



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 02:46 PM UTC

PDB ID : 6J55 / pdb_00006j55
Title : Crystal structure of an iron superoxide dismutase (FeSOD) from a pathogenic *Acanthamoeba castellanii*
Authors : Lee, K.H.; Dao, T.O.; Asaithambi, K.; Na, B.K.
Deposited on : 2019-01-10
Resolution : 2.33 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

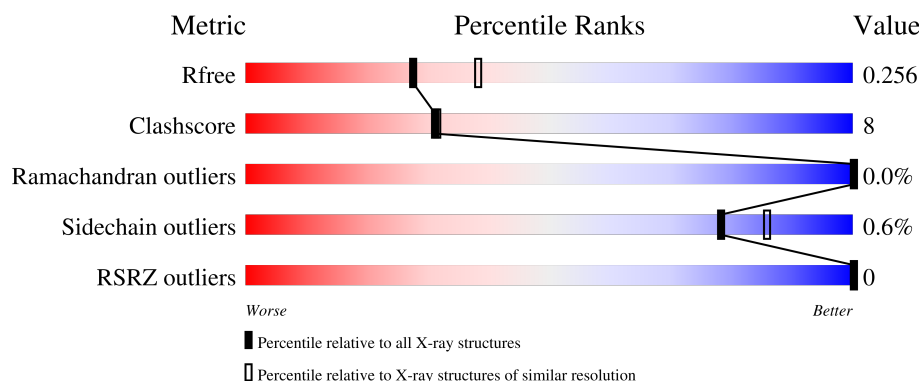
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.33 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	3031 (2.36-2.32)
Clashscore	190562	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)
RSRZ outliers	180081	3033 (2.36-2.32)

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	205	
1	B	205	
1	C	205	
1	D	205	
1	E	205	

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Mol	Chain	Length	Quality of chain
1	F	205	 81%15%.
1	G	205	 77%19%.
1	H	205	 72%24%.
1	I	205	 88%8%.
1	J	205	 71%24%.
1	K	205	 81%14%.
1	L	205	 78%21%.

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 20294 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 Superoxide dismutase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	202	Total	C	N	O	S	0	0	0
			1637	1051	278	305	3			
1	B	202	Total	C	N	O	S	0	1	0
			1643	1056	279	305	3			
1	C	202	Total	C	N	O	S	0	0	0
			1637	1051	278	305	3			
1	D	201	Total	C	N	O	S	0	0	0
			1632	1048	277	304	3			
1	E	197	Total	C	N	O	S	0	0	0
			1602	1031	269	299	3			
1	F	196	Total	C	N	O	S	0	0	0
			1594	1026	268	298	2			
1	G	196	Total	C	N	O	S	0	0	0
			1594	1026	268	298	2			
1	H	197	Total	C	N	O	S	0	0	0
			1602	1031	269	299	3			
1	I	197	Total	C	N	O	S	0	0	0
			1602	1031	269	299	3			
1	J	197	Total	C	N	O	S	0	0	0
			1602	1031	269	299	3			
1	K	197	Total	C	N	O	S	0	0	0
			1602	1031	269	299	3			
1	L	203	Total	C	N	O	S	0	0	0
			1653	1061	284	305	3			

