



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 10, 2022 – 03:49 PM EST

PDB ID : 4GKA
Title : Crystal structure of purine nucleoside phosphorylase (W16Y, W94Y, W178Y, H257W) mutant from human complexed with phosphate
Authors : Haapalainen, A.M.; Ho, M.C.; Suarez, J.J.; Almo, S.C.; Schramm, V.L.
Deposited on : 2012-08-10
Resolution : 2.20 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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 : 2.31.2
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) : 2.31.2

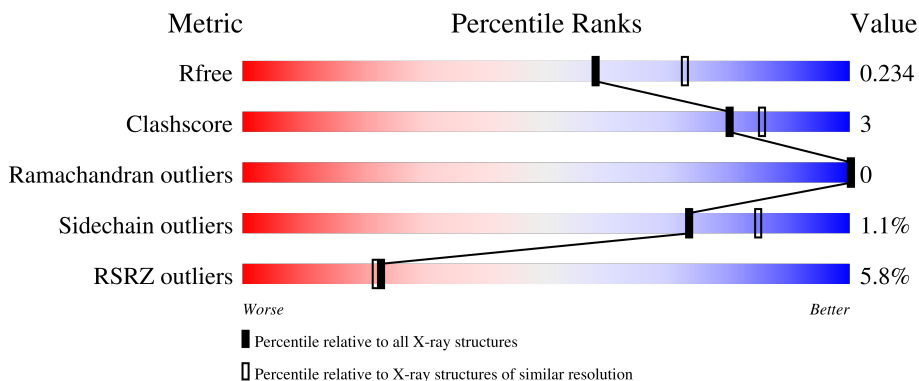
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 of 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	324	 2% 78% 6% 16%
1	B	324	 8% 78% 5% 17%
1	C	324	 4% 77% 5% 18%
1	D	324	 4% 79% 17%
1	E	324	 8% 77% 6% 18%

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Mol	Chain	Length	Quality of chain
1	F	324	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into four segments: a small red segment at the beginning labeled '3%', a large green segment labeled '76%', a small yellow segment labeled '6%', and a grey segment at the end labeled '18%'.</p>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 13091 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 Purine nucleoside phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	271	Total 2130	C 1355	N 371	O 388	S 16	0	2	0
1	B	269	Total 2121	C 1349	N 372	O 385	S 15	0	2	0
1	C	266	Total 2090	C 1332	N 365	O 378	S 15	0	2	0
1	D	268	Total 2105	C 1341	N 368	O 381	S 15	0	1	0
1	E	267	Total 2103	C 1339	N 370	O 379	S 15	0	2	0
1	F	267	Total 2096	C 1336	N 367	O 378	S 15	0	1	0

There are 240 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-34	MET	-	initiating methionine	UNP P00491
A	-33	ARG	-	expression tag	UNP P00491
A	-32	GLY	-	expression tag	UNP P00491
A	-31	SER	-	expression tag	UNP P00491
A	-30	HIS	-	expression tag	UNP P00491
A	-29	HIS	-	expression tag	UNP P00491
A	-28	HIS	-	expression tag	UNP P00491
A	-27	HIS	-	expression tag	UNP P00491
A	-26	HIS	-	expression tag	UNP P00491
A	-25	HIS	-	expression tag	UNP P00491
A	-24	GLY	-	expression tag	UNP P00491
A	-23	MET	-	expression tag	UNP P00491
A	-22	ALA	-	expression tag	UNP P00491
A	-21	SER	-	expression tag	UNP P00491
A	-20	MET	-	expression tag	UNP P00491
A	-19	THR	-	expression tag	UNP P00491
A	-18	GLY	-	expression tag	UNP P00491

