A (PutA) from *Geobacter sulfurreducens* PCA inactivated by N-propargylglycine and complexed with menadione bisulfite
Authors : Singh, H.; Tanner, J.J.
Deposited on : 2013-11-14
Resolution : 1.95 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

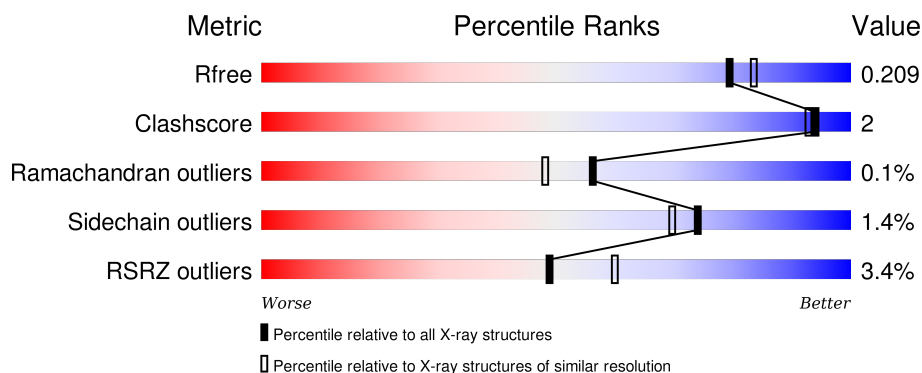
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	91344	1833 (1.96-1.96)
Clashscore	102246	1953 (1.96-1.96)
Ramachandran outliers	100387	1936 (1.96-1.96)
Sidechain outliers	100360	1936 (1.96-1.96)
RSRZ outliers	91569	1835 (1.96-1.96)

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. 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	1005	<div> <div>5%</div> <div>92%</div> <div>6%</div> <div>.</div> <div>.</div> </div>
1	B	1005	<div> <div>2%</div> <div>92%</div> <div>6%</div> <div>.</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	2L3	B	1102[A]	-	-	-	X
4	EDO	A	1107	-	-	-	X
4	EDO	B	1106	-	-	-	X
5	2LB	B	1103[B]	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 16394 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.

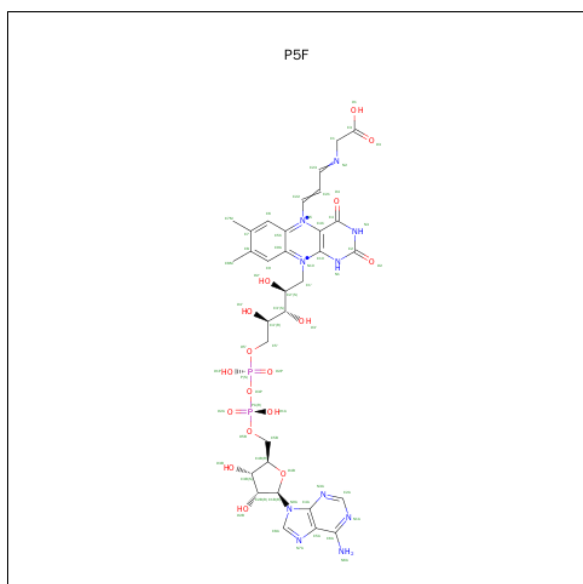
- Molecule 1 is a protein called Proline dehydrogenase and Delta-1-pyrroline-5-carboxylate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	973	Total	C	N	O	S	0	4	0
			7568	4837	1313	1379	39			
1	B	979	Total	C	N	O	S	0	2	0
			7624	4864	1323	1399	38			

There are 2 discrepancies between the modelled and reference sequences:

