



wwPDB X-ray Structure Validation Summary Report ⓘ

May 27, 2018 – 07:39 AM EDT

PDB ID : 6C1K
Title : HypoPP mutant with ligand1
Authors : Catterall, W.A.; Zheng, N.; Jiang, D.; Gamal El-Din, T.M.
Deposited on : 2018-01-04
Resolution : 2.70 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : rb-20031172
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20031172

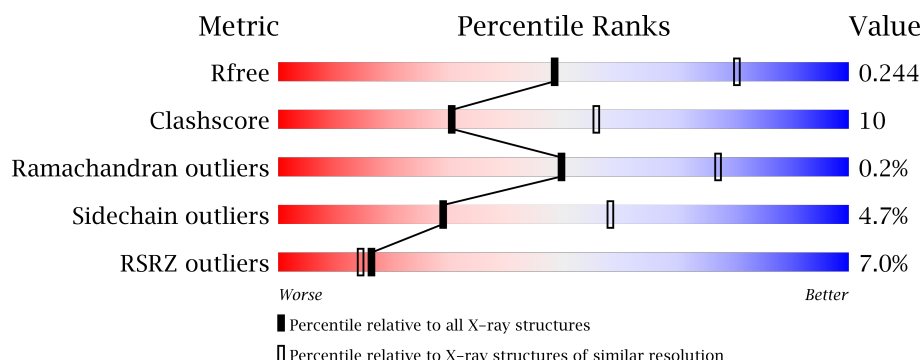
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	111664	2449 (2.70-2.70)
Clashscore	122126	2756 (2.70-2.70)
Ramachandran outliers	120053	2716 (2.70-2.70)
Sidechain outliers	120020	2716 (2.70-2.70)
RSRZ outliers	108989	2376 (2.70-2.70)

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	285	<div> <div>5%</div> <div>59%</div> <div>16%</div> <div>•</div> <div>22%</div> </div>
1	B	285	<div> <div>6%</div> <div>59%</div> <div>18%</div> <div>•</div> <div>22%</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
2	GAI	A	1301	-	X	-	-
3	PX4	A	1308	-	-	-	X
5	SO4	A	1313	-	-	X	-
5	SO4	B	2312	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4059 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 Ion transport protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	S	0	0	0
			1802	1228	267	294	13			
1	B	221	Total	C	N	O	S	0	0	0
			1803	1229	267	294	13			

There are 40 discrepancies between the modelled and reference sequences:

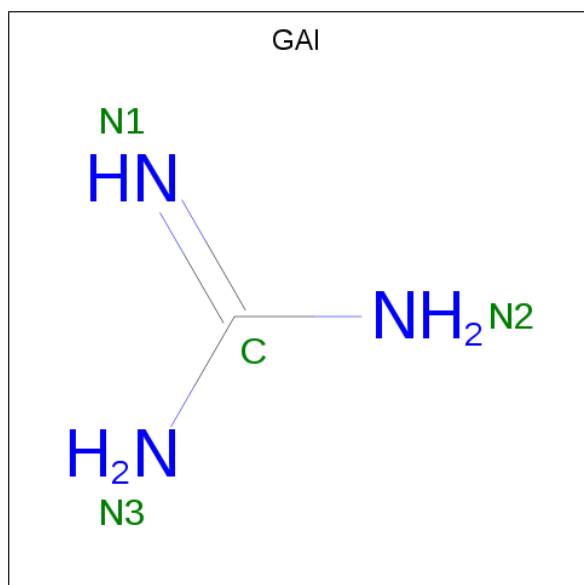
Chain	Residue	Modelled	Actual	Comment	Reference
A	983	MET	-	initiating methionine	UNP A8EVM5
A	984	ASP	-	expression tag	UNP A8EVM5
A	985	TYR	-	expression tag	UNP A8EVM5
A	986	LYS	-	expression tag	UNP A8EVM5
A	987	ASP	-	expression tag	UNP A8EVM5
A	988	ASP	-	expression tag	UNP A8EVM5
A	989	ASP	-	expression tag	UNP A8EVM5
A	990	ASP	-	expression tag	UNP A8EVM5
A	991	LYS	-	expression tag	UNP A8EVM5
A	992	GLY	-	expression tag	UNP A8EVM5
A	993	SER	-	expression tag	UNP A8EVM5
A	994	LEU	-	expression tag	UNP A8EVM5
A	995	VAL	-	expression tag	UNP A8EVM5
A	996	PRO	-	expression tag	UNP A8EVM5
A	997	ARG	-	expression tag	UNP A8EVM5
A	998	GLY	-	expression tag	UNP A8EVM5
A	999	SER	-	expression tag	UNP A8EVM5
A	1000	HIS	-	expression tag	UNP A8EVM5
A	1102	GLY	ARG	engineered mutation	UNP A8EVM5
A	1217	CYS	ILE	engineered mutation	UNP A8EVM5
B	1983	MET	-	initiating methionine	UNP A8EVM5
B	1984	ASP	-	expression tag	UNP A8EVM5
B	1985	TYR	-	expression tag	UNP A8EVM5
B	1986	LYS	-	expression tag	UNP A8EVM5
B	1987	ASP	-	expression tag	UNP A8EVM5

