



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 15, 2026 – 10:20 AM UTC

PDB ID : 6SB4 / pdb_00006sb4
Title : Crystal structure of murine perforin-2 P2 domain crystal form 2
Authors : Ni, T.; Yu, X.; Ginger, L.; Gilbert, R.J.C.
Deposited on : 2019-07-18
Resolution : 3.17 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

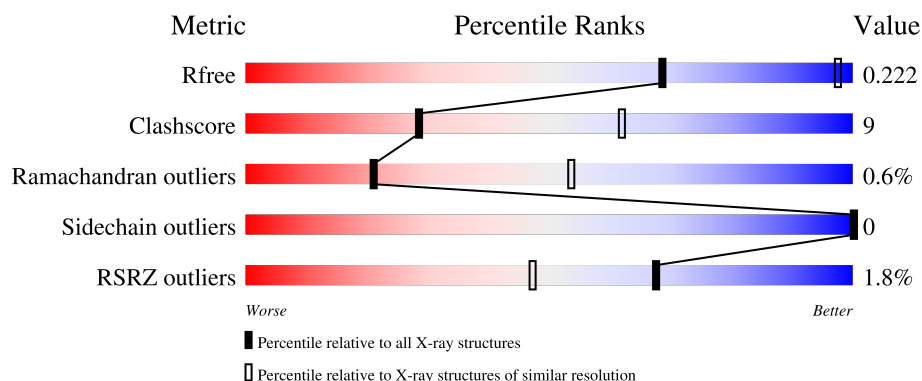
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.17 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}	180053	2001 (3.20-3.16)
Clashscore	190562	2119 (3.20-3.16)
Ramachandran outliers	187476	2070 (3.20-3.16)
Sidechain outliers	187428	2069 (3.20-3.16)
RSRZ outliers	180081	2001 (3.20-3.16)

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	295	 2% 52% 14% 34%
1	B	295	 2% 55% 13% 33%
1	C	295	 % 56% 11% 33%
1	D	295	 % 50% 16% 34%
1	E	295	 57% 10% 33%

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Mol	Chain	Length	Quality of chain
1	F	295	% 51% 15% 34%
1	G	295	% 51% 16% 34%
1	H	295	2% 53% 14% 34%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 11992 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 Macrophage-expressed gene 1 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	196	Total	C	N	O	S	0	0	0
			1493	958	241	278	16			
1	B	198	Total	C	N	O	S	0	0	0
			1511	972	243	280	16			
1	C	197	Total	C	N	O	S	0	0	0
			1504	968	242	278	16			
1	D	195	Total	C	N	O	S	0	0	0
			1492	960	240	276	16			
1	E	197	Total	C	N	O	S	0	0	0
			1504	968	242	278	16			
1	F	196	Total	C	N	O	S	0	0	0
			1497	965	240	276	16			
1	G	196	Total	C	N	O	S	0	0	0
			1495	960	241	278	16			
1	H	196	Total	C	N	O	S	0	0	0
			1496	961	241	278	16			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	346	GLU	-	expression tag	UNP A1L314
A	347	THR	-	expression tag	UNP A1L314
A	348	GLY	-	expression tag	UNP A1L314
A	632	GLY	-	expression tag	UNP A1L314
A	633	THR	-	expression tag	UNP A1L314
A	634	LYS	-	expression tag	UNP A1L314
A	635	HIS	-	expression tag	UNP A1L314
A	636	HIS	-	expression tag	UNP A1L314
A	637	HIS	-	expression tag	UNP A1L314
A	638	HIS	-	expression tag	UNP A1L314
A	639	HIS	-	expression tag	UNP A1L314
A	640	HIS	-	expression tag	UNP A1L314
B	346	GLU	-	expression tag	UNP A1L314

