



Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 12:32 PM GMT

PDB ID : 4ECE
Title : Crystal structure of purine nucleoside phosphorylase (W16Y, W94Y, W178Y, H257W) mutant from human complexed with guanine
Authors : Haapalainen, A.M.; Ho, M.C.; Suarez, J.J.; Almo, S.C.; Schramm, V.L.
Deposited on : 2012-03-26
Resolution : 2.60 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

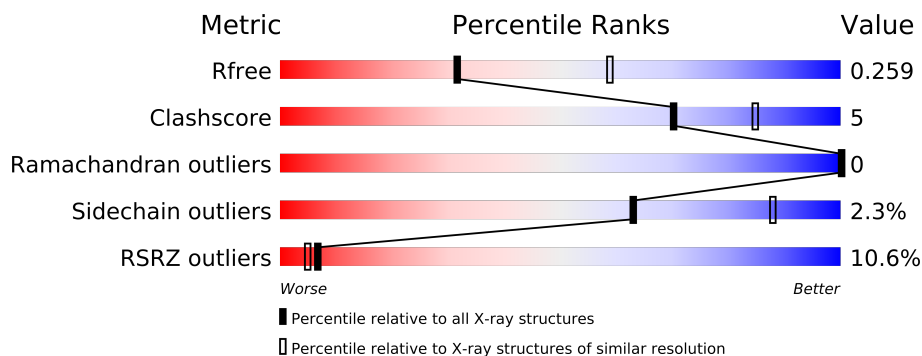
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.60 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}	66092	1718 (2.60-2.60)
Clashscore	79885	2154 (2.60-2.60)
Ramachandran outliers	78287	2113 (2.60-2.60)
Sidechain outliers	78261	2113 (2.60-2.60)
RSRZ outliers	66119	1718 (2.60-2.60)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	324	
1	B	324	
1	C	324	
1	D	324	
1	E	324	
1	F	324	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13632 atoms, of which 0 are hydrogen and 0 are deuterium.

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
1	A	282	Total	C	N	O	S	0	1	0
			2206	1405	382	403	16			
1	B	283	Total	C	N	O	S	0	1	0
			2216	1411	383	406	16			
1	C	283	Total	C	N	O	S	0	2	0
			2219	1413	383	406	17			
1	D	282	Total	C	N	O	S	0	2	0
			2214	1410	385	403	16			
1	E	282	Total	C	N	O	S	0	0	0
			2203	1403	382	403	15			
1	F	282	Total	C	N	O	S	0	0	0
			2203	1403	382	403	15			

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	ENGINEERED MUTATION	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	ENGINEERED MUTATION	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	ENGINEERED MUTATION	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	ENGINEERED MUTATION	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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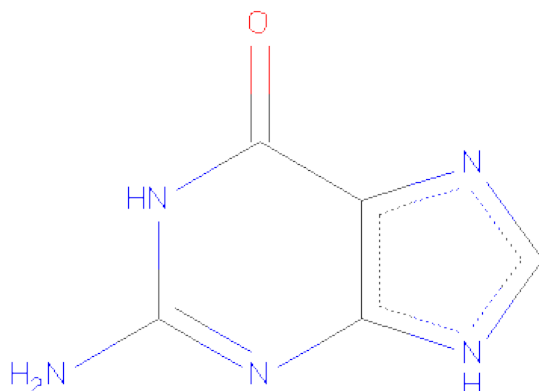
Chain	Residue	Modelled	Actual	Comment	Reference
E	-9	TYR	-	EXPRESSION TAG	UNP P00491
E	-8	ASP	-	EXPRESSION TAG	UNP P00491
E	-7	ASP	-	EXPRESSION TAG	UNP P00491
E	-6	ASP	-	EXPRESSION TAG	UNP P00491
E	-5	ASP	-	EXPRESSION TAG	UNP P00491
E	-4	LYS	-	EXPRESSION TAG	UNP P00491
E	-3	ASP	-	EXPRESSION TAG	UNP P00491
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	ENGINEERED MUTATION	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	ENGINEERED MUTATION	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 GUANINE (three-letter code: GUN) (formula: C₅H₅N₅O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			11	5	5	1		
2	B	1	Total	C	N	O	0	0
			11	5	5	1		
2	C	1	Total	C	N	O	0	0
			11	5	5	1		
2	D	1	Total	C	N	O	0	0
			11	5	5	1		
2	E	1	Total	C	N	O	0	0
			11	5	5	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	F	1	Total	C	N	O	0	0
			11	5	5	1		