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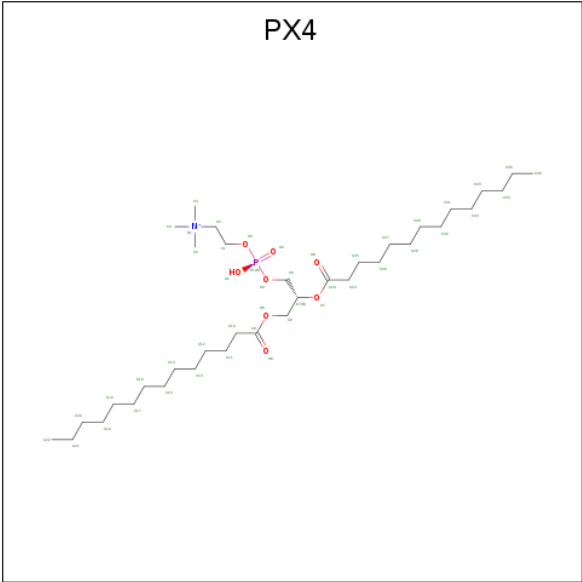
Chain	Residue	Modelled	Actual	Comment	Reference
B	1988	ASP	-	expression tag	UNP A8EVM5
B	1989	ASP	-	expression tag	UNP A8EVM5
B	1990	ASP	-	expression tag	UNP A8EVM5
B	1991	LYS	-	expression tag	UNP A8EVM5
B	1992	GLY	-	expression tag	UNP A8EVM5
B	1993	SER	-	expression tag	UNP A8EVM5
B	1994	LEU	-	expression tag	UNP A8EVM5
B	1995	VAL	-	expression tag	UNP A8EVM5
B	1996	PRO	-	expression tag	UNP A8EVM5
B	1997	ARG	-	expression tag	UNP A8EVM5
B	1998	GLY	-	expression tag	UNP A8EVM5
B	1999	SER	-	expression tag	UNP A8EVM5
B	2000	HIS	-	expression tag	UNP A8EVM5
B	2102	GLY	ARG	engineered mutation	UNP A8EVM5
B	2217	CYS	ILE	engineered mutation	UNP A8EVM5

- Molecule 2 is GUANIDINE (three-letter code: GAI) (formula: CH_5N_3).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	N	0	0
			4	1	3		
2	B	1	Total	C	N	0	0
			4	1	3		

