



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 27, 2023 – 09:21 AM EDT

PDB ID : 3HN6
Title : Crystal structure of glucosamine-6-phosphate deaminase from *Borrelia burgdorferi*
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2009-05-29
Resolution : 2.20 Å (reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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 : 2.35
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) : 2.35

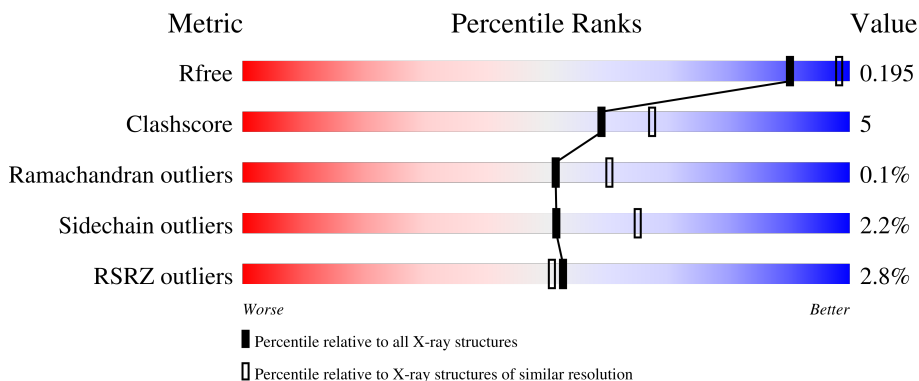
1 Overall quality at a glance i

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.



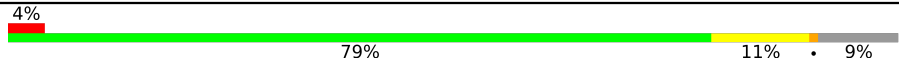
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	289	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 86%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 8%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 6%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center; margin-top: 5px;">86% 8% 6%</p>
1	B	289	<div style="display: flex; align-items: center;"> <div style="width: 3%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 81%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 12%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 7%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center; margin-top: 5px;">81% 12% 7%</p>
1	C	289	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 89%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 5%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 6%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center; margin-top: 5px;">89% 5% 6%</p>
1	D	289	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 83%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 10%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 7%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center; margin-top: 5px;">83% 10% 7%</p>
1	E	289	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 2px;"></div> <div style="width: 80%; height: 10px; background-color: green; margin-right: 2px;"></div> <div style="width: 11%; height: 10px; background-color: yellow; margin-right: 2px;"></div> <div style="width: 8%; height: 10px; background-color: grey;"></div> </div> <p style="text-align: center; margin-top: 5px;">80% 11% 8%</p>

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Mol	Chain	Length	Quality of chain
1	F	289	 <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 '4%', a large green segment labeled '79%', a yellow segment labeled '11%', and a small grey segment at the end labeled '9%'.</p>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 13486 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 Glucosamine-6-phosphate deaminase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	271	2115	1345	361	400	9	0	1	0
1	B	270	2105	1337	360	399	9	0	2	0
1	C	271	2131	1355	365	402	9	0	2	0
1	D	270	2122	1351	358	404	9	0	4	0
1	E	266	2101	1338	360	394	9	0	3	0
1	F	262	2030	1291	346	384	9	0	1	0

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	expression tag	UNP O30564
A	-19	ALA	-	expression tag	UNP O30564
A	-18	HIS	-	expression tag	UNP O30564
A	-17	HIS	-	expression tag	UNP O30564
A	-16	HIS	-	expression tag	UNP O30564
A	-15	HIS	-	expression tag	UNP O30564
A	-14	HIS	-	expression tag	UNP O30564
A	-13	HIS	-	expression tag	UNP O30564
A	-12	MET	-	expression tag	UNP O30564
A	-11	GLY	-	expression tag	UNP O30564
A	-10	THR	-	expression tag	UNP O30564
A	-9	LEU	-	expression tag	UNP O30564
A	-8	GLU	-	expression tag	UNP O30564
A	-7	ALA	-	expression tag	UNP O30564
A	-6	GLN	-	expression tag	UNP O30564
A	-5	THR	-	expression tag	UNP O30564
A	-4	GLN	-	expression tag	UNP O30564