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Chain	Residue	Modelled	Actual	Comment	Reference
B	347	THR	-	expression tag	UNP A1L314
B	348	GLY	-	expression tag	UNP A1L314
B	632	GLY	-	expression tag	UNP A1L314
B	633	THR	-	expression tag	UNP A1L314
B	634	LYS	-	expression tag	UNP A1L314
B	635	HIS	-	expression tag	UNP A1L314
B	636	HIS	-	expression tag	UNP A1L314
B	637	HIS	-	expression tag	UNP A1L314
B	638	HIS	-	expression tag	UNP A1L314
B	639	HIS	-	expression tag	UNP A1L314
B	640	HIS	-	expression tag	UNP A1L314
C	346	GLU	-	expression tag	UNP A1L314
C	347	THR	-	expression tag	UNP A1L314
C	348	GLY	-	expression tag	UNP A1L314
C	632	GLY	-	expression tag	UNP A1L314
C	633	THR	-	expression tag	UNP A1L314
C	634	LYS	-	expression tag	UNP A1L314
C	635	HIS	-	expression tag	UNP A1L314
C	636	HIS	-	expression tag	UNP A1L314
C	637	HIS	-	expression tag	UNP A1L314
C	638	HIS	-	expression tag	UNP A1L314
C	639	HIS	-	expression tag	UNP A1L314
C	640	HIS	-	expression tag	UNP A1L314
D	346	GLU	-	expression tag	UNP A1L314
D	347	THR	-	expression tag	UNP A1L314
D	348	GLY	-	expression tag	UNP A1L314
D	632	GLY	-	expression tag	UNP A1L314
D	633	THR	-	expression tag	UNP A1L314
D	634	LYS	-	expression tag	UNP A1L314
D	635	HIS	-	expression tag	UNP A1L314
D	636	HIS	-	expression tag	UNP A1L314
D	637	HIS	-	expression tag	UNP A1L314
D	638	HIS	-	expression tag	UNP A1L314
D	639	HIS	-	expression tag	UNP A1L314
D	640	HIS	-	expression tag	UNP A1L314
E	346	GLU	-	expression tag	UNP A1L314
E	347	THR	-	expression tag	UNP A1L314
E	348	GLY	-	expression tag	UNP A1L314
E	632	GLY	-	expression tag	UNP A1L314
E	633	THR	-	expression tag	UNP A1L314
E	634	LYS	-	expression tag	UNP A1L314
E	635	HIS	-	expression tag	UNP A1L314

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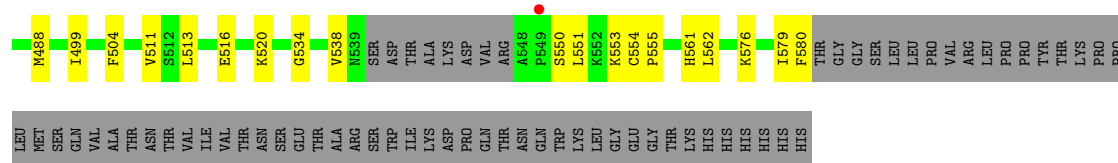
Chain	Residue	Modelled	Actual	Comment	Reference
E	636	HIS	-	expression tag	UNP A1L314
E	637	HIS	-	expression tag	UNP A1L314
E	638	HIS	-	expression tag	UNP A1L314
E	639	HIS	-	expression tag	UNP A1L314
E	640	HIS	-	expression tag	UNP A1L314
F	346	GLU	-	expression tag	UNP A1L314
F	347	THR	-	expression tag	UNP A1L314
F	348	GLY	-	expression tag	UNP A1L314
F	632	GLY	-	expression tag	UNP A1L314
F	633	THR	-	expression tag	UNP A1L314
F	634	LYS	-	expression tag	UNP A1L314
F	635	HIS	-	expression tag	UNP A1L314
F	636	HIS	-	expression tag	UNP A1L314
F	637	HIS	-	expression tag	UNP A1L314
F	638	HIS	-	expression tag	UNP A1L314
F	639	HIS	-	expression tag	UNP A1L314
F	640	HIS	-	expression tag	UNP A1L314
G	346	GLU	-	expression tag	UNP A1L314
G	347	THR	-	expression tag	UNP A1L314
G	348	GLY	-	expression tag	UNP A1L314
G	632	GLY	-	expression tag	UNP A1L314
G	633	THR	-	expression tag	UNP A1L314
G	634	LYS	-	expression tag	UNP A1L314
G	635	HIS	-	expression tag	UNP A1L314
G	636	HIS	-	expression tag	UNP A1L314
G	637	HIS	-	expression tag	UNP A1L314
G	638	HIS	-	expression tag	UNP A1L314
G	639	HIS	-	expression tag	UNP A1L314
G	640	HIS	-	expression tag	UNP A1L314
H	346	GLU	-	expression tag	UNP A1L314
H	347	THR	-	expression tag	UNP A1L314
H	348	GLY	-	expression tag	UNP A1L314
H	632	GLY	-	expression tag	UNP A1L314
H	633	THR	-	expression tag	UNP A1L314
H	634	LYS	-	expression tag	UNP A1L314
H	635	HIS	-	expression tag	UNP A1L314
H	636	HIS	-	expression tag	UNP A1L314
H	637	HIS	-	expression tag	UNP A1L314
H	638	HIS	-	expression tag	UNP A1L314
H	639	HIS	-	expression tag	UNP A1L314
H	640	HIS	-	expression tag	UNP A1L314