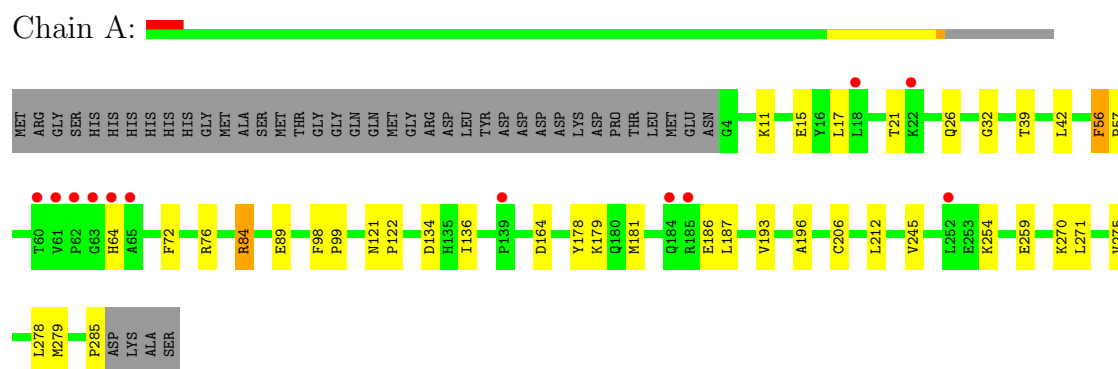
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	72	Total	O	0	0
			72	72		
3	B	80	Total	O	0	0
			80	80		
3	C	59	Total	O	0	0
			59	59		
3	D	40	Total	O	0	0
			40	40		
3	E	45	Total	O	0	0
			45	45		
3	F	9	Total	O	0	0
			9	9		

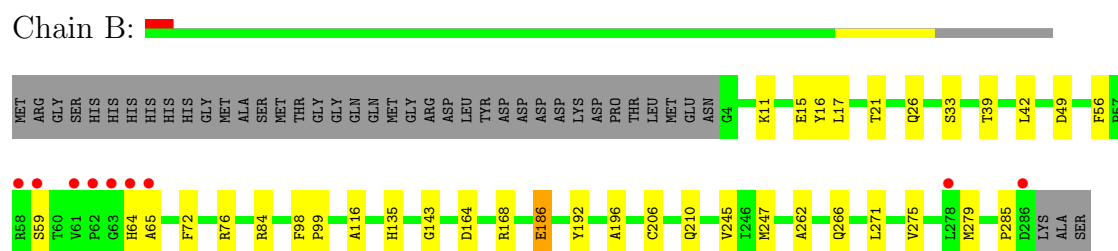
3 Residue-property plots

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.

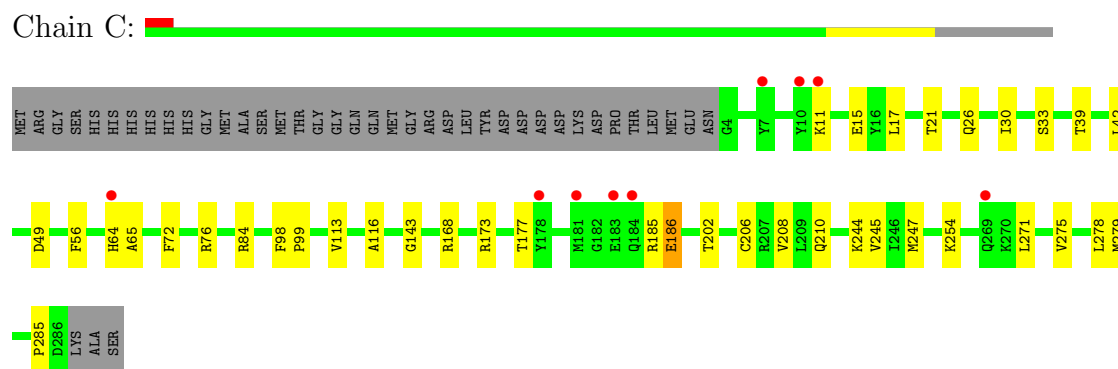
- Molecule 1: Purine nucleoside phosphorylase