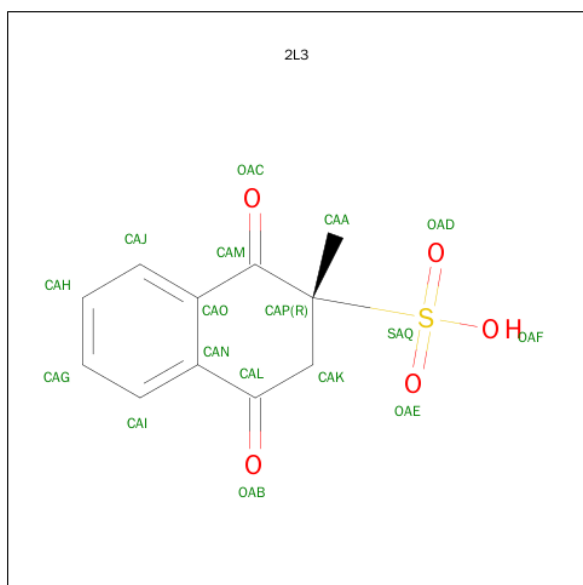
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	EXPRESSION TAG	UNP Q746X3
B	0	SER	-	EXPRESSION TAG	UNP Q746X3

- Molecule 2 is N-PROPARGYLGLYCINE-MODIFIED FLAVIN ADENINE DINUCLEOTIDE (three-letter code: P5F) (formula: $C_{32}H_{40}N_{10}O_{17}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			56	30	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			56	30	9	15	2		

- Molecule 3 is (2R)-2-METHYL-1,4-DIOXO-1,2,3,4-TETRAHYDRONAPHTHALENE-2-SULFONIC ACID (three-letter code: 2L3) (formula: C₁₁H₁₀O₅S).



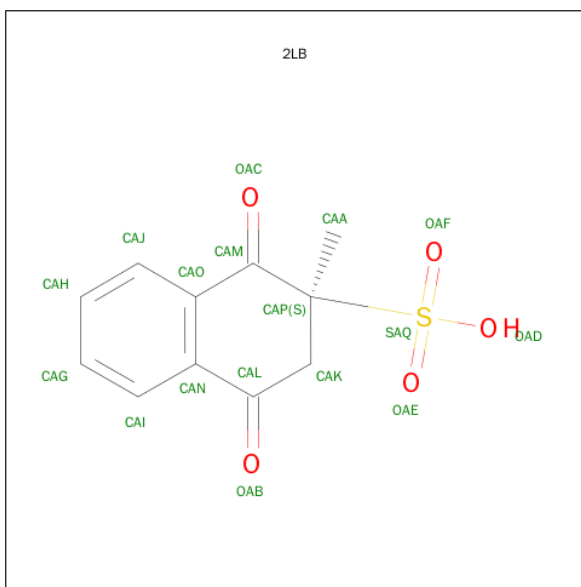
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	S	0	0
			17	11	5	1		
3	B	1	Total	C	O	S	0	1
			17	11	5	1		

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

- Molecule 5 is (2S)-2-METHYL-1,4-DIOXO-1,2,3,4-TETRAHYDRONAPHTHALENE-2-SULFONIC ACID (three-letter code: 2LB) (formula: C₁₁H₁₀O₅S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	O	S	0	1
			17	11	5	1		