- Molecule 3 is 1,2-DIMYRISTOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PX4) (formula: $\text{C}_{36}\text{H}_{73}\text{NO}_8\text{P}$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	O	P		0	0
			10	3	6	1			
3	A	1	Total	C	N	O	P	0	0
			46	36	1	8	1		
3	A	1	Total	C	O			0	0
			16	14	2				
3	A	1	Total	C	O	P		0	0
			23	16	6	1			
3	A	1	Total	C				0	0
			6	6					
3	A	1	Total	C	O	P		0	0
			41	32	8	1			
3	A	1	Total	C	O			0	0
			20	17	3				
3	A	1	Total	C	O			0	0
			17	15	2				
3	A	1	Total	C	O			0	0
			17	15	2				
3	B	1	Total	C	N	O	P	0	0
			37	27	1	8	1		
3	B	1	Total	C	N	O	P	0	0
			46	36	1	8	1		
3	B	1	Total	C	O			0	0
			16	14	2				
3	B	1	Total	C	O			0	0
			17	15	2				
3	B	1	Total	C	N	O	P	0	0
			38	28	1	8	1		

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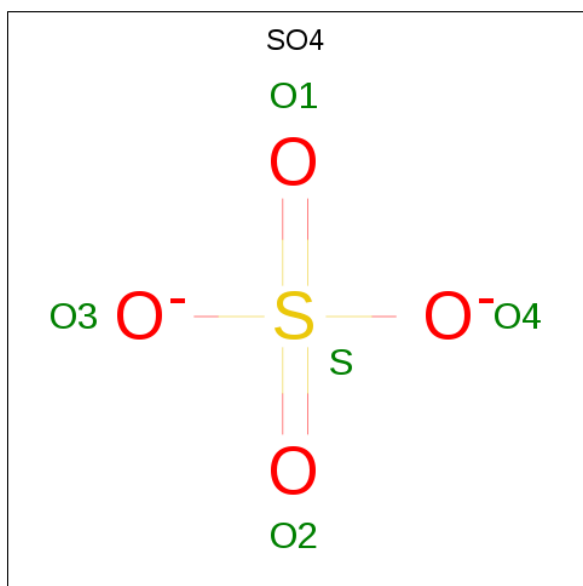
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	0	0
			46	36	1	8	1		
3	B	1	Total	C	O	P		0	0
			25	17	7	1			
3	B	1	Total	C				0	0
			6	6					

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Na	0	0
			2	2		
4	A	2	Total	Na	0	0
			2	2		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

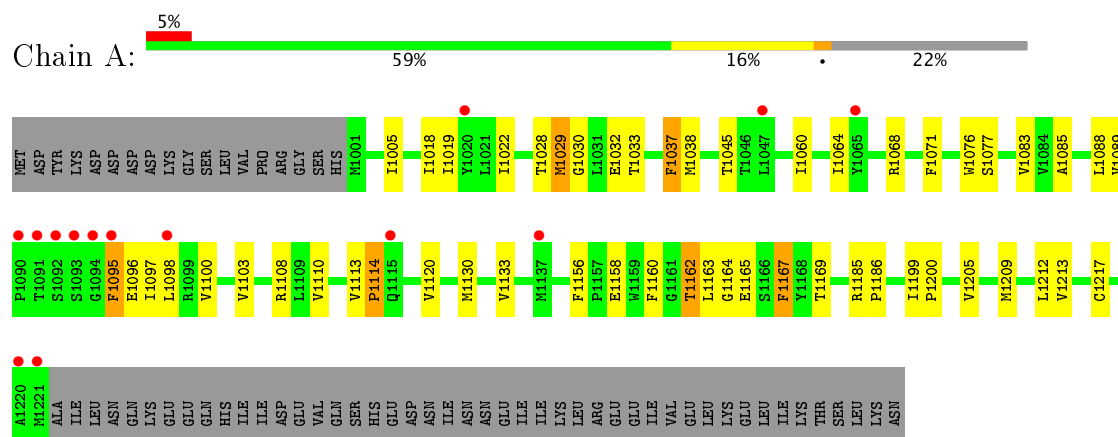
- Molecule 6 is water.