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP O30564
A	-2	PRO	-	expression tag	UNP O30564
A	-1	GLY	-	expression tag	UNP O30564
A	0	SER	-	expression tag	UNP O30564
B	-20	MET	-	expression tag	UNP O30564
B	-19	ALA	-	expression tag	UNP O30564
B	-18	HIS	-	expression tag	UNP O30564
B	-17	HIS	-	expression tag	UNP O30564
B	-16	HIS	-	expression tag	UNP O30564
B	-15	HIS	-	expression tag	UNP O30564
B	-14	HIS	-	expression tag	UNP O30564
B	-13	HIS	-	expression tag	UNP O30564
B	-12	MET	-	expression tag	UNP O30564
B	-11	GLY	-	expression tag	UNP O30564
B	-10	THR	-	expression tag	UNP O30564
B	-9	LEU	-	expression tag	UNP O30564
B	-8	GLU	-	expression tag	UNP O30564
B	-7	ALA	-	expression tag	UNP O30564
B	-6	GLN	-	expression tag	UNP O30564
B	-5	THR	-	expression tag	UNP O30564
B	-4	GLN	-	expression tag	UNP O30564
B	-3	GLY	-	expression tag	UNP O30564
B	-2	PRO	-	expression tag	UNP O30564
B	-1	GLY	-	expression tag	UNP O30564
B	0	SER	-	expression tag	UNP O30564
C	-20	MET	-	expression tag	UNP O30564
C	-19	ALA	-	expression tag	UNP O30564
C	-18	HIS	-	expression tag	UNP O30564
C	-17	HIS	-	expression tag	UNP O30564
C	-16	HIS	-	expression tag	UNP O30564
C	-15	HIS	-	expression tag	UNP O30564
C	-14	HIS	-	expression tag	UNP O30564
C	-13	HIS	-	expression tag	UNP O30564
C	-12	MET	-	expression tag	UNP O30564
C	-11	GLY	-	expression tag	UNP O30564
C	-10	THR	-	expression tag	UNP O30564
C	-9	LEU	-	expression tag	UNP O30564
C	-8	GLU	-	expression tag	UNP O30564
C	-7	ALA	-	expression tag	UNP O30564
C	-6	GLN	-	expression tag	UNP O30564
C	-5	THR	-	expression tag	UNP O30564
C	-4	GLN	-	expression tag	UNP O30564

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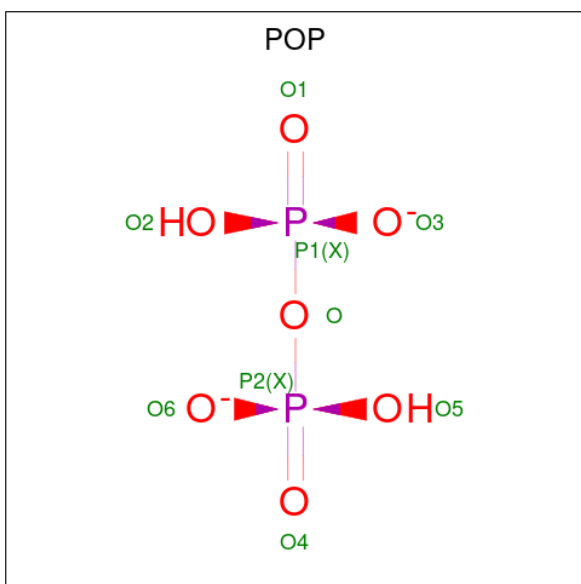
Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	expression tag	UNP O30564
C	-2	PRO	-	expression tag	UNP O30564
C	-1	GLY	-	expression tag	UNP O30564
C	0	SER	-	expression tag	UNP O30564
D	-20	MET	-	expression tag	UNP O30564
D	-19	ALA	-	expression tag	UNP O30564
D	-18	HIS	-	expression tag	UNP O30564
D	-17	HIS	-	expression tag	UNP O30564
D	-16	HIS	-	expression tag	UNP O30564
D	-15	HIS	-	expression tag	UNP O30564
D	-14	HIS	-	expression tag	UNP O30564
D	-13	HIS	-	expression tag	UNP O30564
D	-12	MET	-	expression tag	UNP O30564
D	-11	GLY	-	expression tag	UNP O30564
D	-10	THR	-	expression tag	UNP O30564
D	-9	LEU	-	expression tag	UNP O30564
D	-8	GLU	-	expression tag	UNP O30564
D	-7	ALA	-	expression tag	UNP O30564
D	-6	GLN	-	expression tag	UNP O30564
D	-5	THR	-	expression tag	UNP O30564
D	-4	GLN	-	expression tag	UNP O30564
D	-3	GLY	-	expression tag	UNP O30564
D	-2	PRO	-	expression tag	UNP O30564
D	-1	GLY	-	expression tag	UNP O30564
D	0	SER	-	expression tag	UNP O30564
E	-20	MET	-	expression tag	UNP O30564
E	-19	ALA	-	expression tag	UNP O30564
E	-18	HIS	-	expression tag	UNP O30564
E	-17	HIS	-	expression tag	UNP O30564
E	-16	HIS	-	expression tag	UNP O30564
E	-15	HIS	-	expression tag	UNP O30564
E	-14	HIS	-	expression tag	UNP O30564
E	-13	HIS	-	expression tag	UNP O30564
E	-12	MET	-	expression tag	UNP O30564
E	-11	GLY	-	expression tag	UNP O30564
E	-10	THR	-	expression tag	UNP O30564
E	-9	LEU	-	expression tag	UNP O30564
E	-8	GLU	-	expression tag	UNP O30564
E	-7	ALA	-	expression tag	UNP O30564
E	-6	GLN	-	expression tag	UNP O30564
E	-5	THR	-	expression tag	UNP O30564
E	-4	GLN	-	expression tag	UNP O30564