- Molecule 1: Purine nucleoside phosphorylase

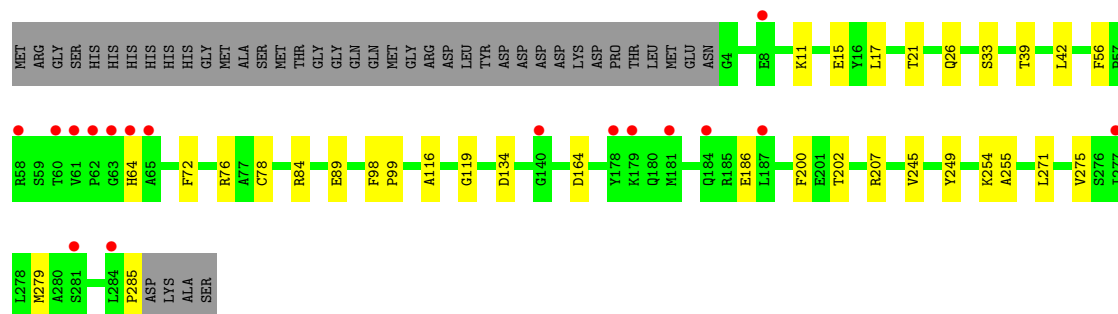


- Molecule 1: Purine nucleoside phosphorylase



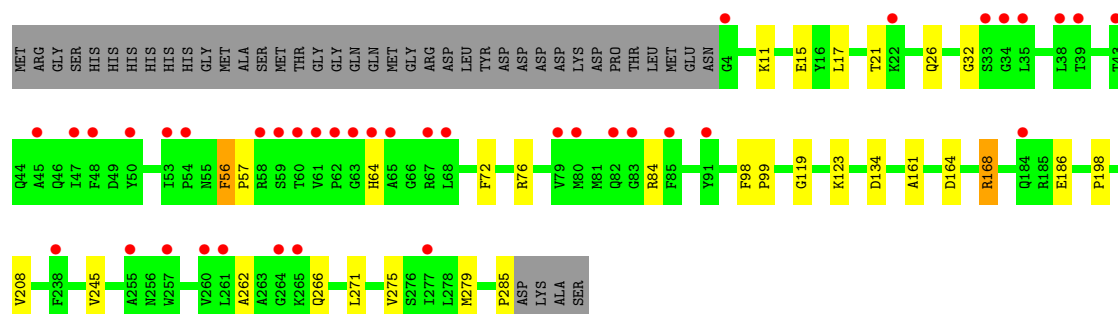
- Molecule 1: Purine nucleoside phosphorylase





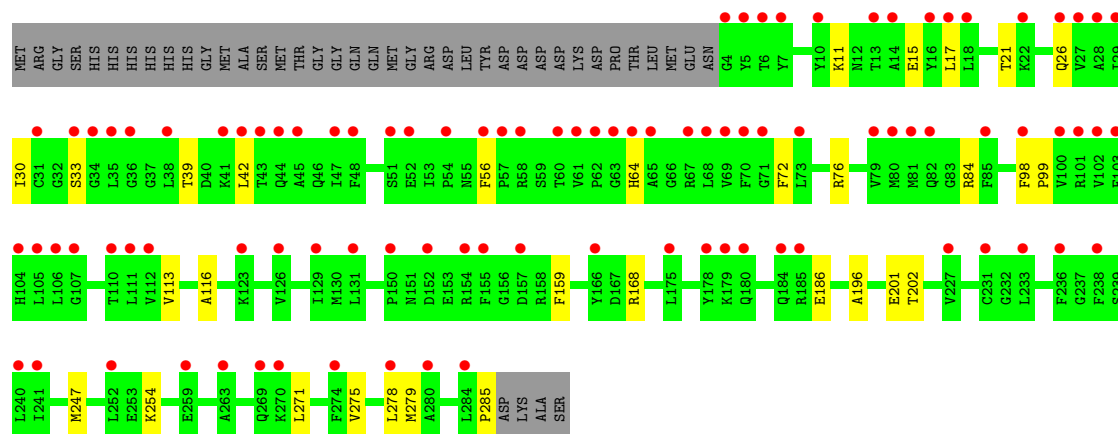
- Molecule 1: Purine nucleoside phosphorylase

Chain E:



- Molecule 1: Purine nucleoside phosphorylase

Chain F:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	77.55Å 129.68Å 104.35Å 90.00° 105.29° 90.00°	Depositor
Resolution (Å)	49.04 – 2.60 49.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.04-2.60) 99.9 (49.00-2.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.7.0025	Depositor
R, R_{free}	0.222 , 0.261 0.220 , 0.259	Depositor DCC
R_{free} test set	3106 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	60.0	Xtriage
Anisotropy	0.290	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 61129 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13632	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GUN

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	0.63	0/2259	0.76	0/3056
1	B	0.67	0/2269	0.72	0/3069
1	C	0.55	0/2275	0.65	0/3077
1	D	0.55	0/2270	0.67	0/3070
1	E	0.50	0/2253	0.62	0/3048
1	F	0.43	0/2253	0.61	0/3048
All	All	0.56	0/13579	0.67	0/18368

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2206	0	2189	26	0
1	B	2216	0	2197	27	1
1	C	2219	0	2202	26	0
1	D	2214	0	2202	21	1
1	E	2203	0	2184	22	0
1	F	2203	0	2184	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	11	0	5	0	0
2	B	11	0	5	0	0
2	C	11	0	5	0	0
2	D	11	0	5	0	0
2	E	11	0	5	0	0
2	F	11	0	5	2	0
3	A	72	0	0	2	0
3	B	80	0	0	4	0
3	C	59	0	0	3	0
3	D	40	0	0	0	0
3	E	45	0	0	5	0
3	F	9	0	0	1	0
All	All	13632	0	13188	123	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 5.