There are 108 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	HIS	-	expression tag	UNP Q5IZD9
A	-6	HIS	-	expression tag	UNP Q5IZD9
A	-5	HIS	-	expression tag	UNP Q5IZD9
A	-4	HIS	-	expression tag	UNP Q5IZD9
A	-3	HIS	-	expression tag	UNP Q5IZD9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	HIS	-	expression tag	UNP Q5IZD9
A	-1	GLY	-	expression tag	UNP Q5IZD9
A	0	SER	-	expression tag	UNP Q5IZD9
A	34	THR	ALA	conflict	UNP Q5IZD9
B	-7	HIS	-	expression tag	UNP Q5IZD9
B	-6	HIS	-	expression tag	UNP Q5IZD9
B	-5	HIS	-	expression tag	UNP Q5IZD9
B	-4	HIS	-	expression tag	UNP Q5IZD9
B	-3	HIS	-	expression tag	UNP Q5IZD9
B	-2	HIS	-	expression tag	UNP Q5IZD9
B	-1	GLY	-	expression tag	UNP Q5IZD9
B	0	SER	-	expression tag	UNP Q5IZD9
B	34	THR	ALA	conflict	UNP Q5IZD9
C	-7	HIS	-	expression tag	UNP Q5IZD9
C	-6	HIS	-	expression tag	UNP Q5IZD9
C	-5	HIS	-	expression tag	UNP Q5IZD9
C	-4	HIS	-	expression tag	UNP Q5IZD9
C	-3	HIS	-	expression tag	UNP Q5IZD9
C	-2	HIS	-	expression tag	UNP Q5IZD9
C	-1	GLY	-	expression tag	UNP Q5IZD9
C	0	SER	-	expression tag	UNP Q5IZD9
C	34	THR	ALA	conflict	UNP Q5IZD9
D	-7	HIS	-	expression tag	UNP Q5IZD9
D	-6	HIS	-	expression tag	UNP Q5IZD9
D	-5	HIS	-	expression tag	UNP Q5IZD9
D	-4	HIS	-	expression tag	UNP Q5IZD9
D	-3	HIS	-	expression tag	UNP Q5IZD9
D	-2	HIS	-	expression tag	UNP Q5IZD9
D	-1	GLY	-	expression tag	UNP Q5IZD9
D	0	SER	-	expression tag	UNP Q5IZD9
D	34	THR	ALA	conflict	UNP Q5IZD9
E	-7	HIS	-	expression tag	UNP Q5IZD9
E	-6	HIS	-	expression tag	UNP Q5IZD9
E	-5	HIS	-	expression tag	UNP Q5IZD9
E	-4	HIS	-	expression tag	UNP Q5IZD9
E	-3	HIS	-	expression tag	UNP Q5IZD9
E	-2	HIS	-	expression tag	UNP Q5IZD9
E	-1	GLY	-	expression tag	UNP Q5IZD9
E	0	SER	-	expression tag	UNP Q5IZD9
E	34	THR	ALA	conflict	UNP Q5IZD9
F	-7	HIS	-	expression tag	UNP Q5IZD9
F	-6	HIS	-	expression tag	UNP Q5IZD9

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-5	HIS	-	expression tag	UNP Q5IZD9
F	-4	HIS	-	expression tag	UNP Q5IZD9
F	-3	HIS	-	expression tag	UNP Q5IZD9
F	-2	HIS	-	expression tag	UNP Q5IZD9
F	-1	GLY	-	expression tag	UNP Q5IZD9
F	0	SER	-	expression tag	UNP Q5IZD9
F	34	THR	ALA	conflict	UNP Q5IZD9
G	-7	HIS	-	expression tag	UNP Q5IZD9
G	-6	HIS	-	expression tag	UNP Q5IZD9
G	-5	HIS	-	expression tag	UNP Q5IZD9
G	-4	HIS	-	expression tag	UNP Q5IZD9
G	-3	HIS	-	expression tag	UNP Q5IZD9
G	-2	HIS	-	expression tag	UNP Q5IZD9
G	-1	GLY	-	expression tag	UNP Q5IZD9
G	0	SER	-	expression tag	UNP Q5IZD9
G	34	THR	ALA	conflict	UNP Q5IZD9
H	-7	HIS	-	expression tag	UNP Q5IZD9
H	-6	HIS	-	expression tag	UNP Q5IZD9
H	-5	HIS	-	expression tag	UNP Q5IZD9
H	-4	HIS	-	expression tag	UNP Q5IZD9
H	-3	HIS	-	expression tag	UNP Q5IZD9
H	-2	HIS	-	expression tag	UNP Q5IZD9
H	-1	GLY	-	expression tag	UNP Q5IZD9
H	0	SER	-	expression tag	UNP Q5IZD9
H	34	THR	ALA	conflict	UNP Q5IZD9
I	-7	HIS	-	expression tag	UNP Q5IZD9
I	-6	HIS	-	expression tag	UNP Q5IZD9
I	-5	HIS	-	expression tag	UNP Q5IZD9
I	-4	HIS	-	expression tag	UNP Q5IZD9
I	-3	HIS	-	expression tag	UNP Q5IZD9
I	-2	HIS	-	expression tag	UNP Q5IZD9
I	-1	GLY	-	expression tag	UNP Q5IZD9
I	0	SER	-	expression tag	UNP Q5IZD9
I	34	THR	ALA	conflict	UNP Q5IZD9
J	-7	HIS	-	expression tag	UNP Q5IZD9
J	-6	HIS	-	expression tag	UNP Q5IZD9
J	-5	HIS	-	expression tag	UNP Q5IZD9
J	-4	HIS	-	expression tag	UNP Q5IZD9
J	-3	HIS	-	expression tag	UNP Q5IZD9
J	-2	HIS	-	expression tag	UNP Q5IZD9
J	-1	GLY	-	expression tag	UNP Q5IZD9
J	0	SER	-	expression tag	UNP Q5IZD9