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-3	GLY	-	expression tag	UNP O30564
E	-2	PRO	-	expression tag	UNP O30564
E	-1	GLY	-	expression tag	UNP O30564
E	0	SER	-	expression tag	UNP O30564
F	-20	MET	-	expression tag	UNP O30564
F	-19	ALA	-	expression tag	UNP O30564
F	-18	HIS	-	expression tag	UNP O30564
F	-17	HIS	-	expression tag	UNP O30564
F	-16	HIS	-	expression tag	UNP O30564
F	-15	HIS	-	expression tag	UNP O30564
F	-14	HIS	-	expression tag	UNP O30564
F	-13	HIS	-	expression tag	UNP O30564
F	-12	MET	-	expression tag	UNP O30564
F	-11	GLY	-	expression tag	UNP O30564
F	-10	THR	-	expression tag	UNP O30564
F	-9	LEU	-	expression tag	UNP O30564
F	-8	GLU	-	expression tag	UNP O30564
F	-7	ALA	-	expression tag	UNP O30564
F	-6	GLN	-	expression tag	UNP O30564
F	-5	THR	-	expression tag	UNP O30564
F	-4	GLN	-	expression tag	UNP O30564
F	-3	GLY	-	expression tag	UNP O30564
F	-2	PRO	-	expression tag	UNP O30564
F	-1	GLY	-	expression tag	UNP O30564
F	0	SER	-	expression tag	UNP O30564

- Molecule 2 is PYROPHOSPHATE 2- (three-letter code: POP) (formula: $\text{H}_2\text{O}_7\text{P}_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	P	0	0
			9	7	2		
2	C	1	Total	O	P	0	0
			9	7	2		
2	D	1	Total	O	P	0	0
			9	7	2		

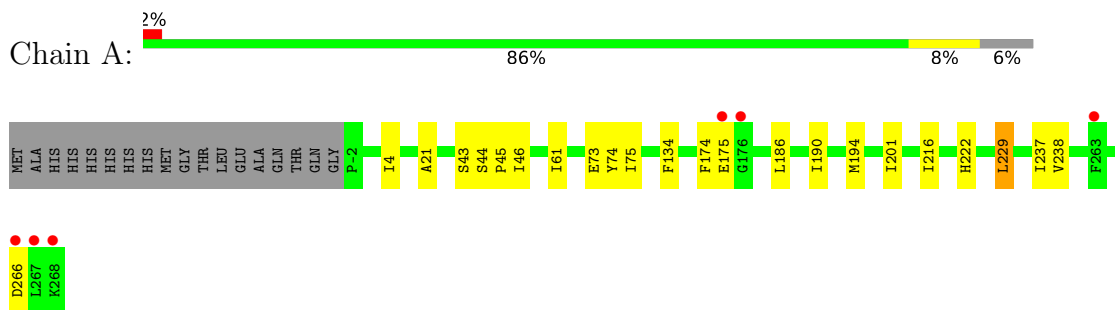
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	169	Total	O	0	0
			169	169		
3	B	121	Total	O	0	0
			121	121		
3	C	182	Total	O	0	0
			182	182		
3	D	139	Total	O	0	0
			139	139		
3	E	141	Total	O	0	0
			141	141		
3	F	103	Total	O	0	0
			103	103		