All (123) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:206[B]:CYS:SG	1:C:245:VAL:CG1	2.34	1.14
1:A:89:GLU:HG2	3:A:418:HOH:O	1.50	1.08
1:C:206[B]:CYS:SG	1:C:245:VAL:HG11	1.94	1.06
1:C:206[B]:CYS:SG	1:C:245:VAL:HG12	1.97	1.02
1:A:206[B]:CYS:SG	1:A:245:VAL:CG1	2.58	0.92
1:B:206:CYS:SG	1:B:245:VAL:CG1	2.61	0.89
1:F:201:GLU:OE2	2:F:301:GUN:N2	2.05	0.88
1:B:206:CYS:SG	1:B:245:VAL:HG11	2.17	0.85
1:A:259:GLU:HG3	3:A:459:HOH:O	1.77	0.84
1:A:206[B]:CYS:SG	1:A:245:VAL:HG11	2.19	0.83
1:A:206[B]:CYS:SG	1:A:245:VAL:HG12	2.18	0.83
1:B:49:ASP:HB3	3:B:475:HOH:O	1.83	0.79
1:E:198:PRO:O	1:F:159:PHE:HD1	1.68	0.77
1:B:206:CYS:SG	1:B:245:VAL:HG12	2.26	0.76
1:A:11:LYS:HE2	1:A:15:GLU:OE2	1.92	0.70
1:C:49:ASP:HB3	3:C:458:HOH:O	1.91	0.70
1:E:32:GLY:HA2	3:E:436:HOH:O	1.93	0.68
1:D:89:GLU:HG2	3:E:432:HOH:O	1.95	0.67
1:C:244:LYS:HE2	3:C:459:HOH:O	1.94	0.67
1:F:11:LYS:HE2	1:F:15:GLU:OE2	1.98	0.64
1:E:11:LYS:HE2	1:E:15:GLU:OE2	1.98	0.64
1:D:11:LYS:HE2	1:D:15:GLU:OE2	1.99	0.63
1:C:11:LYS:HE2	1:C:15:GLU:OE2	1.99	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:11:LYS:HE2	1:B:15:GLU:OE2	1.98	0.63
1:C:210:GLN:OE1	1:C:247[B]:MET:SD	2.57	0.63
1:F:201:GLU:CD	2:F:301:GUN:HN21	1.99	0.61
1:C:65:ALA:HB3	3:C:458:HOH:O	2.01	0.59
1:C:206[B]:CYS:HG	1:C:245:VAL:HG11	1.64	0.59
1:D:202:THR:HB	1:E:134:ASP:OD1	2.04	0.57
1:D:271:LEU:O	1:D:275:VAL:HG23	2.04	0.57
1:B:59:SER:HB2	3:B:449:HOH:O	2.03	0.57
1:D:164:ASP:OD2	1:F:254:LYS:NZ	2.33	0.56
1:C:271:LEU:O	1:C:275:VAL:HG23	2.07	0.55
1:D:254:LYS:NZ	1:E:164:ASP:OD2	2.36	0.55
1:D:254:LYS:HD2	1:E:164:ASP:OD2	2.08	0.54
1:F:271:LEU:O	1:F:275:VAL:HG23	2.08	0.53
1:B:98:PHE:HB3	1:B:99:PRO:HD3	1.88	0.53
1:E:168:ARG:HD3	3:E:411:HOH:O	2.09	0.53
1:A:76:ARG:HG2	1:A:279:MET:HE3	1.90	0.53
1:A:271:LEU:O	1:A:275:VAL:HG23	2.09	0.52
1:B:65:ALA:HB3	3:B:475:HOH:O	2.11	0.51
1:E:271:LEU:O	1:E:275:VAL:HG23	2.09	0.51
1:E:98:PHE:HB3	1:E:99:PRO:HD3	1.94	0.50
1:B:271:LEU:O	1:B:275:VAL:HG23	2.12	0.50
1:D:134:ASP:OD1	1:F:202:THR:HB	2.13	0.49
1:B:206:CYS:HB3	1:B:247:MET:SD	2.53	0.48
1:A:98:PHE:HB3	1:A:99:PRO:HD3	1.95	0.48
1:B:76:ARG:HG2	1:B:279:MET:HE3	1.94	0.48
1:D:72:PHE:HA	1:D:76:ARG:O	2.14	0.48
1:B:210:GLN:OE1	1:B:247:MET:SD	2.72	0.48
1:C:76:ARG:HG2	1:C:279:MET:HE3	1.96	0.48
1:C:17:LEU:O	1:C:21:THR:HG22	2.13	0.48
1:C:72:PHE:HA	1:C:76:ARG:O	2.14	0.48
1:D:42:LEU:HD21	1:D:78[B]:CYS:SG	2.54	0.48
1:C:98:PHE:HB3	1:C:99:PRO:HD3	1.96	0.47
1:F:196:ALA:O	3:F:408:HOH:O	2.20	0.47
1:B:76:ARG:HB3	1:B:279:MET:HE2	1.97	0.47
1:F:76:ARG:HG2	1:F:279:MET:HE3	1.97	0.47
1:F:17:LEU:O	1:F:21:THR:HG22	2.16	0.46
1:A:134:ASP:OD1	1:C:202:THR:HB	2.16	0.46
1:E:119:GLY:O	1:E:245:VAL:HG23	2.16	0.46
1:A:32:GLY:HA2	1:A:84:ARG:HH21	1.80	0.45