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.

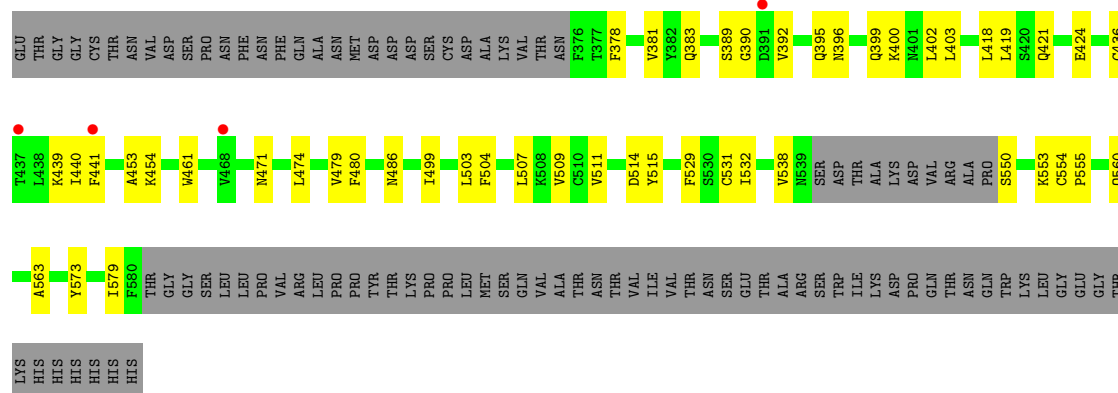
- [illegible]

- Chain B:
-
- Sequence logo for Chain B. The y-axis represents information content in bits (0.00 to 0.10). The x-axis shows positions 1 to 100. A color key at the top indicates amino acid categories: GLU (blue), THR (green), GLY (yellow), CYS (red), THR (purple), ASN (brown), VAL (pink), SER (grey), PRO (light blue), PHE (light green), ASN (light brown), PHE (light yellow), GLN (light purple), ALA (light pink), ASN (light grey), MET (light blue), ASP (light green), ASP (light yellow), SER (light purple), CYS (light brown), ASP (light pink), LYS (light grey), LYS (light blue), VAL (light green), THR (light yellow), ASN (light purple), F376 (light pink), D391 (light grey), V392 (light blue), L393 (light green), L403 (light yellow), H417 (light purple), L418 (light brown), L419 (light pink), S420 (light grey), E424 (light blue), E425 (light green), L430 (light yellow), C432 (light purple), E431 (light brown), L438 (light pink), K439 (light grey), V445 (light blue), C446 (light green), K454 (light yellow), V461 (light purple).