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

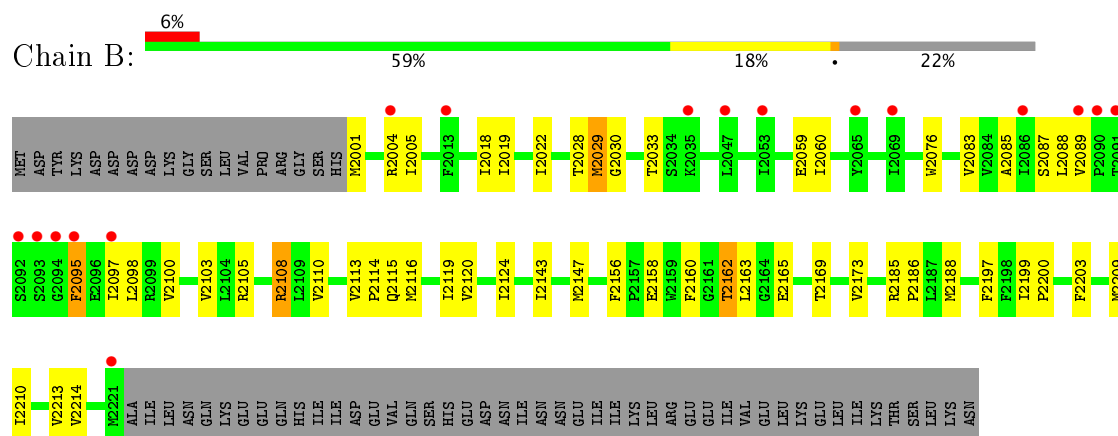
3 Residue-property plots [i](#)

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: Ion transport protein



- Molecule 1: Ion transport protein



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	126.39Å 126.23Å 191.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.31 – 2.70 42.31 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.0 (42.31-2.70) 97.0 (42.31-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.210 , 0.246 0.214 , 0.244	Depositor DCC
R_{free} test set	1981 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å ²)	68.6	Xtriage
Anisotropy	0.407	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 82.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.469 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4059	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.71% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, SO4, GAI, PX4

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	0.51	0/1852	0.58	1/2519 (0.0%)
1	B	0.50	0/1854	0.58	0/2522
All	All	0.50	0/3706	0.58	1/5041 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1037	PHE	CG-CD1-CE1	5.58	126.94	120.80

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	1802	0	1870	37	0
1	B	1803	0	1873	38	0
2	A	4	0	5	0	0
2	B	4	0	4	0	0
3	A	196	0	281	9	0
3	B	231	0	339	17	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	5	0	0	2	0
5	B	5	0	0	2	0
6	A	1	0	0	0	0
6	B	4	0	0	0	0
All	All	4059	0	4372	84	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.

The worst 5 of 84 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:1162:THR:HG22	1:A:1165:GLU:H	1.41	0.84
1:B:2162:THR:HG22	1:B:2165:GLU:H	1.43	0.83
1:B:2197:PHE:HB2	3:B:2307:PX4:H50	1.64	0.80
1:A:1085:ALA:HA	1:A:1088:LEU:HD12	1.74	0.70
3:A:1308:PX4:H45	3:B:2307:PX4:H40	1.75	0.69

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	219/285 (77%)	202 (92%)	16 (7%)	1 (0%)	31	58
1	B	219/285 (77%)	203 (93%)	16 (7%)	0	100	100
All	All	438/570 (77%)	405 (92%)	32 (7%)	1 (0%)	49	77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1114	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	202/263 (77%)	191 (95%)	11 (5%)	24	51
1	B	202/263 (77%)	194 (96%)	8 (4%)	34	64
All	All	404/526 (77%)	385 (95%)	19 (5%)	29	58

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1163	LEU
1	A	1205	VAL
1	B	2083	VAL
1	A	1162	THR
1	B	2095	PHE

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

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 carbohydrates in this entry.