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	GLY	-	expression tag	UNP P00491
A	-16	GLN	-	expression tag	UNP P00491
A	-15	GLN	-	expression tag	UNP P00491
A	-14	MET	-	expression tag	UNP P00491
A	-13	GLY	-	expression tag	UNP P00491
A	-12	ARG	-	expression tag	UNP P00491
A	-11	ASP	-	expression tag	UNP P00491
A	-10	LEU	-	expression tag	UNP P00491
A	-9	TYR	-	expression tag	UNP P00491
A	-8	ASP	-	expression tag	UNP P00491
A	-7	ASP	-	expression tag	UNP P00491
A	-6	ASP	-	expression tag	UNP P00491
A	-5	ASP	-	expression tag	UNP P00491
A	-4	LYS	-	expression tag	UNP P00491
A	-3	ASP	-	expression tag	UNP P00491
A	-2	PRO	-	expression tag	UNP P00491
A	-1	THR	-	expression tag	UNP P00491
A	0	LEU	-	expression tag	UNP P00491
A	16	TYR	TRP	engineered mutation	UNP P00491
A	51	SER	GLY	variant	UNP P00491
A	94	TYR	TRP	engineered mutation	UNP P00491
A	178	TYR	TRP	engineered mutation	UNP P00491
A	257	TRP	HIS	engineered mutation	UNP P00491
B	-34	MET	-	initiating methionine	UNP P00491
B	-33	ARG	-	expression tag	UNP P00491
B	-32	GLY	-	expression tag	UNP P00491
B	-31	SER	-	expression tag	UNP P00491
B	-30	HIS	-	expression tag	UNP P00491
B	-29	HIS	-	expression tag	UNP P00491
B	-28	HIS	-	expression tag	UNP P00491
B	-27	HIS	-	expression tag	UNP P00491
B	-26	HIS	-	expression tag	UNP P00491
B	-25	HIS	-	expression tag	UNP P00491
B	-24	GLY	-	expression tag	UNP P00491
B	-23	MET	-	expression tag	UNP P00491
B	-22	ALA	-	expression tag	UNP P00491
B	-21	SER	-	expression tag	UNP P00491
B	-20	MET	-	expression tag	UNP P00491
B	-19	THR	-	expression tag	UNP P00491
B	-18	GLY	-	expression tag	UNP P00491
B	-17	GLY	-	expression tag	UNP P00491
B	-16	GLN	-	expression tag	UNP P00491

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	GLN	-	expression tag	UNP P00491
B	-14	MET	-	expression tag	UNP P00491
B	-13	GLY	-	expression tag	UNP P00491
B	-12	ARG	-	expression tag	UNP P00491
B	-11	ASP	-	expression tag	UNP P00491
B	-10	LEU	-	expression tag	UNP P00491
B	-9	TYR	-	expression tag	UNP P00491
B	-8	ASP	-	expression tag	UNP P00491
B	-7	ASP	-	expression tag	UNP P00491
B	-6	ASP	-	expression tag	UNP P00491
B	-5	ASP	-	expression tag	UNP P00491
B	-4	LYS	-	expression tag	UNP P00491
B	-3	ASP	-	expression tag	UNP P00491
B	-2	PRO	-	expression tag	UNP P00491
B	-1	THR	-	expression tag	UNP P00491
B	0	LEU	-	expression tag	UNP P00491
B	16	TYR	TRP	engineered mutation	UNP P00491
B	51	SER	GLY	variant	UNP P00491
B	94	TYR	TRP	engineered mutation	UNP P00491
B	178	TYR	TRP	engineered mutation	UNP P00491
B	257	TRP	HIS	engineered mutation	UNP P00491
C	-34	MET	-	initiating methionine	UNP P00491
C	-33	ARG	-	expression tag	UNP P00491
C	-32	GLY	-	expression tag	UNP P00491
C	-31	SER	-	expression tag	UNP P00491
C	-30	HIS	-	expression tag	UNP P00491
C	-29	HIS	-	expression tag	UNP P00491
C	-28	HIS	-	expression tag	UNP P00491
C	-27	HIS	-	expression tag	UNP P00491
C	-26	HIS	-	expression tag	UNP P00491
C	-25	HIS	-	expression tag	UNP P00491
C	-24	GLY	-	expression tag	UNP P00491
C	-23	MET	-	expression tag	UNP P00491
C	-22	ALA	-	expression tag	UNP P00491
C	-21	SER	-	expression tag	UNP P00491
C	-20	MET	-	expression tag	UNP P00491
C	-19	THR	-	expression tag	UNP P00491
C	-18	GLY	-	expression tag	UNP P00491
C	-17	GLY	-	expression tag	UNP P00491
C	-16	GLN	-	expression tag	UNP P00491
C	-15	GLN	-	expression tag	UNP P00491
C	-14	MET	-	expression tag	UNP P00491