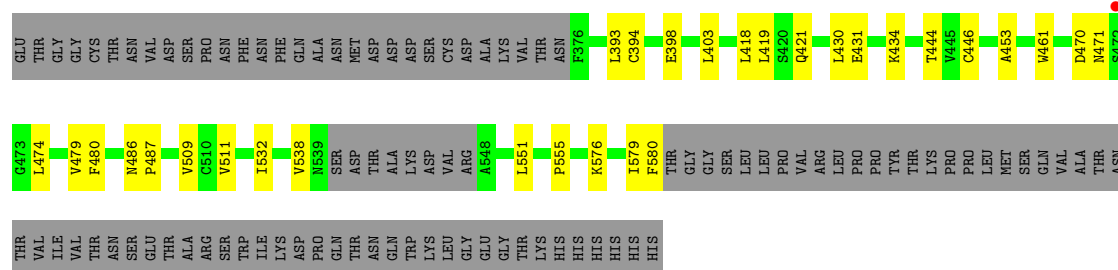
- Chain C: 
- 
- 56% 11% 33%
- GLU THR GLY CYS THR ASN VAL ASP SER PRO PHE ASN PHE GLN ALA ASP MET ASP ASP ASP CYS ASP ALA LYS VAL THR ASN F376 L388 V392 Q395 L403 L419 S420 Q421 E424 S427 S428 R429 R451 K454 F457 D470 N471 I477



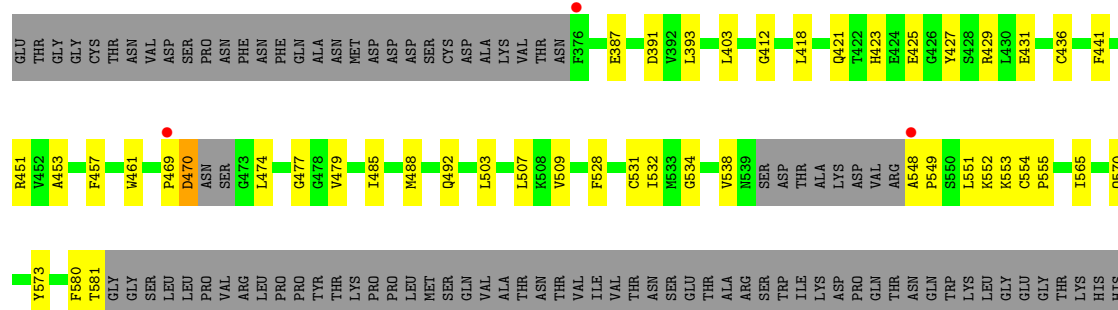
• Molecule 1: Macrophage-expressed gene 1 protein