5.6 Ligand geometry

Of 25 ligands modelled in this entry, 4 are monoatomic - leaving 21 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
2	GAI	A	1301	-	3,3,3	4.27	3 (100%)	3,3,3	1.10	0
3	PX4	A	1302	-	9,9,45	0.89	1 (11%)	11,12,53	0.63	0
3	PX4	A	1303	-	45,45,45	1.19	3 (6%)	51,53,53	1.09	2 (3%)
3	PX4	A	1304	-	12,15,45	0.78	0	11,15,53	0.69	0
3	PX4	A	1305	-	22,22,45	1.03	2 (9%)	25,26,53	1.43	2 (8%)
3	PX4	A	1306	-	5,5,45	0.74	0	4,4,53	0.48	0
3	PX4	A	1307	-	40,40,45	1.07	2 (5%)	43,45,53	1.18	3 (6%)
3	PX4	A	1308	-	19,19,45	1.23	1 (5%)	19,19,53	1.11	1 (5%)
3	PX4	A	1309	-	16,16,45	1.32	2 (12%)	16,16,53	0.91	1 (6%)
3	PX4	A	1310	-	16,16,45	1.16	1 (6%)	16,16,53	0.97	1 (6%)
5	SO4	A	1313	-	4,4,4	0.22	0	6,6,6	0.34	0
3	PX4	B	2301	-	36,36,45	1.31	5 (13%)	42,44,53	1.32	3 (7%)
3	PX4	B	2302	-	45,45,45	1.14	3 (6%)	51,53,53	1.04	2 (3%)
3	PX4	B	2303	-	12,15,45	0.74	0	11,15,53	0.79	0
3	PX4	B	2304	-	16,16,45	1.20	1 (6%)	16,16,53	0.87	1 (6%)
2	GAI	B	2305	-	3,3,3	2.97	2 (66%)	3,3,3	1.27	0
3	PX4	B	2306	-	37,37,45	1.22	3 (8%)	43,45,53	1.17	3 (6%)
3	PX4	B	2307	-	45,45,45	1.15	3 (6%)	51,53,53	1.44	7 (13%)
3	PX4	B	2308	-	24,24,45	1.10	1 (4%)	27,28,53	1.19	1 (3%)
3	PX4	B	2309	-	5,5,45	0.76	0	4,4,53	0.47	0
5	SO4	B	2312	-	4,4,4	0.17	0	6,6,6	0.25	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	GAI	A	1301	-	-	0/0/0/0	0/0/0/0
3	PX4	A	1302	-	-	0/8/8/49	0/0/0/0
3	PX4	A	1303	-	-	0/49/49/49	0/0/0/0
3	PX4	A	1304	-	-	0/11/13/49	0/0/0/0
3	PX4	A	1305	-	-	0/22/22/49	0/0/0/0
3	PX4	A	1306	-	-	0/3/3/49	0/0/0/0
3	PX4	A	1307	-	-	0/44/44/49	0/0/0/0
3	PX4	A	1308	-	-	0/18/18/49	0/0/0/0
3	PX4	A	1309	-	-	0/15/15/49	0/0/0/0
3	PX4	A	1310	-	-	0/15/15/49	0/0/0/0
5	SO4	A	1313	-	-	0/0/0/0	0/0/0/0
3	PX4	B	2301	-	-	0/40/40/49	0/0/0/0
3	PX4	B	2302	-	-	0/49/49/49	0/0/0/0
3	PX4	B	2303	-	-	0/11/13/49	0/0/0/0
3	PX4	B	2304	-	-	0/15/15/49	0/0/0/0
2	GAI	B	2305	-	-	0/0/0/0	0/0/0/0
3	PX4	B	2306	-	-	0/41/41/49	0/0/0/0
3	PX4	B	2307	-	-	0/49/49/49	0/0/0/0
3	PX4	B	2308	-	-	0/24/24/49	0/0/0/0
3	PX4	B	2309	-	-	0/3/3/49	0/0/0/0
5	SO4	B	2312	-	-	0/0/0/0	0/0/0/0