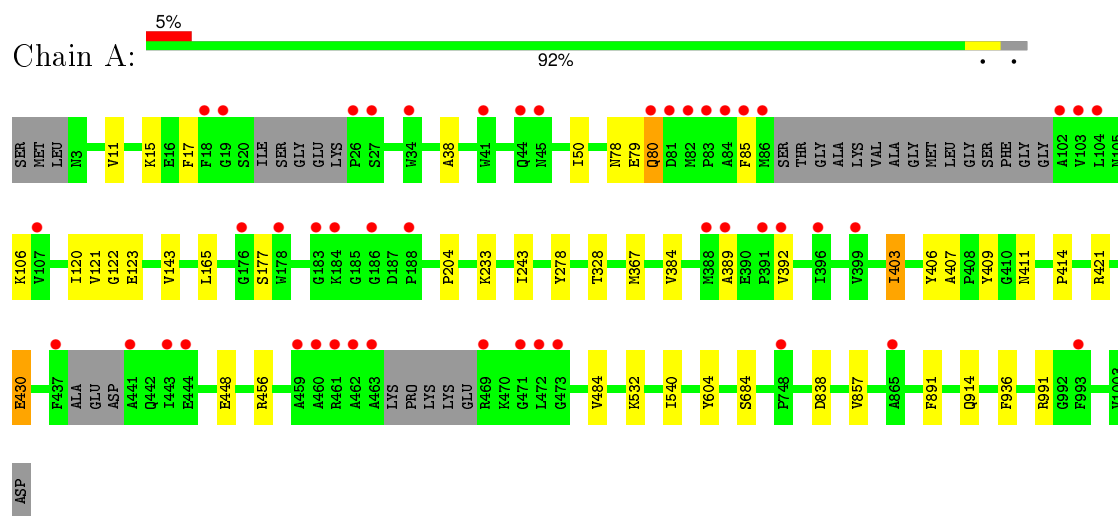
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	497	Total	O	0	0
			497	497		
6	B	510	Total	O	0	0
			510	510		

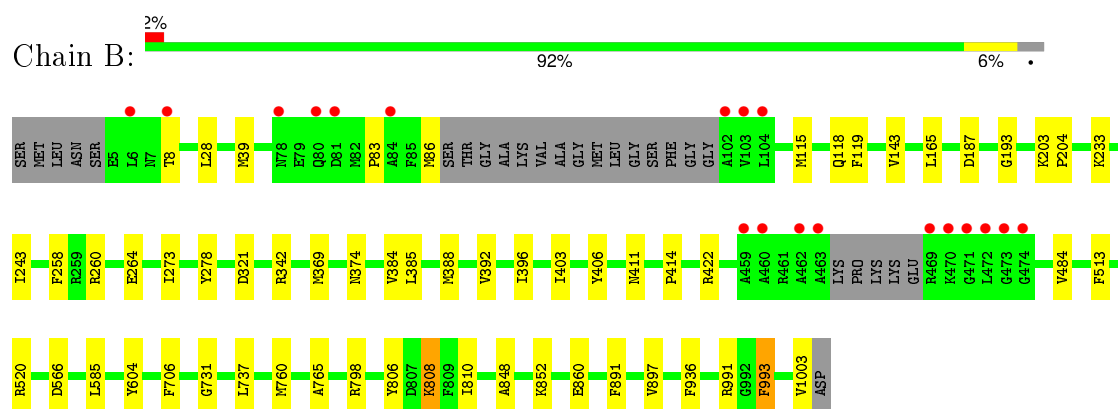
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Proline dehydrogenase and Delta-1-pyrroline-5-carboxylate dehydrogenase



- Molecule 1: Proline dehydrogenase and Delta-1-pyrroline-5-carboxylate dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.59Å 151.74Å 176.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.60 – 1.95 47.60 – 1.95	Depositor EDS
% Data completeness (in resolution range)	98.2 (47.60-1.95) 98.2 (47.60-1.95)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 1.95Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.173 , 0.203 0.182 , 0.209	Depositor DCC
R_{free} test set	9211 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	24.3	Xtriage
Anisotropy	0.486	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	2 of 183462 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16394	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.45% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: P5F, EDO, 2L3, 2LB

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	0.36	0/7751	0.51	0/10500
1	B	0.37	0/7802	0.50	0/10570
All	All	0.36	0/15553	0.51	0/21070

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	7568	0	7425	24	0
1	B	7624	0	7485	32	0
2	A	56	0	35	1	0
2	B	56	0	35	3	0
3	A	17	0	9	1	0
3	B	17	0	9	1	0
4	A	20	0	30	0	0
4	B	12	0	18	0	0
5	B	17	0	9	3	0
6	A	497	0	0	1	0
6	B	510	0	0	1	0
All	All	16394	0	15055	56	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 2.