• Molecule 1: Macrophage-expressed gene 1 protein

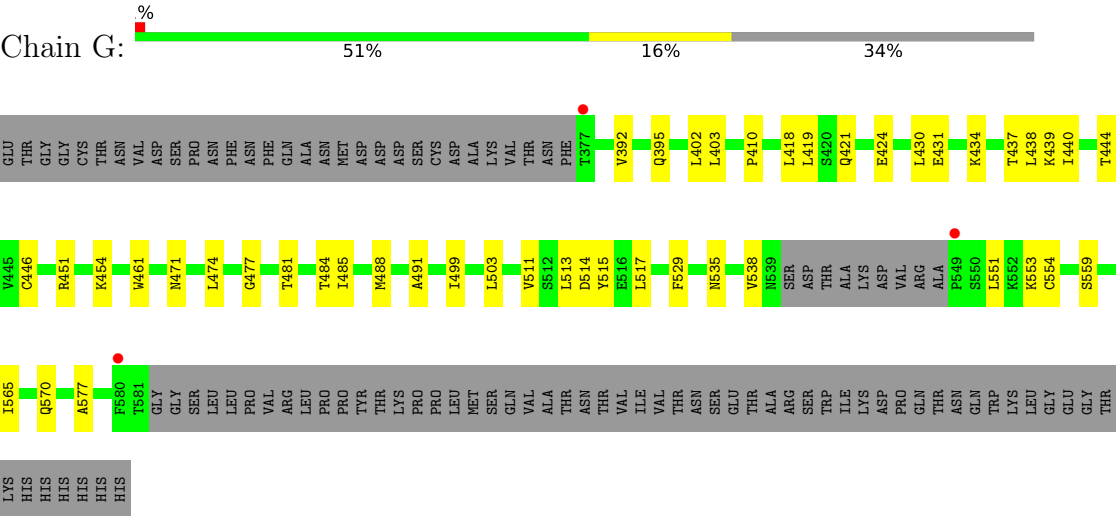


• Molecule 1: Macrophage-expressed gene 1 protein

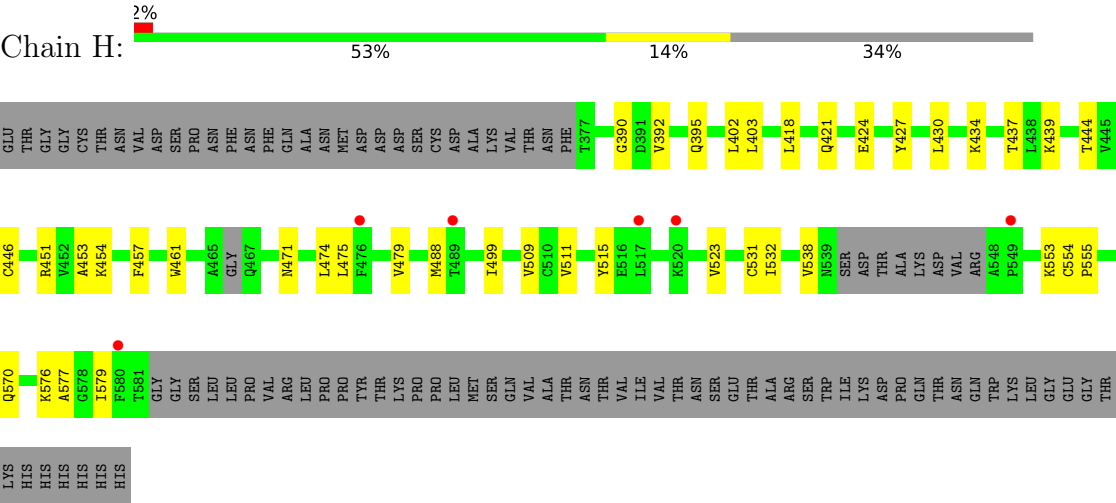


HIS
HIS
HIS

● Molecule 1: Macrophage-expressed gene 1 protein



● Molecule 1: Macrophage-expressed gene 1 protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	70.23Å 70.05Å 128.14Å 78.50° 79.05° 85.01°	Depositor
Resolution (Å)	56.09 – 3.17 56.09 – 3.17	Depositor EDS
% Data completeness (in resolution range)	95.3 (56.09-3.17) 95.4 (56.09-3.17)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 3.19Å)	Xtriage
Refinement program	PHENIX dev_3488, PHENIX dev_3488	Depositor
R, R_{free}	0.189 , 0.225 0.190 , 0.222	Depositor DCC
R_{free} test set	1976 reflections (5.20%)	wwPDB-VP
Wilson B-factor (Å ²)	72.0	Xtriage
Anisotropy	0.664	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 71.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.016 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11992	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.01% 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](#)

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	0.15	0/1528	0.44	0/2064
1	B	0.14	0/1548	0.45	0/2094
1	C	0.14	0/1541	0.44	0/2084
1	D	0.15	0/1528	0.46	0/2065
1	E	0.14	0/1541	0.46	0/2084
1	F	0.16	0/1534	0.45	0/2075
1	G	0.14	0/1531	0.45	0/2070
1	H	0.14	0/1531	0.45	0/2070
All	All	0.15	0/12282	0.45	0/16606

There are no bond length outliers.