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-13	GLY	-	expression tag	UNP P00491
C	-12	ARG	-	expression tag	UNP P00491
C	-11	ASP	-	expression tag	UNP P00491
C	-10	LEU	-	expression tag	UNP P00491
C	-9	TYR	-	expression tag	UNP P00491
C	-8	ASP	-	expression tag	UNP P00491
C	-7	ASP	-	expression tag	UNP P00491
C	-6	ASP	-	expression tag	UNP P00491
C	-5	ASP	-	expression tag	UNP P00491
C	-4	LYS	-	expression tag	UNP P00491
C	-3	ASP	-	expression tag	UNP P00491
C	-2	PRO	-	expression tag	UNP P00491
C	-1	THR	-	expression tag	UNP P00491
C	0	LEU	-	expression tag	UNP P00491
C	16	TYR	TRP	engineered mutation	UNP P00491
C	51	SER	GLY	variant	UNP P00491
C	94	TYR	TRP	engineered mutation	UNP P00491
C	178	TYR	TRP	engineered mutation	UNP P00491
C	257	TRP	HIS	engineered mutation	UNP P00491
D	-34	MET	-	initiating methionine	UNP P00491
D	-33	ARG	-	expression tag	UNP P00491
D	-32	GLY	-	expression tag	UNP P00491
D	-31	SER	-	expression tag	UNP P00491
D	-30	HIS	-	expression tag	UNP P00491
D	-29	HIS	-	expression tag	UNP P00491
D	-28	HIS	-	expression tag	UNP P00491
D	-27	HIS	-	expression tag	UNP P00491
D	-26	HIS	-	expression tag	UNP P00491
D	-25	HIS	-	expression tag	UNP P00491
D	-24	GLY	-	expression tag	UNP P00491
D	-23	MET	-	expression tag	UNP P00491
D	-22	ALA	-	expression tag	UNP P00491
D	-21	SER	-	expression tag	UNP P00491
D	-20	MET	-	expression tag	UNP P00491
D	-19	THR	-	expression tag	UNP P00491
D	-18	GLY	-	expression tag	UNP P00491
D	-17	GLY	-	expression tag	UNP P00491
D	-16	GLN	-	expression tag	UNP P00491
D	-15	GLN	-	expression tag	UNP P00491
D	-14	MET	-	expression tag	UNP P00491
D	-13	GLY	-	expression tag	UNP P00491
D	-12	ARG	-	expression tag	UNP P00491

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-11	ASP	-	expression tag	UNP P00491
D	-10	LEU	-	expression tag	UNP P00491
D	-9	TYR	-	expression tag	UNP P00491
D	-8	ASP	-	expression tag	UNP P00491
D	-7	ASP	-	expression tag	UNP P00491
D	-6	ASP	-	expression tag	UNP P00491
D	-5	ASP	-	expression tag	UNP P00491
D	-4	LYS	-	expression tag	UNP P00491
D	-3	ASP	-	expression tag	UNP P00491
D	-2	PRO	-	expression tag	UNP P00491
D	-1	THR	-	expression tag	UNP P00491
D	0	LEU	-	expression tag	UNP P00491
D	16	TYR	TRP	engineered mutation	UNP P00491
D	51	SER	GLY	variant	UNP P00491
D	94	TYR	TRP	engineered mutation	UNP P00491
D	178	TYR	TRP	engineered mutation	UNP P00491
D	257	TRP	HIS	engineered mutation	UNP P00491
E	-34	MET	-	initiating methionine	UNP P00491
E	-33	ARG	-	expression tag	UNP P00491
E	-32	GLY	-	expression tag	UNP P00491
E	-31	SER	-	expression tag	UNP P00491
E	-30	HIS	-	expression tag	UNP P00491
E	-29	HIS	-	expression tag	UNP P00491
E	-28	HIS	-	expression tag	UNP P00491
E	-27	HIS	-	expression tag	UNP P00491
E	-26	HIS	-	expression tag	UNP P00491
E	-25	HIS	-	expression tag	UNP P00491
E	-24	GLY	-	expression tag	UNP P00491
E	-23	MET	-	expression tag	UNP P00491
E	-22	ALA	-	expression tag	UNP P00491
E	-21	SER	-	expression tag	UNP P00491
E	-20	MET	-	expression tag	UNP P00491
E	-19	THR	-	expression tag	UNP P00491
E	-18	GLY	-	expression tag	UNP P00491
E	-17	GLY	-	expression tag	UNP P00491
E	-16	GLN	-	expression tag	UNP P00491
E	-15	GLN	-	expression tag	UNP P00491
E	-14	MET	-	expression tag	UNP P00491
E	-13	GLY	-	expression tag	UNP P00491
E	-12	ARG	-	expression tag	UNP P00491
E	-11	ASP	-	expression tag	UNP P00491
E	-10	LEU	-	expression tag	UNP P00491