All (56) 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:B:422:ARG:NH1	3:B:1102[A]:2L3:OAF	2.25	0.69
1:B:28:LEU:HD22	1:B:39:MET:HG3	1.77	0.66
1:A:389:ALA:HB1	1:A:392:VAL:HB	1.77	0.66
1:A:406:TYR:HB2	2:A:1101:P5F:H18	1.81	0.62
1:B:321:ASP:HB2	6:B:1649:HOH:O	2.00	0.62
1:B:143:VAL:HG13	1:B:406:TYR:HA	1.83	0.61
1:A:120:ILE:HG22	1:A:122:GLY:H	1.66	0.59
1:B:203:LYS:HE3	5:B:1103[B]:2LB:H5	1.85	0.58
1:B:810:ILE:HD11	1:B:897:VAL:HG11	1.86	0.56
1:B:852:LYS:NZ	1:B:860:GLU:OE2	2.39	0.54
2:B:1101:P5F:C1'	5:B:1103[B]:2LB:H10	2.39	0.53
1:B:83:PRO:HD2	1:B:86:MET:HG3	1.90	0.53
1:B:187:ASP:O	1:B:193:GLY:HA2	2.10	0.52
1:B:406:TYR:HB2	2:B:1101:P5F:H18	1.92	0.51
1:A:78:ASN:O	1:A:80:GLN:N	2.43	0.51
1:A:384:VAL:HG22	1:A:403:ILE:HD11	1.92	0.51
1:B:808:LYS:NZ	1:B:808:LYS:HB2	2.25	0.50
1:A:448:GLU:OE2	1:A:456:ARG:NH1	2.45	0.49
1:A:121:VAL:HG11	1:A:407:ALA:HB1	1.93	0.49
1:B:731:GLY:O	1:B:760:MET:HA	2.14	0.48
1:A:143:VAL:HG13	1:A:406:TYR:HA	1.96	0.47
1:A:17:PHE:CE2	1:A:367:MET:HE1	2.50	0.47
1:A:50:ILE:HG12	1:B:993:PHE:HZ	1.81	0.45
1:A:914:GLN:NE2	6:A:1490:HOH:O	2.38	0.45
1:B:385:LEU:HD21	5:B:1103[B]:2LB:H9	2.00	0.44
1:A:484:VAL:HB	1:A:604:TYR:CG	2.53	0.44
1:B:806:TYR:O	1:B:810:ILE:HG12	2.18	0.43
1:A:120:ILE:HG23	1:A:409:TYR:HA	2.00	0.43
1:B:848:ALA:O	1:B:852:LYS:HG3	2.18	0.43
1:A:421:ARG:NE	3:A:1102:2L3:OAF	2.43	0.43
1:B:484:VAL:HB	1:B:604:TYR:CG	2.54	0.43
1:B:258:PHE:HB2	1:B:273:ILE:HD13	2.01	0.43
1:B:991:ARG:HD3	1:B:991:ARG:HA	1.92	0.42
1:B:411:ASN:HB3	1:B:414:PRO:HD2	2.01	0.42
1:B:342:ARG:HB2	1:B:369:MET:SD	2.59	0.42
2:B:1101:P5F:H35	2:B:1101:P5F:C4	2.49	0.42
1:A:11:VAL:O	1:A:15:LYS:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:765:ALA:HA	1:B:798:ARG:O	2.20	0.42
1:A:328:THR:HG21	1:B:1003:VAL:HG11	2.02	0.42
1:B:165:LEU:HD22	1:B:233:LYS:HG3	2.01	0.42
1:A:411:ASN:HB3	1:A:414:PRO:HD2	2.02	0.41
1:A:165:LEU:HD22	1:A:233:LYS:HG3	2.01	0.41
1:B:384:VAL:HG22	1:B:403:ILE:HD11	2.02	0.41
1:A:484:VAL:HB	1:A:604:TYR:CD1	2.55	0.41
1:A:204:PRO:HG3	1:A:243:ILE:HG23	2.02	0.41
1:B:392:VAL:O	1:B:396:ILE:HG13	2.20	0.41
1:A:430:GLU:H	1:A:430:GLU:CD	2.24	0.41
1:A:38:ALA:HA	1:A:85:PHE:CZ	2.56	0.41
1:A:540:ILE:HG13	1:A:684:SER:HB2	2.03	0.41
1:B:513:PHE:HB3	1:B:706:PHE:HB3	2.03	0.41
1:B:119:PHE:HE1	1:B:388:MET:HB3	1.87	0.41
1:A:991:ARG:HA	1:A:991:ARG:HD3	1.89	0.40
1:B:204:PRO:HG3	1:B:243:ILE:HG23	2.03	0.40
1:B:115:MET:O	1:B:118:GLN:HB3	2.21	0.40
1:B:737:LEU:HD23	1:B:737:LEU:HA	1.90	0.40
1:B:260:ARG:O	1:B:264:GLU:HG3	2.22	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	967/1005 (96%)	948 (98%)	17 (2%)	2 (0%)	52 43
1	B	975/1005 (97%)	953 (98%)	22 (2%)	0	100 100
All	All	1942/2010 (97%)	1901 (98%)	39 (2%)	2 (0%)	56 48