There are no bond angle outliers.

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	1493	0	1450	28	0
1	B	1511	0	1468	29	0
1	C	1504	0	1461	24	0
1	D	1492	0	1449	31	0
1	E	1504	0	1465	20	0
1	F	1497	0	1455	29	0
1	G	1495	0	1453	32	0
1	H	1496	0	1453	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	11992	0	11654	208	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 9.

The worst 5 of 208 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:B:430:LEU:HD21	1:B:446:CYS:HB3	1.52	0.91
1:G:485:ILE:HD11	1:G:491:ALA:HA	1.54	0.88
1:C:516:GLU:O	1:C:520:LYS:NZ	2.15	0.80
1:H:427:TYR:OH	1:H:451:ARG:NH1	2.16	0.79
1:B:524:PRO:HG2	1:B:576:LYS:HD2	1.64	0.78

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	190/295 (64%)	182 (96%)	7 (4%)	1 (0%)	24	57
1	B	194/295 (66%)	189 (97%)	4 (2%)	1 (0%)	24	57
1	C	193/295 (65%)	186 (96%)	7 (4%)	0	100	100
1	D	191/295 (65%)	181 (95%)	7 (4%)	3 (2%)	7	34
1	E	193/295 (65%)	185 (96%)	8 (4%)	0	100	100
1	F	192/295 (65%)	184 (96%)	7 (4%)	1 (0%)	24	57
1	G	192/295 (65%)	182 (95%)	9 (5%)	1 (0%)	24	57
1	H	190/295 (64%)	182 (96%)	6 (3%)	2 (1%)	11	41
All	All	1535/2360 (65%)	1471 (96%)	55 (4%)	9 (1%)	21	53

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	579	ILE
1	H	390	GLY
1	G	439	LYS
1	H	577	ALA
1	A	439	LYS

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	167/255 (66%)	167 (100%)	0	100	100
1	B	169/255 (66%)	169 (100%)	0	100	100
1	C	168/255 (66%)	168 (100%)	0	100	100
1	D	167/255 (66%)	167 (100%)	0	100	100
1	E	168/255 (66%)	168 (100%)	0	100	100
1	F	167/255 (66%)	167 (100%)	0	100	100
1	G	168/255 (66%)	168 (100%)	0	100	100
1	H	168/255 (66%)	168 (100%)	0	100	100
All	All	1342/2040 (66%)	1342 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	421	GLN
1	F	423	HIS
1	H	395	GLN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å ²)	Q < 0.9
1	A	196/295 (66%)	0.01	5 (2%) 57 36	41, 72, 144, 178	0
1	B	198/295 (67%)	0.02	5 (2%) 58 37	38, 73, 167, 205	0
1	C	197/295 (66%)	-0.10	2 (1%) 79 62	44, 74, 133, 196	0
1	D	195/295 (66%)	0.13	4 (2%) 63 42	46, 88, 183, 214	0
1	E	197/295 (66%)	-0.00	1 (0%) 87 75	43, 75, 145, 192	0
1	F	196/295 (66%)	0.01	3 (1%) 72 51	48, 90, 138, 166	0
1	G	196/295 (66%)	0.01	3 (1%) 72 51	47, 85, 141, 152	0
1	H	196/295 (66%)	0.15	6 (3%) 51 31	53, 100, 149, 180	0
All	All	1571/2360 (66%)	0.03	29 (1%) 67 47	38, 83, 150, 214	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	549	PRO	3.6
1	H	549	PRO	3.3
1	C	549	PRO	3.2
1	A	469	PRO	3.2
1	H	517	LEU	2.8

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.