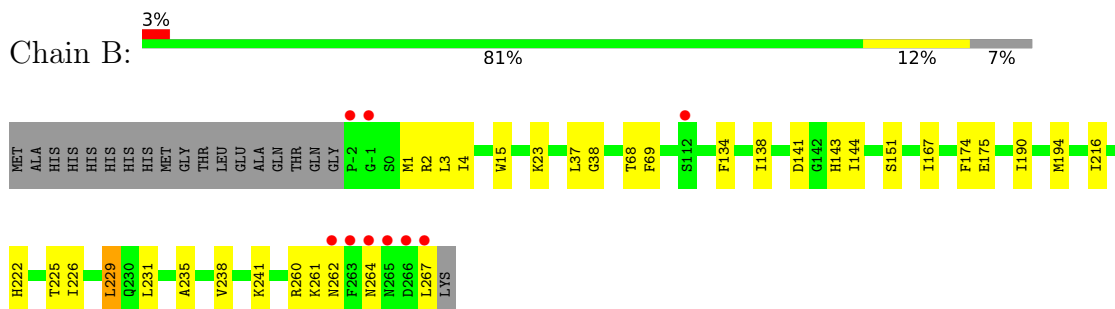
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

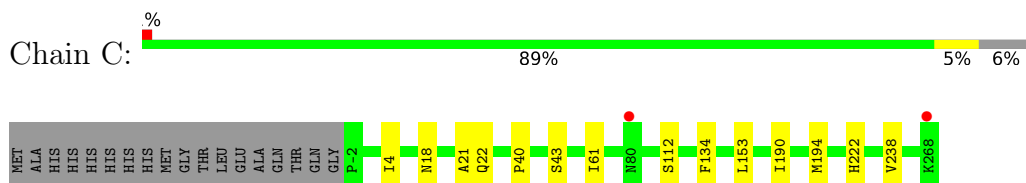
- Molecule 1: Glucosamine-6-phosphate deaminase



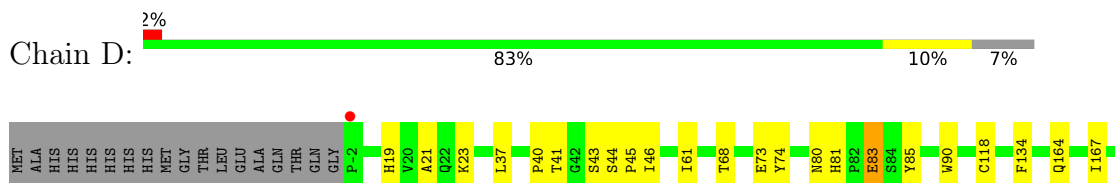
- Molecule 1: Glucosamine-6-phosphate deaminase



- Molecule 1: Glucosamine-6-phosphate deaminase

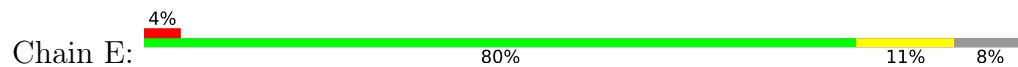


- Molecule 1: Glucosamine-6-phosphate deaminase

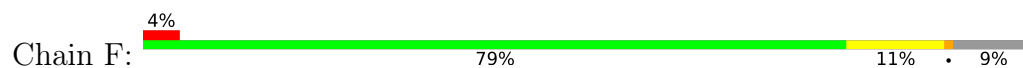




- Molecule 1: Glucosamine-6-phosphate deaminase



- Molecule 1: Glucosamine-6-phosphate deaminase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	89.90Å 82.79Å 126.99Å 90.00° 109.58° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 19.74 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.2 (50.00-2.20) 96.4 (19.74-2.20)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.38 (at 2.19Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.185 , 0.237 0.187 , 0.195	Depositor DCC
R_{free} test set	4299 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	24.1	Xtrriage
Anisotropy	0.056	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.016 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13486	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.36% 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: POP