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	79	GLU
1	A	80	GLN

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	768/821 (94%)	757 (99%)	11 (1%)	74	70
1	B	777/821 (95%)	767 (99%)	10 (1%)	76	72
All	All	1545/1642 (94%)	1524 (99%)	21 (1%)	74	70

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106	LYS
1	A	123	GLU
1	A	177	SER
1	A	278	TYR
1	A	403	ILE
1	A	430	GLU
1	A	532	LYS
1	A	838	ASP
1	A	857	VAL
1	A	891	PHE
1	A	936	PHE
1	B	8	THR
1	B	278	TYR
1	B	374	ASN
1	B	520	ARG
1	B	566	ASP
1	B	585	LEU
1	B	808	LYS
1	B	891	PHE
1	B	936	PHE
1	B	993	PHE

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 ⓘ

13 ligands are 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	$\# Z > 2$
2	P5F	A	1101	1	46,61,66	2.29	14 (30%)	52,93,99	2.37	12 (23%)
3	2L3	A	1102	-	15,18,18	3.93	6 (40%)	18,29,29	1.37	3 (16%)
4	EDO	A	1103	-	3,3,3	0.48	0	2,2,2	0.52	0
4	EDO	A	1104	-	3,3,3	0.56	0	2,2,2	0.42	0
4	EDO	A	1105	-	3,3,3	0.43	0	2,2,2	0.41	0
4	EDO	A	1106	-	3,3,3	0.50	0	2,2,2	0.36	0
4	EDO	A	1107	-	3,3,3	0.56	0	2,2,2	0.44	0
2	P5F	B	1101	1	46,61,66	2.23	14 (30%)	52,93,99	2.43	15 (28%)
3	2L3	B	1102[A]	-	15,18,18	3.98	6 (40%)	18,29,29	1.42	4 (22%)
5	2LB	B	1103[B]	-	15,18,18	3.95	6 (40%)	18,29,29	1.49	6 (33%)
4	EDO	B	1104	-	3,3,3	0.51	0	2,2,2	0.21	0
4	EDO	B	1105	-	3,3,3	0.53	0	2,2,2	0.52	0
4	EDO	B	1106	-	3,3,3	0.54	0	2,2,2	0.56	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
2	P5F	A	1101	1	-	0/31/53/58	0/6/6/6
3	2L3	A	1102	-	-	0/2/28/28	0/2/2/2
4	EDO	A	1103	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1104	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1105	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1106	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1107	-	-	0/1/1/1	0/0/0/0
2	P5F	B	1101	1	-	0/31/53/58	0/6/6/6
3	2L3	B	1102[A]	-	-	0/2/28/28	0/2/2/2
5	2LB	B	1103[B]	-	-	0/2/28/28	0/2/2/2
4	EDO	B	1104	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1105	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1106	-	-	0/1/1/1	0/0/0/0

