



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 24, 2017 – 05:48 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 : unknown
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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

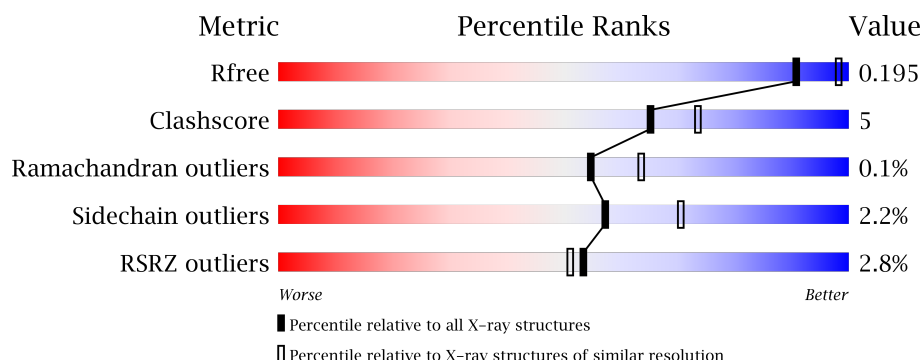
1 Overall quality at a glance

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}	100719	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	289	<div> <div>2%</div> <div> <div></div> <div>86%</div> <div>8%</div> <div>6%</div> </div> </div>
1	B	289	<div> <div>3%</div> <div> <div></div> <div>81%</div> <div>12%</div> <div>7%</div> </div> </div>
1	C	289	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>5%</div> <div>6%</div> </div> </div>
1	D	289	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>10%</div> <div>7%</div> </div> </div>
1	E	289	<div> <div>4%</div> <div> <div></div> <div>80%</div> <div>11%</div> <div>8%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	289	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	POP	B	303	-	-	-	X
2	POP	C	302	-	-	-	X

2 Entry composition

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

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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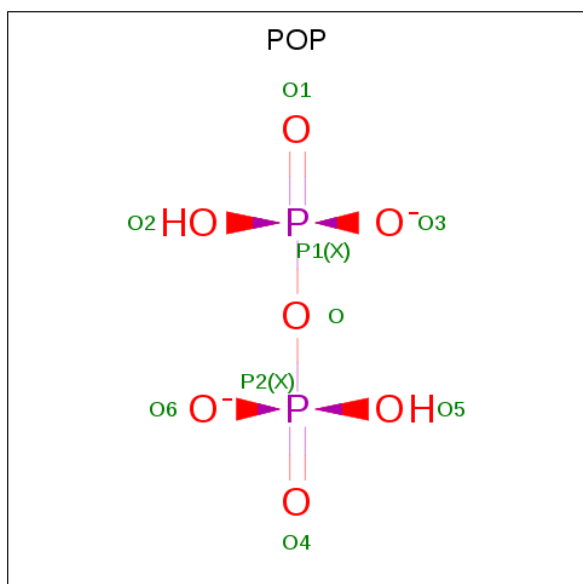
Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	EXPRESSION TAG	UNP O30564
C	-2	PRO	-	EXPRESSION TAG	UNP O30564
C	-1	GLY	-	EXPRESSION TAG	UNP O30564
C	0	SER	-	EXPRESSION TAG	UNP O30564
D	-20	MET	-	EXPRESSION TAG	UNP O30564
D	-19	ALA	-	EXPRESSION TAG	UNP O30564
D	-18	HIS	-	EXPRESSION TAG	UNP 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 9 7 2	0	0
2	C	1	Total O P 9 7 2	0	0
2	D	1	Total O P 9 7 2	0	0

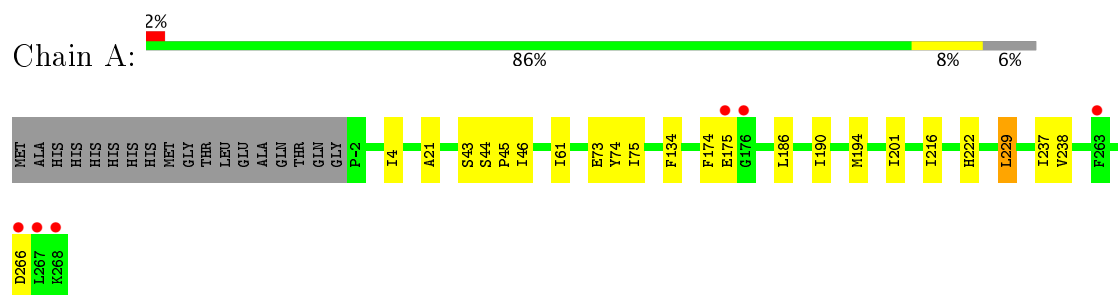
- Molecule 3 is water.