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	0.68	0/2163	0.70	1/2929 (0.0%)
1	B	0.68	0/2155	0.67	0/2919
1	C	0.70	0/2182	0.65	0/2952
1	D	0.67	0/2180	0.65	0/2956
1	E	0.70	0/2154	0.66	0/2912
1	F	0.62	0/2075	0.65	0/2812
All	All	0.68	0/12909	0.66	1/17480 (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	229	LEU	CA-CB-CG	8.55	134.96	115.30

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	2115	0	2060	15	0
1	B	2105	0	2047	21	0
1	C	2131	0	2088	5	0
1	D	2122	0	2061	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2101	0	2068	27	0
1	F	2030	0	1967	34	0
2	B	9	0	0	0	0
2	C	9	0	0	0	0
2	D	9	0	0	0	0
3	A	169	0	0	0	0
3	B	121	0	0	2	0
3	C	182	0	0	0	0
3	D	139	0	0	1	0
3	E	141	0	0	2	0
3	F	103	0	0	1	0
All	All	13486	0	12291	117	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 5.

All (117) 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:E:194[B]:MET:HE1	1:E:228:ALA:HB1	1.18	1.10
1:F:43:SER:HA	1:F:46:ILE:HD12	1.41	0.98
1:E:194[B]:MET:HE1	1:E:228:ALA:CB	1.93	0.97
1:D:90:TRP:HB3	3:D:650:HOH:O	1.65	0.96
1:E:194[B]:MET:CE	1:E:228:ALA:HB1	1.96	0.94
1:B:262:ASN:HB2	3:B:489:HOH:O	1.71	0.90
1:D:164:GLN:HG2	1:F:261:LYS:NZ	1.89	0.88
1:D:190:ILE:HD11	1:D:225[B]:THR:CG2	2.04	0.87
1:D:164:GLN:HG2	1:F:261:LYS:HZ3	1.48	0.78
1:D:190:ILE:HD11	1:D:225[B]:THR:HG21	1.65	0.77
1:E:194[B]:MET:CE	1:E:228:ALA:CB	2.60	0.75
1:E:115:LYS:O	1:E:119:GLU:HG3	1.91	0.70
1:D:21:ALA:HA	1:D:61:ILE:HD12	1.73	0.69
1:E:190[B]:ILE:HG13	1:E:194[B]:MET:HE3	1.74	0.68
1:D:190:ILE:O	1:D:194[B]:MET:HG2	1.93	0.68
1:B:15:TRP:CE3	1:B:238[B]:VAL:HG11	2.29	0.67
1:B:138:ILE:CG2	1:B:226:ILE:HD13	2.26	0.66
1:F:194[A]:MET:HE3	1:F:229:LEU:HD12	1.79	0.64
1:D:190:ILE:CD1	1:D:225[B]:THR:CG2	2.75	0.64
1:F:194[A]:MET:CE	1:F:229:LEU:HD12	2.28	0.64
1:D:164:GLN:HG2	1:F:261:LYS:HZ1	1.63	0.64
1:D:118:CYS:SG	1:D:186:LEU:HD22	2.38	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:194[B]:MET:HE2	1:A:194[B]:MET:HA	1.82	0.62
1:B:190:ILE:O	1:B:194[A]:MET:HG2	2.01	0.60