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1103[B]	2LB	CAN-CAO	-4.47	1.33	1.40
3	B	1102[A]	2L3	CAN-CAO	-4.14	1.34	1.40
3	A	1102	2L3	CAN-CAO	-3.83	1.34	1.40
3	B	1102[A]	2L3	CAA-CAP	-3.71	1.49	1.53
3	A	1102	2L3	CAA-CAP	-3.61	1.49	1.53
5	B	1103[B]	2LB	CAA-CAP	-3.43	1.49	1.53
2	B	1101	P5F	C9A-C5X	-3.14	1.35	1.42
2	A	1101	P5F	C9A-C5X	-2.80	1.36	1.42
2	B	1101	P5F	PA-O5B	-2.21	1.48	1.59
2	A	1101	P5F	PA-O5B	-2.08	1.49	1.59
2	A	1101	P5F	O3B-C3B	-2.05	1.38	1.43
2	B	1101	P5F	O3B-C3B	-2.05	1.38	1.43
2	A	1101	P5F	C2B-C3B	-2.03	1.47	1.53
2	B	1101	P5F	C2B-C3B	-2.03	1.47	1.53
2	B	1101	P5F	C2A-N3A	2.59	1.36	1.32
2	A	1101	P5F	C2A-N3A	2.93	1.37	1.32
2	B	1101	P5F	C6A-N6A	3.09	1.44	1.34
2	B	1101	P5F	C10-N10	3.11	1.42	1.39
2	B	1101	P5F	C9-C9A	3.17	1.47	1.40
2	A	1101	P5F	C6A-N6A	3.18	1.44	1.34
2	A	1101	P5F	C9-C9A	3.52	1.48	1.40
2	B	1101	P5F	C4-N3	3.64	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1101	P5F	C6-C5X	3.74	1.48	1.40
2	A	1101	P5F	C4-C4X	3.94	1.49	1.41
2	A	1101	P5F	C10-N10	3.95	1.43	1.39
2	A	1101	P5F	C4-N3	3.95	1.40	1.33
2	B	1101	P5F	C4-C4X	4.11	1.49	1.41
2	A	1101	P5F	C6-C5X	4.17	1.49	1.40
2	B	1101	P5F	C9A-N10	4.59	1.45	1.38
5	B	1103[B]	2LB	CAJ-CAO	4.86	1.48	1.39
3	B	1102[A]	2L3	CAJ-CAO	5.04	1.48	1.39
3	A	1102	2L3	CAJ-CAO	5.10	1.48	1.39
3	A	1102	2L3	CAI-CAN	5.16	1.48	1.39
5	B	1103[B]	2LB	CAI-CAN	5.37	1.49	1.39
2	A	1101	P5F	C10-N1	5.38	1.44	1.35
2	A	1101	P5F	C9A-N10	5.38	1.46	1.38
3	B	1102[A]	2L3	CAI-CAN	5.49	1.49	1.39
2	A	1101	P5F	O4-C4	5.53	1.37	1.24
2	B	1101	P5F	O4-C4	5.61	1.38	1.24
2	B	1101	P5F	C10-N1	5.62	1.44	1.35
3	A	1102	2L3	OAC-CAM	8.19	1.37	1.21
5	B	1103[B]	2LB	OAC-CAM	8.28	1.37	1.21
3	B	1102[A]	2L3	OAC-CAM	8.35	1.37	1.21
3	B	1102[A]	2L3	OAB-CAL	8.78	1.37	1.22
5	B	1103[B]	2LB	OAB-CAL	8.82	1.37	1.22
3	A	1102	2L3	OAB-CAL	8.89	1.37	1.22