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

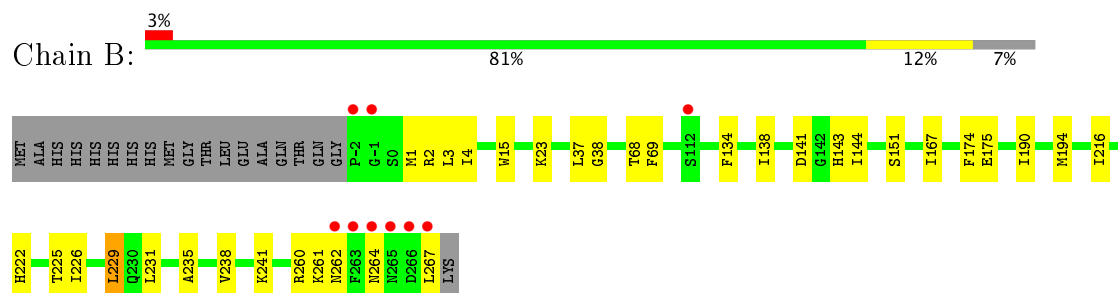
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

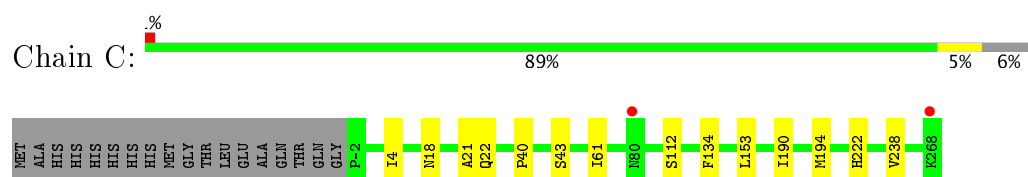
- Molecule 1: Glucosamine-6-phosphate deaminase



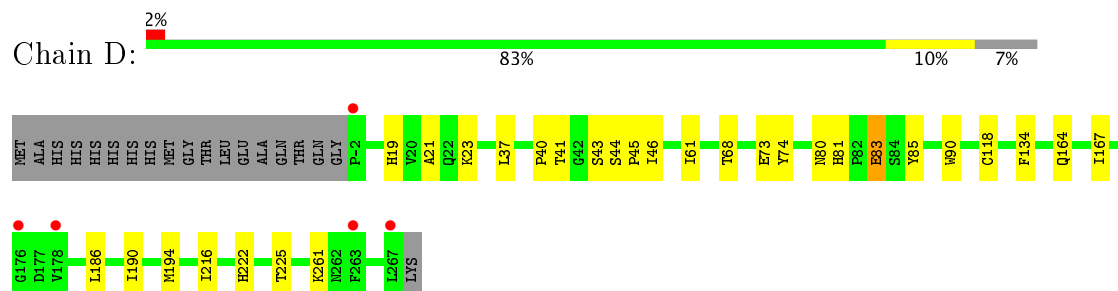
- Molecule 1: Glucosamine-6-phosphate deaminase




- Molecule 1: Glucosamine-6-phosphate deaminase

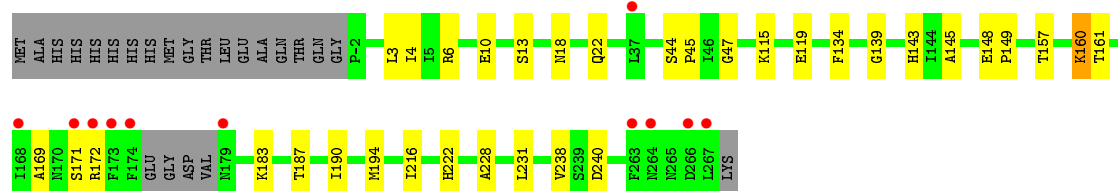


- Molecule 1: Glucosamine-6-phosphate deaminase




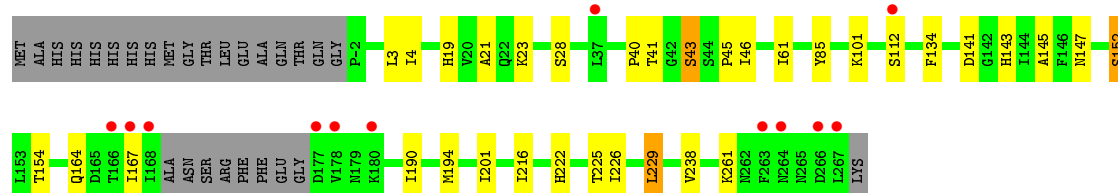
- Molecule 1: Glucosamine-6-phosphate deaminase