1:E:44:SER:HB2	1:E:45:PRO:HD3	1.83	0.60
1:F:3:LEU:HD22	1:F:216:ILE:HD13	1.84	0.60
1:F:19:HIS:O	1:F:23:LYS:HG2	2.02	0.59
1:F:226:ILE:HD12	1:F:229:LEU:HD22	1.84	0.59
1:A:190:ILE:O	1:A:194[B]:MET:HG2	2.02	0.59
1:F:194[A]:MET:HE3	1:F:229:LEU:CD1	2.33	0.59
1:A:75:ILE:HD11	1:A:186:LEU:HD23	1.85	0.58
1:B:260:ARG:NH1	3:B:386:HOH:O	2.36	0.56
1:F:145:ALA:HB3	3:F:304:HOH:O	2.05	0.56
1:D:190:ILE:O	1:D:194[A]:MET:HG2	2.04	0.56
1:F:194[A]:MET:HA	1:F:194[A]:MET:HE2	1.88	0.55
1:E:145:ALA:HB3	3:E:679:HOH:O	2.06	0.55
1:F:152:SER:C	1:F:154:THR:H	2.10	0.55
1:D:43:SER:HA	1:D:46:ILE:HD12	1.89	0.55
1:E:190[B]:ILE:HG13	1:E:194[B]:MET:CE	2.38	0.54
1:E:6:ARG:O	1:E:240:ASP:HA	2.08	0.54
1:A:194[B]:MET:HE2	1:A:194[B]:MET:CA	2.38	0.54
1:B:151:SER:HB2	1:B:225:THR:HG21	1.90	0.54
1:A:201:ILE:HG13	1:A:229:LEU:HD11	1.90	0.54
1:E:143:HIS:CD2	1:E:145:ALA:O	2.61	0.54
1:B:138:ILE:HG21	1:B:226:ILE:HD13	1.91	0.53
1:B:1:MET:HG2	1:B:2:ARG:N	2.25	0.52
1:B:229:LEU:HD23	1:B:235:ALA:HB1	1.90	0.52
1:F:190:ILE:HD11	1:F:225:THR:CG2	2.39	0.52
1:B:3:LEU:HD22	1:B:216:ILE:HD13	1.92	0.52
1:B:4:ILE:HB	1:B:238[B]:VAL:HG12	1.91	0.52
1:C:190:ILE:O	1:C:194[A]:MET:HG2	2.09	0.52
1:D:194[A]:MET:HA	1:D:194[A]:MET:HE2	1.91	0.52
1:E:148:GLU:HB3	1:E:149:PRO:HD2	1.93	0.51
1:A:194[B]:MET:HA	1:A:194[B]:MET:CE	2.41	0.51
1:A:44:SER:HB2	1:A:45:PRO:HD3	1.93	0.51
1:D:41:THR:HG21	1:D:85[B]:TYR:HD1	1.76	0.51
1:D:19:HIS:O	1:D:23:LYS:HG2	2.12	0.50
1:E:143:HIS:HD2	1:E:145:ALA:O	1.94	0.49
1:E:10:GLU:HG3	3:E:296:HOH:O	2.13	0.49
1:A:75:ILE:HD11	1:A:186:LEU:CD2	2.42	0.49
1:E:4:ILE:HB	1:E:238:VAL:HG23	1.95	0.49
1:F:190:ILE:O	1:F:194[A]:MET:HG2	2.13	0.49
1:B:167:ILE:HD12	1:D:261:LYS:HE3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:38:GLY:HA2	1:B:69:PHE:O	2.13	0.48
1:D:167:ILE:HD12	1:F:261:LYS:HE3	1.96	0.48
1:E:160:LYS:HE3	1:E:161:THR:O	2.13	0.48
1:E:13:SER:HB3	1:E:47:GLY:C	2.35	0.46
1:A:4:ILE:HB	1:A:238:VAL:HG23	1.97	0.46
1:D:81:HIS:CE1	1:D:83:GLU:HB2	2.50	0.46
1:F:226:ILE:CD1	1:F:229:LEU:HD22	2.46	0.46