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	P5F	N3A-C2A-N1A	-11.03	120.45	128.89
2	B	1101	P5F	N3A-C2A-N1A	-10.16	121.11	128.89
2	B	1101	P5F	C4X-N5-C5X	-5.71	114.24	121.64
2	A	1101	P5F	C4X-N5-C5X	-4.77	115.45	121.64
2	B	1101	P5F	C4X-C4-N3	-3.56	118.72	123.59
2	A	1101	P5F	C4X-C4-N3	-3.27	119.11	123.59
2	A	1101	P5F	PA-O3P-P	-3.22	123.70	132.73
3	A	1102	2L3	OAD-SAQ-OAE	-3.19	103.82	115.58
2	A	1101	P5F	C1B-N9A-C4A	-3.17	122.15	126.94
2	B	1101	P5F	O5B-PA-O2A	-2.98	98.05	109.62
2	B	1101	P5F	C4X-C10-N10	-2.92	118.80	120.52
2	B	1101	P5F	C21-C22-N5	-2.66	115.74	125.20
3	A	1102	2L3	OAF-SAQ-OAE	-2.61	102.97	113.86
2	A	1101	P5F	O5B-PA-O2A	-2.58	99.60	109.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1101	P5F	O3P-P-O5'	-2.54	96.19	102.94
5	B	1103[B]	2LB	OAF-SAQ-OAE	-2.53	106.27	115.58
2	A	1101	P5F	O5'-P-O2P	-2.52	99.85	109.62
5	B	1103[B]	2LB	OAD-SAQ-OAE	-2.51	103.40	113.86
3	B	1102[A]	2L3	OAD-SAQ-OAE	-2.49	106.42	115.58
3	B	1102[A]	2L3	OAF-SAQ-OAD	-2.39	103.88	113.86
3	B	1102[A]	2L3	OAF-SAQ-OAE	-2.38	103.95	113.86
2	B	1101	P5F	O5'-P-O2P	-2.29	100.72	109.62
5	B	1103[B]	2LB	OAC-CAM-CAO	-2.21	118.84	122.29
2	B	1101	P5F	C1B-N9A-C4A	-2.15	123.70	126.94
2	B	1101	P5F	O3'-C3'-C4'	-2.14	103.35	108.75
5	B	1103[B]	2LB	OAB-CAL-CAN	-2.10	119.14	121.66
2	B	1101	P5F	C4A-C5A-N7A	-2.09	107.55	109.48
5	B	1103[B]	2LB	OAD-SAQ-OAF	-2.06	105.27	113.86
3	A	1102	2L3	CAK-CAL-CAN	2.05	119.85	116.65
2	B	1101	P5F	O1P-P-O5'	2.09	119.00	108.46
2	A	1101	P5F	C6-C5X-C9A	2.46	121.55	119.06
3	B	1102[A]	2L3	CAK-CAL-CAN	2.77	120.97	116.65
2	A	1101	P5F	O1P-P-O3P	3.07	119.00	105.09
5	B	1103[B]	2LB	CAK-CAL-CAN	3.10	121.48	116.65
2	A	1101	P5F	O1A-PA-O3P	3.19	119.55	105.09
2	B	1101	P5F	O1P-P-O3P	3.52	121.08	105.09
2	B	1101	P5F	C1'-N10-C9A	3.83	123.16	118.86
2	A	1101	P5F	C1'-N10-C9A	4.17	123.54	118.86
2	A	1101	P5F	C4-N3-C2	5.83	120.28	115.25
2	B	1101	P5F	C4-N3-C2	6.87	121.18	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	P5F	1	0
3	A	1102	2L3	1	0
2	B	1101	P5F	3	0
3	B	1102[A]	2L3	1	0
5	B	1103[B]	2LB	3	0