Chain E: 



- Molecule 1: Glucosamine-6-phosphate deaminase

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	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)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.185 , 0.237 0.187 , 0.195	Depositor DCC
R_{free} test set	4299 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	24.1	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.016 for h,-k,-h-l	Xtriage
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

Xtriage'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

5.1 Standard geometry

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

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:HA	1:A:194[B]:MET:HE2	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:HE2	1:F:194[A]:MET:HA	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:CA	1:A:194[B]:MET:HE2	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:CE	1:A:194[B]:MET:HA	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:CE	1:D:194[A]:MET:HA	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:174:PHE:O	1:A:175:GLU:HB2	2.17	0.44
1:A:21:ALA:HA	1:A:61:ILE:HD12	1.98	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: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:B:37:LEU:O	1:B:68:THR:HA	2.19	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:169:ALA:O	1:E:172:ARG:HG2	2.20	0.41
1:E:18:ASN:O	1:E:22:GLN:HB2	2.19	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:153:LEU:HB2	1:E:231:LEU:HD23	2.03	0.40
1:C:21:ALA:HA	1:C:61:ILE:HD12	2.02	0.40
1:F:152:SER:C	1:F:154:THR:N	2.73	0.40
1:F:4:ILE:HB	1:F:238:VAL:HG23	2.03	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%)	38	41
1	D	272/289 (94%)	258 (95%)	13 (5%)	1 (0%)	38	41
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%)	55	63

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	40	PRO
1	C	40	PRO

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	229/253 (90%)	227 (99%)	2 (1%)	82	91
1	B	227/253 (90%)	220 (97%)	7 (3%)	45	57
1	C	232/253 (92%)	228 (98%)	4 (2%)	66	79
1	D	231/253 (91%)	226 (98%)	5 (2%)	57	70
1	E	230/253 (91%)	226 (98%)	4 (2%)	66	79
1	F	218/253 (86%)	210 (96%)	8 (4%)	39	49
All	All	1367/1518 (90%)	1337 (98%)	30 (2%)	57	70

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

Some 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 ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	B	303	-	8,8,8	1.23	1 (12%)	8,13,13	0.59	0
2	POP	C	302	-	8,8,8	0.91	0	8,13,13	0.59	0
2	POP	D	301	-	8,8,8	0.78	0	8,13,13	0.59	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	POP	B	303	-	-	0/6/6/6	0/0/0/0
2	POP	C	302	-	-	0/6/6/6	0/0/0/0
2	POP	D	301	-	-	0/6/6/6	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	303	POP	P1-O	2.53	1.64	1.60

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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 60	10, 20, 45, 62	0
1	B	270/289 (93%)	-0.21	9 (3%) 47 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%) 67 65	10, 23, 43, 55	0
1	E	266/289 (92%)	-0.20	11 (4%) 38 36	11, 22, 50, 75	0
1	F	262/289 (90%)	-0.04	12 (4%) 33 32	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	4.9
1	B	-2	PRO	4.6
1	E	263	PHE	4.2
1	B	263	PHE	4.1
1	B	266	ASP	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	A	267	LEU	3.6
1	E	173	PHE	3.6
1	B	265	ASN	3.6
1	D	176	GLY	3.5
1	E	266	ASP	3.5
1	C	268	LYS	3.3
1	B	-1	GLY	3.3
1	B	264	ASN	3.2
1	F	267	LEU	3.2
1	A	263	PHE	3.2

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Mol	Chain	Res	Type	RSRZ
1	F	263	PHE	3.2
1	F	177	ASP	3.2
1	E	168	ILE	3.1
1	F	168	ILE	3.1
1	E	171	SER	3.0
1	A	175	GLU	3.0
1	E	267	LEU	2.9
1	F	180	LYS	2.8
1	B	267	LEU	2.8
1	B	262	ASN	2.7
1	D	263	PHE	2.6
1	F	264	ASN	2.6
1	E	179	ASN	2.5
1	D	267	LEU	2.5
1	D	-2	PRO	2.5
1	F	166	THR	2.4
1	F	266	ASP	2.4
1	B	112	SER	2.3
1	F	167	ILE	2.3
1	C	80	ASN	2.2
1	A	176	GLY	2.2
1	E	174	PHE	2.1
1	D	178	VAL	2.1
1	F	37	LEU	2.1
1	E	37	LEU	2.0
1	F	112	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	POP	B	303	9/9	0.94	0.18	3.70	47,49,50,50	0
2	POP	C	302	9/9	0.92	0.17	2.49	53,54,55,55	0
2	POP	D	301	9/9	0.95	0.11	-0.36	42,44,45,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.