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Chain	Residue	Modelled	Actual	Comment	Reference
J	34	THR	ALA	conflict	UNP Q5IZD9
K	-7	HIS	-	expression tag	UNP Q5IZD9
K	-6	HIS	-	expression tag	UNP Q5IZD9
K	-5	HIS	-	expression tag	UNP Q5IZD9
K	-4	HIS	-	expression tag	UNP Q5IZD9
K	-3	HIS	-	expression tag	UNP Q5IZD9
K	-2	HIS	-	expression tag	UNP Q5IZD9
K	-1	GLY	-	expression tag	UNP Q5IZD9
K	0	SER	-	expression tag	UNP Q5IZD9
K	34	THR	ALA	conflict	UNP Q5IZD9
L	-7	HIS	-	expression tag	UNP Q5IZD9
L	-6	HIS	-	expression tag	UNP Q5IZD9
L	-5	HIS	-	expression tag	UNP Q5IZD9
L	-4	HIS	-	expression tag	UNP Q5IZD9
L	-3	HIS	-	expression tag	UNP Q5IZD9
L	-2	HIS	-	expression tag	UNP Q5IZD9
L	-1	GLY	-	expression tag	UNP Q5IZD9
L	0	SER	-	expression tag	UNP Q5IZD9
L	34	THR	ALA	conflict	UNP Q5IZD9

- Molecule 2 is FE (II) ION (CCD ID: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Fe 1 1	0	0
2	B	1	Total Fe 1 1	0	0
2	C	1	Total Fe 1 1	0	0
2	D	1	Total Fe 1 1	0	0
2	E	1	Total Fe 1 1	0	0
2	F	1	Total Fe 1 1	0	0
2	G	1	Total Fe 1 1	0	0
2	H	1	Total Fe 1 1	0	0
2	I	1	Total Fe 1 1	0	0
2	J	1	Total Fe 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	K	1	Total 1	Fe 1	0	0
2	L	1	Total 1	Fe 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	121	Total 121	O 121	0	0
3	B	82	Total 82	O 82	0	0
3	C	110	Total 110	O 110	0	0
3	D	108	Total 108	O 108	0	0
3	E	71	Total 71	O 71	0	0
3	F	54	Total 54	O 54	0	0
3	G	50	Total 50	O 50	0	0
3	H	62	Total 62	O 62	0	0
3	I	57	Total 57	O 57	0	0
3	J	42	Total 42	O 42	0	0
3	K	55	Total 55	O 55	0	0
3	L	70	Total 70	O 70	0	0

3 Residue-property plots

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.