1:B:261:LYS:HE2	1:F:164:GLN:CA	2.45	0.46
1:F:190:ILE:HD11	1:F:225:THR:HG21	1.98	0.46
1:D:194[A]:MET:HA	1:D:194[A]:MET:CE	2.46	0.45
1:F:21:ALA:HA	1:F:61:ILE:HD12	1.98	0.45
1:D:44:SER:HB2	1:D:45:PRO:HD3	1.99	0.44
1:D:43:SER:HA	1:D:46:ILE:CD1	2.47	0.44
1:F:141:ASP:OD1	1:F:143:HIS:CD2	2.70	0.44
1:A:21:ALA:HA	1:A:61:ILE:HD12	1.98	0.44
1:A:174:PHE:O	1:A:175:GLU:HB2	2.17	0.44
1:C:18:ASN:O	1:C:22:GLN:HG3	2.18	0.44
1:C:4:ILE:HB	1:C:238:VAL:HG23	2.00	0.44
1:F:40:PRO:HG2	1:F:45:PRO:HG3	2.00	0.44
1:D:73:GLU:HG3	1:D:74:TYR:N	2.33	0.44
1:F:147:ASN:HB3	1:F:190:ILE:HD11	2.00	0.43
1:F:190:ILE:CD1	1:F:225:THR:CG2	2.96	0.43
1:B:23:LYS:HA	1:B:23:LYS:HD2	1.55	0.43
1:F:152:SER:O	1:F:154:THR:N	2.52	0.43
1:E:139:GLY:HA3	1:E:143:HIS:CE1	2.54	0.43
1:B:37:LEU:O	1:B:68:THR:HA	2.19	0.43
1:B:141:ASP:OD1	1:B:143:HIS:CD2	2.72	0.43
1:B:174:PHE:C	1:B:175:GLU:HG2	2.39	0.43
1:E:194[B]:MET:CE	1:E:228:ALA:HB3	2.45	0.42
1:D:164:GLN:CG	1:F:261:LYS:HZ1	2.30	0.42
1:F:3:LEU:HD22	1:F:216:ILE:CD1	2.48	0.42
1:A:43:SER:HA	1:A:46:ILE:HD12	2.01	0.42
1:D:44:SER:CB	1:D:45:PRO:HD3	2.50	0.42
1:F:194[A]:MET:HE1	1:F:229:LEU:HD12	2.01	0.42
1:D:37:LEU:O	1:D:68:THR:HA	2.20	0.42
1:F:201:ILE:HG13	1:F:229:LEU:HD21	2.01	0.42
1:E:18:ASN:O	1:E:22:GLN:HB2	2.19	0.41
1:E:169:ALA:O	1:E:172:ARG:HG2	2.20	0.41
1:A:266:ASP:OD2	1:E:183:LYS:HE3	2.20	0.41
1:B:261:LYS:HE3	1:F:167:ILE:HD12	2.01	0.41
1:E:157:THR:HA	1:E:187:THR:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:3:LEU:HD22	1:B:216:ILE:CD1	2.50	0.41
1:F:41:THR:HG1	1:F:85:TYR:HE2	1.68	0.41
1:A:216:ILE:HD11	1:A:237:ILE:HD12	2.03	0.41
1:E:183:LYS:HE2	1:E:183:LYS:HB2	1.85	0.41
1:C:21:ALA:HA	1:C:61:ILE:HD12	2.02	0.40
1:C:153:LEU:HB2	1:E:231:LEU:HD23	2.03	0.40
1:F:4:ILE:HB	1:F:238:VAL:HG23	2.03	0.40
1:F:152:SER:C	1:F:154:THR:N	2.73	0.40
1:B:194[B]:MET:HE1	1:B:231:LEU:HB2	2.03	0.40
1:E:148:GLU:HB3	1:E:149:PRO:CD	2.51	0.40
1:F:190:ILE:CD1	1:F:225:THR:HG23	2.51	0.40
1:A:73:GLU:HG3	1:A:74:TYR:O	2.21	0.40
1:E:3:LEU:HD22	1:E:216:ILE:HD13	2.03	0.40