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1303	PX4	C4-N1	-2.96	1.41	1.50
3	B	2301	PX4	C4-N1	-2.81	1.41	1.50
3	B	2306	PX4	C4-N1	-2.80	1.42	1.50
3	B	2307	PX4	C4-N1	-2.71	1.42	1.50
3	B	2302	PX4	C4-N1	-2.63	1.42	1.50

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1305	PX4	C7-O7-C23	-3.78	113.11	117.90
3	B	2307	PX4	O8-C23-C24	-2.38	114.40	123.70
3	B	2307	PX4	C8-O5-C9	-2.36	110.08	117.13
3	B	2307	PX4	C8-C7-C6	-2.30	106.66	111.86
3	B	2301	PX4	C25-C24-C23	-2.11	105.99	113.60

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

12 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1303	PX4	1	0
3	A	1305	PX4	2	0
3	A	1307	PX4	3	0
3	A	1308	PX4	1	0
3	A	1309	PX4	1	0
3	A	1310	PX4	1	0
5	A	1313	SO4	2	0
3	B	2301	PX4	6	0
3	B	2302	PX4	2	0
3	B	2307	PX4	6	0
3	B	2308	PX4	3	0
5	B	2312	SO4	2	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	221/285 (77%)	0.54	14 (6%)	20 19	44, 94, 170, 214	0
1	B	221/285 (77%)	0.57	17 (7%)	13 11	40, 92, 171, 228	0
All	All	442/570 (77%)	0.55	31 (7%)	16 14	40, 93, 171, 228	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1095	PHE	10.1
1	A	1090	PRO	7.0
1	B	2090	PRO	6.4
1	A	1094	GLY	5.6
1	B	2091	THR	5.0

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, 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(\AA^2)	Q<0.9
5	SO4	B	2312	5/5	0.54	0.38	264,265,268,274	0
3	PX4	A	1305	23/46	0.73	0.38	69,122,246,246	0
3	PX4	B	2303	16/46	0.73	0.33	72,96,152,153	0
3	PX4	A	1308	20/46	0.74	0.45	84,103,140,141	0
3	PX4	A	1309	17/46	0.75	0.37	81,110,126,127	0
3	PX4	B	2308	25/46	0.78	0.33	71,104,261,262	0
3	PX4	A	1304	16/46	0.79	0.28	71,105,136,139	0
2	GAI	A	1301	4/4	0.80	0.15	106,108,109,111	0
4	NA	A	1312	1/1	0.81	0.32	88,88,88,88	0
4	NA	B	2311	1/1	0.82	0.24	86,86,86,86	0
3	PX4	B	2309	6/46	0.83	0.41	76,91,93,105	0
3	PX4	A	1302	10/46	0.86	0.21	123,135,168,171	0
3	PX4	A	1303	46/46	0.86	0.25	72,96,123,197	0
5	SO4	A	1313	5/5	0.87	0.24	155,155,156,162	0
3	PX4	A	1310	17/46	0.87	0.27	59,89,127,133	0
4	NA	B	2310	1/1	0.88	0.24	76,76,76,76	0
3	PX4	A	1306	6/46	0.88	0.13	79,88,96,109	0
4	NA	A	1311	1/1	0.88	0.28	82,82,82,82	0
3	PX4	B	2307	46/46	0.88	0.45	79,104,138,148	0
3	PX4	B	2302	46/46	0.89	0.34	52,100,143,162	0
3	PX4	B	2304	17/46	0.91	0.27	48,91,106,113	0
2	GAI	B	2305	4/4	0.92	0.10	104,112,114,121	0
3	PX4	B	2306	38/46	0.94	0.28	49,90,114,116	0
3	PX4	B	2301	37/46	0.95	0.22	62,90,120,134	0
3	PX4	A	1307	41/46	0.95	0.30	65,97,126,139	0

6.5 Other polymers ⓘ

There are no such residues in this entry.