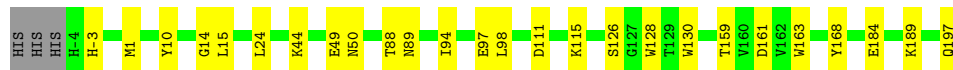
- Molecule 1: Superoxide dismutase

Chain A: 



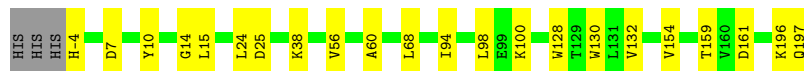
- Molecule 1: Superoxide dismutase

Chain B: 



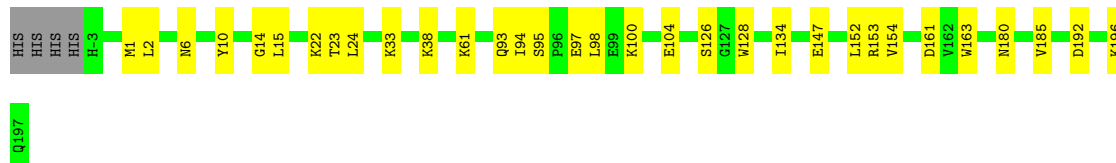
- Molecule 1: Superoxide dismutase

Chain C: 



- Molecule 1: Superoxide dismutase

Chain D: 



- Molecule 1: Superoxide dismutase

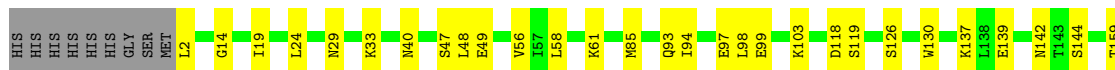
Chain E: 





- Molecule 1: Superoxide dismutase

Chain F: 81% 15% .



- Molecule 1: Superoxide dismutase

Chain G: 77% 19% .



- Molecule 1: Superoxide dismutase

Chain H: 72% 24% .



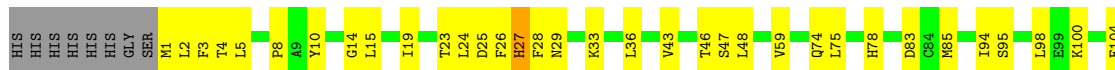
- Molecule 1: Superoxide dismutase

Chain I: 88% 8% .

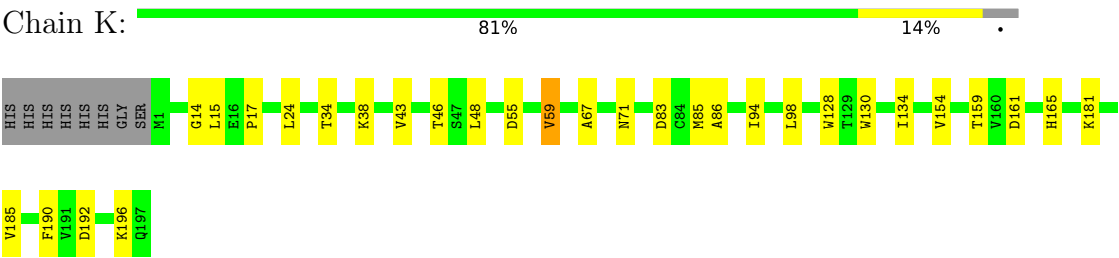


- Molecule 1: Superoxide dismutase

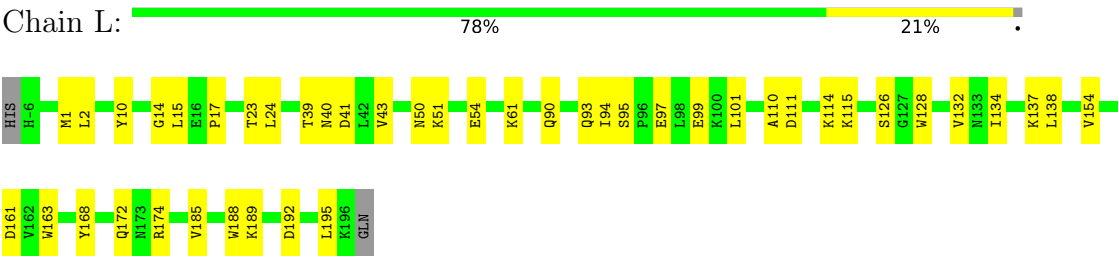
Chain J: 71% 24% .