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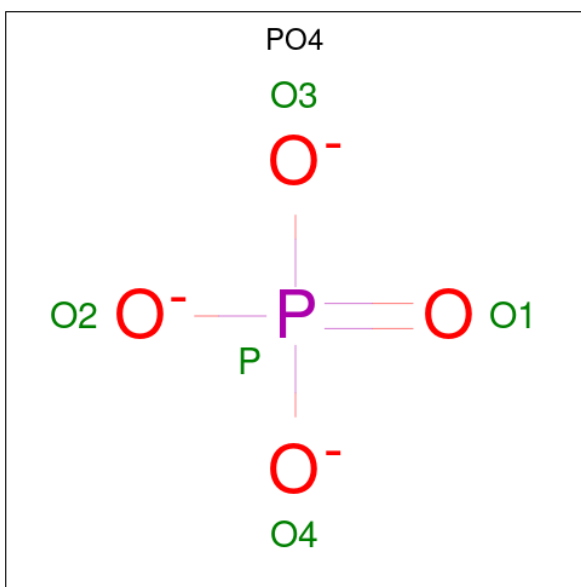
Chain	Residue	Modelled	Actual	Comment	Reference
E	-9	TYR	-	expression tag	UNP P00491
E	-8	ASP	-	expression tag	UNP P00491
E	-7	ASP	-	expression tag	UNP P00491
E	-6	ASP	-	expression tag	UNP P00491
E	-5	ASP	-	expression tag	UNP P00491
E	-4	LYS	-	expression tag	UNP P00491
E	-3	ASP	-	expression tag	UNP P00491
E	-2	PRO	-	expression tag	UNP P00491
E	-1	THR	-	expression tag	UNP P00491
E	0	LEU	-	expression tag	UNP P00491
E	16	TYR	TRP	engineered mutation	UNP P00491
E	51	SER	GLY	variant	UNP P00491
E	94	TYR	TRP	engineered mutation	UNP P00491
E	178	TYR	TRP	engineered mutation	UNP P00491
E	257	TRP	HIS	engineered mutation	UNP P00491
F	-34	MET	-	initiating methionine	UNP P00491
F	-33	ARG	-	expression tag	UNP P00491
F	-32	GLY	-	expression tag	UNP P00491
F	-31	SER	-	expression tag	UNP P00491
F	-30	HIS	-	expression tag	UNP P00491
F	-29	HIS	-	expression tag	UNP P00491
F	-28	HIS	-	expression tag	UNP P00491
F	-27	HIS	-	expression tag	UNP P00491
F	-26	HIS	-	expression tag	UNP P00491
F	-25	HIS	-	expression tag	UNP P00491
F	-24	GLY	-	expression tag	UNP P00491
F	-23	MET	-	expression tag	UNP P00491
F	-22	ALA	-	expression tag	UNP P00491
F	-21	SER	-	expression tag	UNP P00491
F	-20	MET	-	expression tag	UNP P00491
F	-19	THR	-	expression tag	UNP P00491
F	-18	GLY	-	expression tag	UNP P00491
F	-17	GLY	-	expression tag	UNP P00491
F	-16	GLN	-	expression tag	UNP P00491
F	-15	GLN	-	expression tag	UNP P00491
F	-14	MET	-	expression tag	UNP P00491
F	-13	GLY	-	expression tag	UNP P00491
F	-12	ARG	-	expression tag	UNP P00491
F	-11	ASP	-	expression tag	UNP P00491
F	-10	LEU	-	expression tag	UNP P00491
F	-9	TYR	-	expression tag	UNP P00491
F	-8	ASP	-	expression tag	UNP P00491