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	270/289 (93%)	259 (96%)	11 (4%)	0	100	100
1	B	270/289 (93%)	258 (96%)	12 (4%)	0	100	100
1	C	271/289 (94%)	261 (96%)	9 (3%)	1 (0%)	34	37
1	D	272/289 (94%)	258 (95%)	13 (5%)	1 (0%)	34	37
1	E	265/289 (92%)	252 (95%)	13 (5%)	0	100	100
1	F	259/289 (90%)	246 (95%)	13 (5%)	0	100	100
All	All	1607/1734 (93%)	1534 (96%)	71 (4%)	2 (0%)	51	60

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	40	PRO
1	C	40	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	229/253 (90%)	227 (99%)	2 (1%)	78 88
1	B	227/253 (90%)	220 (97%)	7 (3%)	40 51
1	C	232/253 (92%)	228 (98%)	4 (2%)	60 74
1	D	231/253 (91%)	226 (98%)	5 (2%)	52 65
1	E	230/253 (91%)	226 (98%)	4 (2%)	60 74
1	F	218/253 (86%)	210 (96%)	8 (4%)	34 43
All	All	1367/1518 (90%)	1337 (98%)	30 (2%)	52 65

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	134	PHE
1	A	222	HIS
1	B	134	PHE
1	B	144	ILE
1	B	222	HIS
1	B	229	LEU
1	B	241	LYS
1	B	264	ASN
1	B	267	LEU
1	C	43	SER
1	C	112	SER
1	C	134	PHE
1	C	222	HIS
1	D	80	ASN
1	D	83	GLU
1	D	134	PHE
1	D	216	ILE

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Mol	Chain	Res	Type
1	D	222	HIS
1	E	134	PHE
1	E	160	LYS
1	E	171	SER
1	E	222	HIS
1	F	28	SER
1	F	43	SER
1	F	101	LYS
1	F	112	SER
1	F	134	PHE
1	F	152	SER
1	F	222	HIS
1	F	229	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	22	GLN

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](#)

3 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	POP	D	301	-	6,8,8	0.58	0	13,13,13	1.25	3 (23%)
2	POP	C	302	-	6,8,8	0.68	0	13,13,13	1.35	2 (15%)
2	POP	B	303	-	6,8,8	0.69	0	13,13,13	1.16	1 (7%)

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	POP	D	301	-	-	1/6/6/6	-
2	POP	C	302	-	-	1/6/6/6	-
2	POP	B	303	-	-	2/6/6/6	-

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	302	POP	P2-O-P1	-2.90	122.86	132.83
2	D	301	POP	O6-P2-O	2.36	112.54	104.64
2	D	301	POP	O2-P1-O	2.33	112.45	104.64
2	C	302	POP	O2-P1-O	2.26	112.20	104.64
2	B	303	POP	P2-O-P1	-2.08	125.70	132.83
2	D	301	POP	P2-O-P1	-2.02	125.88	132.83

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	303	POP	P1-O-P2-O6
2	D	301	POP	P1-O-P2-O5
2	C	302	POP	P2-O-P1-O1
2	B	303	POP	P1-O-P2-O4

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	271/289 (93%)	-0.28	6 (2%) 62 59	10, 20, 45, 62	0
1	B	270/289 (93%)	-0.21	9 (3%) 46 44	10, 24, 46, 64	0
1	C	271/289 (93%)	-0.47	2 (0%) 87 86	9, 18, 32, 48	0
1	D	270/289 (93%)	-0.25	5 (1%) 66 65	10, 23, 43, 55	0
1	E	266/289 (92%)	-0.20	11 (4%) 37 35	11, 22, 50, 75	0
1	F	262/289 (90%)	-0.03	12 (4%) 32 31	13, 26, 50, 67	0
All	All	1610/1734 (92%)	-0.24	45 (2%) 53 51	9, 22, 45, 75	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	268	LYS	4.8
1	B	-2	PRO	4.6
1	B	266	ASP	4.2
1	E	263	PHE	4.1
1	B	263	PHE	4.1
1	F	178	VAL	4.0
1	E	264	ASN	4.0
1	A	266	ASP	3.9
1	E	172	ARG	3.8
1	B	265	ASN	3.6
1	E	173	PHE	3.5
1	A	267	LEU	3.5
1	D	176	GLY	3.5
1	E	266	ASP	3.5
1	B	264	ASN	3.3
1	C	268	LYS	3.3
1	B	-1	GLY	3.3
1	A	263	PHE	3.2
1	F	267	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	F	177	ASP	3.2
1	F	263	PHE	3.1
1	E	168	ILE	3.1
1	A	175	GLU	3.1
1	F	168	ILE	3.1
1	E	171	SER	3.0
1	E	267	LEU	2.8
1	F	180	LYS	2.8
1	B	262	ASN	2.7
1	B	267	LEU	2.7
1	D	263	PHE	2.6
1	F	264	ASN	2.5
1	E	179	ASN	2.5
1	D	267	LEU	2.5
1	D	-2	PRO	2.4
1	F	166	THR	2.4
1	B	112	SER	2.3
1	F	266	ASP	2.3
1	F	167	ILE	2.3
1	A	176	GLY	2.2
1	C	80	ASN	2.2
1	E	174	PHE	2.2
1	F	37	LEU	2.1
1	E	37	LEU	2.1
1	D	178	VAL	2.1
1	F	112	SER	2.1

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(\AA^2)	Q<0.9
2	POP	C	302	9/9	0.92	0.17	53,54,55,55	0
2	POP	B	303	9/9	0.94	0.18	47,49,50,50	0
2	POP	D	301	9/9	0.95	0.11	42,44,45,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.