• Molecule 1: Superoxide dismutase



• Molecule 1: Superoxide dismutase



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	127.49Å 127.49Å 327.06Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.57 – 2.33 36.57 – 2.33	Depositor EDS
% Data completeness (in resolution range)	100.0 (36.57-2.33) 100.0 (36.57-2.33)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.38 (at 2.31Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.200 , 0.248 0.209 , 0.256	Depositor DCC
R_{free} test set	6498 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	37.6	Xtriage
Anisotropy	0.183	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 30.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.228 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	20294	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.93% 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: FE2

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	0.40	0/1683	0.56	0/2292
1	B	0.41	0/1692	0.56	0/2303
1	C	0.40	0/1683	0.57	0/2292
1	D	0.38	0/1678	0.55	0/2285
1	E	0.36	0/1646	0.57	0/2242
1	F	0.36	0/1638	0.55	0/2232
1	G	0.39	1/1638 (0.1%)	0.58	0/2232
1	H	0.36	0/1646	0.58	0/2242
1	I	0.32	0/1646	0.54	0/2242
1	J	0.38	0/1646	0.57	0/2242
1	K	0.32	0/1646	0.53	0/2242
1	L	0.31	0/1702	0.53	0/2318
All	All	0.37	1/19944 (0.0%)	0.56	0/27164

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	193	GLN	CD-OE1	-5.54	1.13	1.23

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	1637	0	1585	21	0
1	B	1643	0	1598	17	0
1	C	1637	0	1585	15	0
1	D	1632	0	1583	24	0
1	E	1602	0	1561	25	0
1	F	1594	0	1549	25	0
1	G	1594	0	1549	34	0
1	H	1602	0	1561	46	0
1	I	1602	0	1561	18	0
1	J	1602	0	1561	44	0
1	K	1602	0	1561	23	0
1	L	1653	0	1596	34	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
3	A	121	0	0	6	0
3	B	82	0	0	2	0
3	C	110	0	0	5	0
3	D	108	0	0	7	0
3	E	71	0	0	3	0
3	F	54	0	0	9	0
3	G	50	0	0	7	0
3	H	62	0	0	17	0
3	I	57	0	0	0	0
3	J	42	0	0	4	0
3	K	55	0	0	1	0
3	L	70	0	0	9	0
All	All	20294	0	18850	312	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 8.

The worst 5 of 312 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:A:22:LYS:NZ	3:A:303:HOH:O	1.96	0.98
1:F:49:GLU:O	3:F:302:HOH:O	1.86	0.92
1:L:17:PRO:O	3:L:301:HOH:O	1.87	0.92
1:L:90:GLN:O	1:L:189:LYS:NZ	2.02	0.91
1:A:192:ASP:OD2	3:A:302:HOH:O	1.90	0.90

There are no symmetry-related clashes.

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	200/205 (98%)	191 (96%)	9 (4%)	0	100	100
1	B	201/205 (98%)	194 (96%)	7 (4%)	0	100	100
1	C	200/205 (98%)	193 (96%)	7 (4%)	0	100	100
1	D	199/205 (97%)	191 (96%)	8 (4%)	0	100	100
1	E	195/205 (95%)	188 (96%)	7 (4%)	0	100	100
1	F	194/205 (95%)	186 (96%)	8 (4%)	0	100	100
1	G	194/205 (95%)	188 (97%)	6 (3%)	0	100	100
1	H	195/205 (95%)	187 (96%)	7 (4%)	1 (0%)	24	26
1	I	195/205 (95%)	186 (95%)	9 (5%)	0	100	100
1	J	195/205 (95%)	187 (96%)	8 (4%)	0	100	100
1	K	195/205 (95%)	187 (96%)	8 (4%)	0	100	100
1	L	201/205 (98%)	194 (96%)	7 (4%)	0	100	100
All	All	2364/2460 (96%)	2272 (96%)	91 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	50	ASN