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-7	ASP	-	expression tag	UNP P00491
F	-6	ASP	-	expression tag	UNP P00491
F	-5	ASP	-	expression tag	UNP P00491
F	-4	LYS	-	expression tag	UNP P00491
F	-3	ASP	-	expression tag	UNP P00491
F	-2	PRO	-	expression tag	UNP P00491
F	-1	THR	-	expression tag	UNP P00491
F	0	LEU	-	expression tag	UNP P00491
F	16	TYR	TRP	engineered mutation	UNP P00491
F	51	SER	GLY	variant	UNP P00491
F	94	TYR	TRP	engineered mutation	UNP P00491
F	178	TYR	TRP	engineered mutation	UNP P00491
F	257	TRP	HIS	engineered mutation	UNP P00491

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



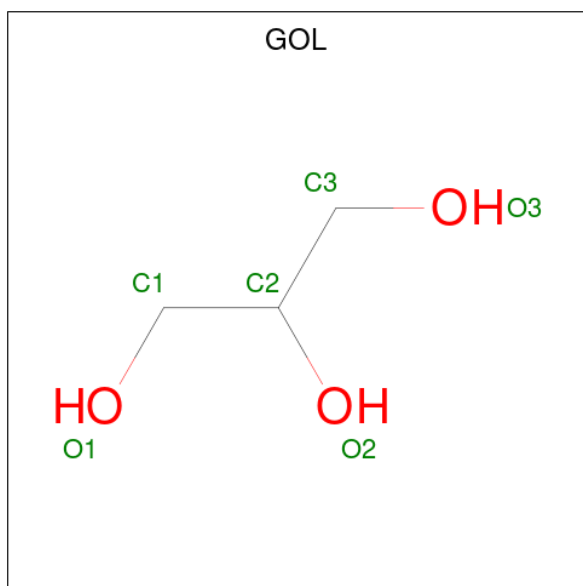
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
2	F	1	5	4	1	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	C	1	6	3	3	0	0
3	F	1	6	3	3	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	56	Total	O	0	0
			56	56		
4	B	45	Total	O	0	0
			45	45		
4	C	100	Total	O	0	0
			100	100		
4	D	46	Total	O	0	0
			46	46		
4	E	38	Total	O	0	0
			38	38		
4	F	119	Total	O	0	0
			119	119		

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.88Å 233.67Å 70.08Å 90.00° 97.33° 90.00°	Depositor
Resolution (Å)	45.29 – 2.20 45.25 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.6 (45.29-2.20) 99.6 (45.25-2.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.37 (at 2.20Å)	Xtrriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.188 , 0.232 0.192 , 0.234	Depositor DCC
R_{free} test set	4320 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	35.9	Xtrriage
Anisotropy	0.703	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 43.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13091	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.44% 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: PO4, GOL

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	0.49	1/2183 (0.0%)	0.66	1/2951 (0.0%)
1	B	0.42	0/2174	0.67	2/2938 (0.1%)
1	C	0.58	0/2143	0.75	3/2897 (0.1%)
1	D	0.47	1/2155 (0.0%)	0.65	1/2912 (0.0%)
1	E	0.42	0/2156	0.65	2/2914 (0.1%)
1	F	0.61	0/2146	0.78	2/2900 (0.1%)
All	All	0.50	2/12957 (0.0%)	0.70	11/17512 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	224	GLU	CD-OE2	-5.13	1.20	1.25
1	A	224	GLU	CD-OE1	-5.07	1.20	1.25

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	133	ARG	NE-CZ-NH2	-11.91	114.34	120.30
1	B	133	ARG	NE-CZ-NH2	-9.07	115.77	120.30
1	E	133	ARG	NE-CZ-NH2	-9.04	115.78	120.30
1	E	133	ARG	NE-CZ-NH1	8.65	124.62	120.30
1	C	133	ARG	NE-CZ-NH2	-8.51	116.04	120.30

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	2130	0	2115	13	0
1	B	2121	0	2107	10	0
1	C	2090	0	2081	12	0
1	D	2105	0	2095	6	0
1	E	2103	0	2095	16	0
1	F	2096	0	2089	14	0
2	A	5	0	0	0	0
2	B	5	0	0	1	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
3	C	6	0	8	0	0
3	F	6	0	8	2	0
4	A	56	0	0	0	0
4	B	45	0	0	0	0
4	C	100	0	0	0	0
4	D	46	0	0	1	0
4	E	38	0	0	0	0
4	F	119	0	0	1	0
All	All	13091	0	12598	67	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.