1:A:17:LEU:O	1:A:21:THR:HG22	2.15	0.45
1:B:26:GLN:HG3	1:B:285:PRO:HG3	1.98	0.45
1:D:249:TYR:O	1:E:168:ARG:NH2	2.49	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:212:LEU:HB3	1:C:208:VAL:HG22	1.99	0.45
1:A:196:ALA:CB	1:B:143:GLY:HA2	2.47	0.45
1:E:76:ARG:HG2	1:E:279:MET:HE3	1.99	0.45
1:A:164:ASP:OD2	1:C:254:LYS:NZ	2.41	0.45
1:E:17:LEU:O	1:E:21:THR:HG22	2.16	0.44
1:A:72:PHE:HA	1:A:76:ARG:O	2.17	0.44
1:D:76:ARG:HB3	1:D:279:MET:HE2	1.99	0.44
1:D:33:SER:HB2	1:D:116:ALA:HB2	1.99	0.44
1:F:72:PHE:HA	1:F:76:ARG:O	2.18	0.44
1:D:119:GLY:O	1:D:245:VAL:HG23	2.17	0.44
1:F:98:PHE:HB3	1:F:99:PRO:HD3	1.99	0.43
1:B:72:PHE:HA	1:B:76:ARG:O	2.18	0.43
1:C:185:ARG:HE	1:C:185:ARG:HB3	1.69	0.43
1:A:179:LYS:HD3	1:A:179:LYS:HA	1.86	0.43
1:E:123:LYS:NZ	3:E:422:HOH:O	2.51	0.43
1:C:186:GLU:HG3	1:C:186:GLU:H	1.68	0.43
1:E:72:PHE:HA	1:E:76:ARG:O	2.19	0.43
1:F:26:GLN:HG3	1:F:285:PRO:HG3	2.00	0.43
1:D:200:PHE:HB2	1:E:161:ALA:HA	2.01	0.43
1:B:17:LEU:O	1:B:21:THR:HG22	2.18	0.43
1:D:17:LEU:O	1:D:21:THR:HG22	2.19	0.42
1:A:56:PHE:HA	1:A:57:PRO:HD3	1.92	0.42
1:E:56:PHE:HA	1:E:57:PRO:HD3	1.95	0.42
1:A:254:LYS:NZ	1:B:164:ASP:OD2	2.42	0.42
1:B:59:SER:CB	3:B:449:HOH:O	2.64	0.42
1:E:26:GLN:HG3	1:E:285:PRO:HG3	2.00	0.42
1:A:121:ASN:HA	1:A:122:PRO:HD3	1.83	0.42
1:D:39:THR:O	1:D:42:LEU:HB2	2.19	0.42
1:A:136:ILE:HB	1:A:193:VAL:HG23	2.02	0.41
1:B:186:GLU:H	1:B:186:GLU:HG3	1.71	0.41
1:B:262:ALA:O	1:B:266:GLN:HG2	2.20	0.41
1:D:255:ALA:O	1:E:161:ALA:HB2	2.20	0.41
1:B:135:HIS:HA	1:B:192:TYR:O	2.20	0.41
1:B:76:ARG:HA	1:B:76:ARG:HD2	1.77	0.41
1:C:76:ARG:HD2	1:C:76:ARG:HA	1.81	0.41
1:B:39:THR:O	1:B:42:LEU:HB2	2.21	0.41
1:D:26:GLN:HG3	1:D:285:PRO:HG3	2.02	0.41
1:E:208:VAL:HG23	3:E:433:HOH:O	2.20	0.41
1:C:173:ARG:O	1:C:177:THR:HG23	2.21	0.41
1:A:76:ARG:HD2	1:A:76:ARG:HA	1.77	0.41
1:A:26:GLN:HG3	1:A:285:PRO:HG3	2.03	0.41
1:C:26:GLN:HG3	1:C:285:PRO:HG3	2.01	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:33:SER:HB2	1:C:116:ALA:HB2	2.03	0.41
1:C:39:THR:O	1:C:42:LEU:HB2	2.21	0.41
1:B:196:ALA:CB	1:C:143:GLY:HA2	2.51	0.41
1:F:33:SER:HB2	1:F:116:ALA:HB2	2.03	0.41
1:E:262:ALA:O	1:E:266:GLN:HG2	2.21	0.40
1:A:178:TYR:CE1	1:A:187:LEU:HD13	2.56	0.40
1:A:39:THR:O	1:A:42:LEU:HB2	2.22	0.40
1:F:39:THR:O	1:F:42:LEU:HB2	2.21	0.40
1:A:181:MET:HE1	1:A:270:LYS:HG3	2.03	0.40
1:D:76:ARG:HA	1:D:76:ARG:HD2	1.81	0.40
1:E:76:ARG:HB3	1:E:279:MET:HE2	2.03	0.40
1:B:33:SER:HB2	1:B:116:ALA:HB2	2.02	0.40
1:B:16:TYR:CD2	1:B:16:TYR:C	2.94	0.40
1:F:30:ILE:HD12	1:F:113:VAL:HG12	2.02	0.40
1:C:30:ILE:HD12	1:C:113:VAL:HG12	2.03	0.40
1:D:98:PHE:HB3	1:D:99:PRO:HD3	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:186:GLU:OE2	1:D:207[B]:ARG:NE[2_545]	2.05	0.15