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	179/183 (98%)	177 (99%)	2 (1%)	65	77
1	B	180/183 (98%)	179 (99%)	1 (1%)	78	86
1	C	179/183 (98%)	178 (99%)	1 (1%)	78	86
1	D	179/183 (98%)	178 (99%)	1 (1%)	78	86
1	E	176/183 (96%)	176 (100%)	0	100	100
1	F	175/183 (96%)	175 (100%)	0	100	100
1	G	175/183 (96%)	175 (100%)	0	100	100
1	H	176/183 (96%)	173 (98%)	3 (2%)	53	66
1	I	176/183 (96%)	175 (99%)	1 (1%)	78	86
1	J	176/183 (96%)	175 (99%)	1 (1%)	78	86
1	K	176/183 (96%)	175 (99%)	1 (1%)	78	86
1	L	181/183 (99%)	180 (99%)	1 (1%)	78	86
All	All	2128/2196 (97%)	2116 (99%)	12 (1%)	78	86

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	38	LYS
1	I	13	THR
1	L	23	THR
1	J	27	HIS
1	C	38	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	90	GLN
1	I	172	GLN
1	L	194	GLN
1	K	197	GLN
1	L	50	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

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 [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	202/205 (98%)	-1.46	0 100 100	21, 31, 54, 69	0
1	B	202/205 (98%)	-1.40	0 100 100	21, 34, 59, 74	1 (0%)
1	C	202/205 (98%)	-1.49	0 100 100	21, 31, 49, 77	0
1	D	201/205 (98%)	-1.48	0 100 100	20, 32, 52, 63	0
1	E	197/205 (96%)	-1.37	0 100 100	27, 39, 56, 84	0
1	F	196/205 (95%)	-1.34	0 100 100	29, 40, 55, 72	0
1	G	196/205 (95%)	-1.27	0 100 100	28, 44, 61, 85	0
1	H	197/205 (96%)	-1.25	0 100 100	31, 44, 64, 83	0
1	I	197/205 (96%)	-1.26	0 100 100	33, 46, 59, 65	0
1	J	197/205 (96%)	-0.98	0 100 100	39, 59, 88, 99	0
1	K	197/205 (96%)	-1.29	0 100 100	33, 45, 63, 90	0
1	L	203/205 (99%)	-1.25	0 100 100	35, 48, 66, 82	0
All	All	2387/2460 (97%)	-1.32	0 100 100	20, 41, 66, 99	1 (0%)

There are no RSRZ outliers to report.

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	FE2	A	201	1/1	1.00	0.01	23,23,23,23	0
2	FE2	B	201	1/1	1.00	0.01	27,27,27,27	0
2	FE2	C	201	1/1	1.00	0.01	24,24,24,24	0
2	FE2	D	201	1/1	1.00	0.01	26,26,26,26	0
2	FE2	E	201	1/1	1.00	0.01	30,30,30,30	0
2	FE2	F	201	1/1	1.00	0.01	32,32,32,32	0
2	FE2	G	201	1/1	1.00	0.01	37,37,37,37	0
2	FE2	H	201	1/1	1.00	0.02	38,38,38,38	0
2	FE2	I	201	1/1	1.00	0.01	40,40,40,40	0
2	FE2	J	201	1/1	1.00	0.01	51,51,51,51	0
2	FE2	K	201	1/1	1.00	0.01	40,40,40,40	0
2	FE2	L	201	1/1	1.00	0.01	40,40,40,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.