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, 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	973/1005 (96%)	0.13	47 (4%)	34 45	10, 19, 47, 64	0
1	B	979/1005 (97%)	-0.02	19 (1%)	70 78	9, 18, 37, 61	0
All	All	1952/2010 (97%)	0.05	66 (3%)	49 60	9, 19, 42, 64	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	103	VAL	5.9
1	A	85	PHE	5.8
1	A	392	VAL	5.4
1	A	102	ALA	5.2
1	A	389	ALA	4.9
1	A	86	MET	4.7
1	A	84	ALA	4.6
1	A	460	ALA	4.5
1	A	748	PRO	4.4
1	A	104	LEU	4.2
1	A	107	VAL	4.1
1	B	463	ALA	4.1
1	A	82	MET	4.0
1	B	103	VAL	4.0
1	A	473	GLY	3.9
1	B	471	GLY	3.7
1	A	178	TRP	3.7
1	B	462	ALA	3.7
1	A	462	ALA	3.6
1	A	441	ALA	3.4
1	B	80	GLN	3.4
1	A	19	GLY	3.3
1	A	463	ALA	3.3
1	B	104	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	83	PRO	3.2
1	B	81	ASP	3.2
1	A	471	GLY	3.2
1	B	459	ALA	3.1
1	A	388	MET	3.0
1	B	84	ALA	3.0
1	A	865	ALA	3.0
1	A	472	LEU	3.0
1	A	18	PHE	3.0
1	A	41	TRP	3.0
1	A	81	ASP	3.0
1	A	80	GLN	2.8
1	B	473	GLY	2.7
1	A	993[A]	PHE	2.7
1	A	176	GLY	2.7
1	A	469	ARG	2.7
1	B	6	LEU	2.7
1	B	472	LEU	2.6
1	B	469	ARG	2.5
1	B	460	ALA	2.5
1	A	396	ILE	2.5
1	A	459	ALA	2.4
1	A	44	GLN	2.4
1	B	78	ASN	2.3
1	A	443	ILE	2.3
1	A	186	GLY	2.3
1	A	391	PRO	2.3
1	A	34	TRP	2.3
1	A	399	VAL	2.3
1	A	461	ARG	2.3
1	A	184	LYS	2.3
1	B	102	ALA	2.3
1	A	26	PRO	2.2
1	A	437	PHE	2.2
1	B	8	THR	2.2
1	A	27	SER	2.2
1	A	188	PRO	2.2
1	A	45	ASN	2.1
1	B	470	LYS	2.1
1	A	444	GLU	2.1
1	A	183	GLY	2.1
1	B	474	GLY	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
4	EDO	A	1107	4/4	0.95	0.22	8.08	19,35,43,47	0
4	EDO	B	1106	4/4	0.95	0.19	4.07	18,28,29,30	0
3	2L3	B	1102[A]	17/17	0.90	0.18	3.03	26,28,33,36	17
5	2LB	B	1103[B]	17/17	0.91	0.17	2.67	23,27,33,37	17
3	2L3	A	1102	17/17	0.91	0.16	1.06	29,34,44,46	0
4	EDO	B	1105	4/4	0.95	0.10	0.63	20,21,22,29	0
2	P5F	B	1101	56/61	0.97	0.11	0.29	10,15,26,37	0
4	EDO	B	1104	4/4	0.98	0.09	-0.35	20,26,27,28	0
2	P5F	A	1101	56/61	0.96	0.11	-0.35	8,15,27,30	0
4	EDO	A	1106	4/4	0.98	0.09	-0.37	14,21,25,29	0
4	EDO	A	1105	4/4	0.95	0.10	-0.37	19,19,20,23	0
4	EDO	A	1104	4/4	0.94	0.11	-0.86	31,32,32,33	0
4	EDO	A	1103	4/4	0.97	0.09	-0.89	15,21,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.