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	281/324 (87%)	272 (97%)	9 (3%)	0	100	100
1	B	282/324 (87%)	277 (98%)	5 (2%)	0	100	100
1	C	283/324 (87%)	277 (98%)	6 (2%)	0	100	100
1	D	282/324 (87%)	277 (98%)	5 (2%)	0	100	100
1	E	280/324 (86%)	275 (98%)	5 (2%)	0	100	100
1	F	280/324 (86%)	274 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1688/1944 (87%)	1652 (98%)	36 (2%)	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	235/269 (87%)	230 (98%)	5 (2%)	66	90
1	B	236/269 (88%)	231 (98%)	5 (2%)	66	90
1	C	237/269 (88%)	231 (98%)	6 (2%)	60	86
1	D	236/269 (88%)	232 (98%)	4 (2%)	73	92
1	E	234/269 (87%)	229 (98%)	5 (2%)	66	90
1	F	234/269 (87%)	227 (97%)	7 (3%)	53	82
All	All	1412/1614 (88%)	1380 (98%)	32 (2%)	63	88

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	PHE
1	A	64	HIS
1	A	84	ARG
1	A	186	GLU
1	A	278	LEU
1	B	56	PHE
1	B	64	HIS
1	B	84	ARG
1	B	168	ARG
1	B	186	GLU
1	C	56	PHE
1	C	64	HIS
1	C	84	ARG
1	C	168	ARG
1	C	186	GLU
1	C	278	LEU

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Mol	Chain	Res	Type
1	D	56	PHE
1	D	64	HIS
1	D	84	ARG
1	D	186	GLU
1	E	56	PHE
1	E	64	HIS
1	E	84	ARG
1	E	168	ARG
1	E	186	GLU
1	F	56	PHE
1	F	64	HIS
1	F	84	ARG
1	F	168	ARG
1	F	186	GLU
1	F	247	MET
1	F	278	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	188	GLN
1	B	243	ASN
1	C	243	ASN
1	D	243	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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

6 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	GUN	A	301	-	12,12,12	2.09	4 (33%)	14,17,17	4.38	5 (35%)
2	GUN	B	301	-	12,12,12	1.95	3 (25%)	14,17,17	5.14	6 (42%)
2	GUN	C	301	-	12,12,12	2.15	3 (25%)	14,17,17	4.75	4 (28%)
2	GUN	D	301	-	12,12,12	1.94	3 (25%)	14,17,17	6.52	5 (35%)
2	GUN	E	301	-	12,12,12	2.38	4 (33%)	14,17,17	6.36	6 (42%)
2	GUN	F	301	-	12,12,12	2.23	5 (41%)	14,17,17	5.03	5 (35%)

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	GUN	A	301	-	-	0/0/0/0	0/0/2/2
2	GUN	B	301	-	-	0/0/0/0	0/0/2/2
2	GUN	C	301	-	-	0/0/0/0	0/0/2/2
2	GUN	D	301	-	-	0/0/0/0	0/0/2/2
2	GUN	E	301	-	-	0/0/0/0	0/0/2/2
2	GUN	F	301	-	-	0/0/0/0	0/0/2/2

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	301	GUN	C6-C5	5.17	1.49	1.41
2	F	301	GUN	C6-C5	4.64	1.48	1.41
2	D	301	GUN	C6-C5	4.38	1.48	1.41
2	B	301	GUN	C6-C5	4.06	1.47	1.41
2	E	301	GUN	C5-C4	4.00	1.49	1.40
2	B	301	GUN	C2-N3	3.89	1.38	1.33
2	C	301	GUN	C2-N3	3.69	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	GUN	C6-C5	3.60	1.47	1.41
2	A	301	GUN	C6-C5	3.59	1.47	1.41
2	A	301	GUN	C5-C4	3.39	1.48	1.40
2	A	301	GUN	C2-N3	3.28	1.37	1.33
2	F	301	GUN	C5-C4	3.17	1.47	1.40
2	F	301	GUN	C2-N2	3.09	1.37	1.32
2	C	301	GUN	C5-C4	2.97	1.47	1.40
2	E	301	GUN	C2-N3	2.80	1.37	1.33
2	E	301	GUN	C4-N3	2.73	1.37	1.34
2	F	301	GUN	C2-N3	2.65	1.36	1.33
2	D	301	GUN	C5-C4	2.61	1.46	1.40
2	D	301	GUN	C2-N2	2.53	1.36	1.32
2	A	301	GUN	C8-N9	2.52	1.38	1.34
2	B	301	GUN	C2-N2	2.36	1.36	1.32
2	F	301	GUN	C4-N3	2.33	1.37	1.34