The worst 5 of 67 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:F:133:ARG:HG2	1:F:133:ARG:HH21	1.21	1.01
1:C:133:ARG:HG2	1:C:133:ARG:HH21	1.33	0.94
1:E:173[B]:ARG:HH21	1:E:173[B]:ARG:CG	1.82	0.93
1:F:133:ARG:HH21	1:F:133:ARG:CG	1.85	0.87
1:E:173[B]:ARG:HH21	1:E:173[B]:ARG:HG2	1.44	0.82

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	269/324 (83%)	268 (100%)	1 (0%)	0	100	100
1	B	267/324 (82%)	264 (99%)	3 (1%)	0	100	100
1	C	264/324 (82%)	258 (98%)	6 (2%)	0	100	100
1	D	265/324 (82%)	264 (100%)	1 (0%)	0	100	100
1	E	265/324 (82%)	258 (97%)	7 (3%)	0	100	100
1	F	264/324 (82%)	260 (98%)	4 (2%)	0	100	100
All	All	1594/1944 (82%)	1572 (99%)	22 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	229/269 (85%)	228 (100%)	1 (0%)	91	96
1	B	227/269 (84%)	224 (99%)	3 (1%)	69	81
1	C	224/269 (83%)	220 (98%)	4 (2%)	59	72
1	D	225/269 (84%)	224 (100%)	1 (0%)	91	96
1	E	225/269 (84%)	223 (99%)	2 (1%)	78	88
1	F	224/269 (83%)	220 (98%)	4 (2%)	59	72
All	All	1354/1614 (84%)	1339 (99%)	15 (1%)	73	85

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	180	GLN
1	F	84	ARG
1	D	56	PHE
1	F	133	ARG
1	F	56	PHE

Sometimes 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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 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	PO4	C	301	-	4,4,4	1.74	1 (25%)	6,6,6	1.37	1 (16%)
2	PO4	B	301	-	4,4,4	1.07	0	6,6,6	0.89	0
2	PO4	D	301	-	4,4,4	0.79	0	6,6,6	0.75	0
3	GOL	F	302	-	5,5,5	0.58	0	5,5,5	0.97	0
2	PO4	A	301	-	4,4,4	1.26	0	6,6,6	0.90	0
3	GOL	C	302	-	5,5,5	0.55	0	5,5,5	0.57	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PO4	F	301	-	4,4,4	1.54	0	6,6,6	0.55	0
2	PO4	E	301	-	4,4,4	0.95	0	6,6,6	0.84	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
3	GOL	C	302	-	-	0/4/4/4	-
3	GOL	F	302	-	-	0/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	PO4	P-O2	-2.01	1.48	1.54

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	301	PO4	O3-P-O1	-2.88	100.37	110.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	301	PO4	1	0
3	F	302	GOL	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	271/324 (83%)	0.13	7 (2%) 56 53	24, 47, 72, 113	0
1	B	269/324 (83%)	0.42	25 (9%) 8 7	29, 53, 87, 135	0
1	C	266/324 (82%)	-0.02	12 (4%) 33 32	21, 33, 76, 104	0
1	D	268/324 (82%)	0.24	14 (5%) 27 26	25, 51, 76, 100	0
1	E	267/324 (82%)	0.59	27 (10%) 7 6	31, 55, 83, 127	0
1	F	267/324 (82%)	-0.19	9 (3%) 45 43	20, 31, 60, 115	0
All	All	1608/1944 (82%)	0.20	94 (5%) 23 22	20, 44, 79, 135	0

The worst 5 of 94 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	180	GLN	10.1
1	E	64	HIS	8.1
1	E	62	PRO	7.0
1	E	65	ALA	6.9
1	B	60	THR	6.6

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 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, 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
3	GOL	F	302	6/6	0.79	0.24	33,44,47,47	0
3	GOL	C	302	6/6	0.91	0.13	43,52,54,56	0
2	PO4	B	301	5/5	0.97	0.13	46,47,50,53	0
2	PO4	D	301	5/5	0.97	0.14	33,34,37,38	0
2	PO4	A	301	5/5	0.98	0.14	30,31,33,34	0
2	PO4	E	301	5/5	0.98	0.12	45,46,51,51	0
2	PO4	C	301	5/5	0.99	0.15	35,35,37,39	0
2	PO4	F	301	5/5	0.99	0.14	35,36,40,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.