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	301	GUN	C6-C5-N7	18.80	136.67	134.14
2	E	301	GUN	C6-C5-N7	18.55	136.64	134.14
2	B	301	GUN	N9-C4-N3	13.73	135.78	124.37
2	C	301	GUN	N9-C4-N3	13.32	135.44	124.37
2	A	301	GUN	N9-C4-N3	13.29	135.41	124.37
2	D	301	GUN	N9-C4-N3	13.00	135.18	124.37
2	E	301	GUN	N9-C4-N3	11.88	134.25	124.37
2	F	301	GUN	C6-C5-N7	11.82	135.73	134.14
2	F	301	GUN	N9-C4-N3	11.81	134.19	124.37
2	B	301	GUN	C6-C5-N7	10.12	135.50	134.14
2	C	301	GUN	C6-C5-N7	9.49	135.42	134.14
2	A	301	GUN	C6-C5-N7	-6.42	133.28	134.14
2	B	301	GUN	C5-C4-N3	-5.35	118.19	125.94
2	D	301	GUN	C5-C4-N3	-5.24	118.36	125.94
2	E	301	GUN	C5-C4-N3	-5.21	118.39	125.94
2	F	301	GUN	C5-C4-N3	-5.14	118.50	125.94
2	C	301	GUN	C5-C4-N3	-4.76	119.05	125.94
2	A	301	GUN	C5-C4-N3	-4.75	119.06	125.94
2	D	301	GUN	C2-N3-C4	4.64	121.60	115.09
2	F	301	GUN	C2-N3-C4	4.53	121.46	115.09
2	E	301	GUN	C4-C5-N7	-4.44	105.61	109.93
2	B	301	GUN	C4-C5-N7	-4.27	105.78	109.93
2	B	301	GUN	C2-N3-C4	3.95	120.63	115.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	301	GUN	C4-C5-N7	-3.85	106.18	109.93
2	C	301	GUN	C2-N3-C4	3.85	120.50	115.09
2	F	301	GUN	C4-C5-N7	-3.73	106.31	109.93
2	E	301	GUN	C2-N3-C4	3.62	120.18	115.09
2	A	301	GUN	N2-C2-N1	-3.32	114.21	117.86
2	A	301	GUN	C2-N3-C4	3.05	119.37	115.09
2	E	301	GUN	N2-C2-N3	-2.96	116.29	120.30
2	B	301	GUN	C8-N7-C5	2.18	110.34	103.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	282/324 (87%)	0.30	12 (4%) 34 30	34, 57, 100, 169	0
1	B	283/324 (87%)	0.16	9 (3%) 45 42	31, 48, 86, 165	0
1	C	283/324 (87%)	0.33	9 (3%) 45 42	33, 62, 103, 144	0
1	D	282/324 (87%)	0.45	17 (6%) 21 18	39, 63, 107, 169	0
1	E	282/324 (87%)	0.87	39 (13%) 4 2	38, 75, 123, 200	0
1	F	282/324 (87%)	1.77	95 (33%) 1 1	52, 112, 157, 192	0
All	All	1694/1944 (87%)	0.65	181 (10%) 7 5	31, 66, 138, 200	0

All (181) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	64	HIS	12.7
1	B	62	PRO	9.3
1	D	62	PRO	8.6
1	F	155	PHE	8.1
1	E	62	PRO	8.0
1	B	64	HIS	7.4
1	F	63	GLY	7.1
1	E	63	GLY	7.1
1	F	68	LEU	7.1
1	F	62	PRO	7.0
1	F	106	LEU	7.0
1	F	38	LEU	6.9
1	E	65	ALA	6.5
1	A	63	GLY	6.5
1	F	18	LEU	6.4
1	E	58	ARG	6.0
1	F	58	ARG	5.9
1	F	100	VAL	5.9
1	F	22	LYS	5.9

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Mol	Chain	Res	Type	RSRZ
1	B	63	GLY	5.8
1	F	7	TYR	5.7
1	A	64	HIS	5.7
1	F	184	GLN	5.6
1	F	48	PHE	5.6
1	E	60	THR	5.1
1	F	107	GLY	5.1
1	B	61	VAL	5.1
1	F	61	VAL	5.0
1	D	64	HIS	5.0
1	E	38	LEU	4.9
1	F	80	MET	4.9
1	F	280	ALA	4.8
1	A	62	PRO	4.7
1	F	52	GLU	4.7
1	F	14	ALA	4.6
1	E	59	SER	4.6
1	F	10	TYR	4.6
1	F	4	GLY	4.6
1	F	69	VAL	4.5
1	F	154	ARG	4.5
1	E	35	LEU	4.5
1	F	274	PHE	4.4
1	B	65	ALA	4.3
1	F	29	ILE	4.3
1	F	34	GLY	4.3
1	F	65	ALA	4.3
1	E	53	ILE	4.3
1	D	61	VAL	4.2
1	F	41	LYS	4.1
1	F	126	VAL	4.1
1	D	63	GLY	4.0
1	B	58	ARG	4.0
1	F	17	LEU	3.9
1	E	39	THR	3.9
1	F	51	SER	3.8
1	F	27	VAL	3.8
1	F	240	LEU	3.8
1	D	284	LEU	3.8
1	E	61	VAL	3.7
1	F	111	LEU	3.7
1	D	184	GLN	3.6

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Mol	Chain	Res	Type	RSRZ
1	F	175	LEU	3.6
1	D	58	ARG	3.6
1	F	35	LEU	3.6
1	F	81	MET	3.5
1	A	65	ALA	3.5
1	E	34	GLY	3.5
1	F	67	ARG	3.5
1	F	33	SER	3.5
1	F	28	ALA	3.5
1	E	265	LYS	3.4
1	F	45	ALA	3.4
1	E	43	THR	3.4
1	F	123	LYS	3.4
1	E	184	GLN	3.4
1	C	184	GLN	3.4
1	A	61	VAL	3.3
1	F	110	THR	3.3
1	F	269	GLN	3.3
1	E	67	ARG	3.3
1	F	26	GLN	3.2
1	E	50	TYR	3.2
1	F	179	LYS	3.2
1	E	85	PHE	3.2
1	E	4	GLY	3.2
1	F	79	VAL	3.2
1	C	269	GLN	3.2
1	F	36	GLY	3.2
1	E	82	GLN	3.2
1	F	5	TYR	3.2
1	E	261	LEU	3.1
1	F	105	LEU	3.1
1	D	8	GLU	3.1
1	F	178	TYR	3.0
1	F	152	ASP	3.0
1	F	102	VAL	3.0
1	E	47	ILE	3.0
1	E	80	MET	3.0
1	F	71	GLY	3.0
1	B	286	ASP	3.0
1	F	47	ILE	3.0
1	F	157	ASP	3.0
1	E	260	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	F	227	VAL	2.9
1	F	73	LEU	2.9
1	A	60	THR	2.9
1	F	98	PHE	2.9
1	F	263	ALA	2.9
1	E	33	SER	2.9
1	C	178	TYR	2.8
1	F	236	PHE	2.8
1	E	68	LEU	2.8
1	F	13	THR	2.8
1	F	82	GLN	2.8
1	E	48	PHE	2.7
1	E	22	LYS	2.7
1	F	129	ILE	2.7
1	E	83	GLY	2.7
1	F	112	VAL	2.7
1	F	284	LEU	2.7
1	F	6	THR	2.7
1	F	103	PHE	2.6
1	B	59	SER	2.6
1	F	150	PRO	2.6
1	C	7	TYR	2.6
1	F	44	GLN	2.6
1	F	180	GLN	2.6
1	F	278	LEU	2.6
1	F	104	HIS	2.6
1	C	181	MET	2.6
1	E	54	PRO	2.5
1	F	252	LEU	2.5
1	F	42	LEU	2.5
1	F	131	LEU	2.5
1	D	65	ALA	2.5
1	F	56	PHE	2.5
1	C	183	GLU	2.5
1	C	10	TYR	2.5
1	C	11	LYS	2.4
1	D	181	MET	2.4
1	F	259	GLU	2.4
1	F	166	TYR	2.4
1	E	79	VAL	2.3
1	F	241	ILE	2.3
1	C	64	HIS	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	22	LYS	2.3
1	D	187	LEU	2.3
1	F	60	THR	2.3
1	F	70	PHE	2.3
1	F	238	PHE	2.3
1	F	85	PHE	2.3
1	D	281	SER	2.3
1	F	16	TYR	2.3
1	D	60	THR	2.3
1	E	277	ILE	2.3
1	F	231	CYS	2.3
1	E	264	GLY	2.2
1	F	31	CYS	2.2
1	F	185	ARG	2.2
1	A	184	GLN	2.2
1	E	91	TYR	2.2
1	F	233	LEU	2.2
1	A	185	ARG	2.2
1	A	139	PRO	2.2
1	A	252	LEU	2.2
1	D	179	LYS	2.2
1	D	277	ILE	2.2
1	E	45	ALA	2.1
1	F	43	THR	2.1
1	D	178	TYR	2.1
1	F	57	PRO	2.1
1	D	140	GLY	2.1
1	B	278	LEU	2.1
1	F	101	ARG	2.1
1	E	255	ALA	2.1
1	E	257	TRP	2.1
1	F	64	HIS	2.1
1	F	54	PRO	2.1
1	F	270	LYS	2.0
1	E	238	PHE	2.0
1	A	18	LEU	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. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	GUN	C	301	11/11	0.16	-0.43	38,44,45,46	0
2	GUN	D	301	11/11	0.14	-0.55	42,43,44,46	0
2	GUN	E	301	11/11	0.17	-0.76	64,66,68,69	0
2	GUN	A	301	11/11	0.14	-0.80	37,37,39,39	0
2	GUN	B	301	11/11	0.14	-1.27	40,41,43,43	0
2	GUN	F	301	11/11	0.15	-1.42	55,57,58,58	0

6.5 Other polymers

There are no such residues in this entry.