



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 04:29 AM UTC

PDB ID : 8PP3 / pdb_00008pp3
Title : Binary crystal structure of positively supercharged ferritin variant Ftn(pos) and crystal contact tuned negatively supercharged ferritin variant Ftn(neg)-m1 (Mg formate condition)
Authors : Lang, L.; Beck, T.
Deposited on : 2023-07-06
Resolution : 1.55 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
Mogul : 2022.3.0, CSD as543be (2022)
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

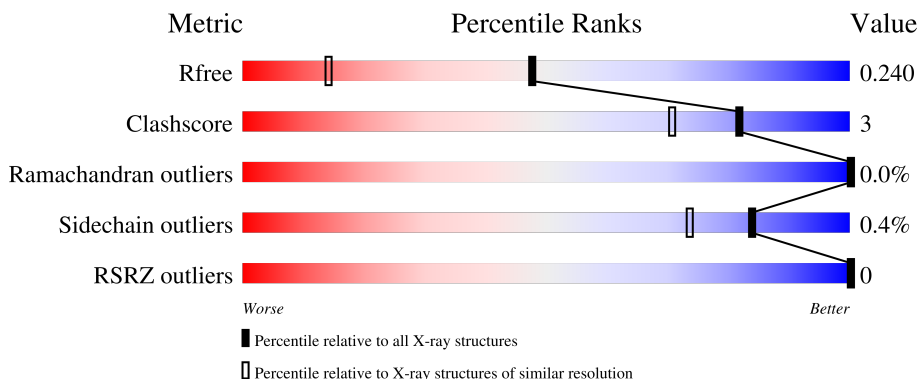
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.55 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	2145 (1.56-1.56)
Clashscore	190562	2189 (1.56-1.56)
Ramachandran outliers	187476	2153 (1.56-1.56)
Sidechain outliers	187428	2150 (1.56-1.56)
RSRZ outliers	180081	2146 (1.56-1.56)

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	183	
1	B	183	
1	C	183	
1	D	183	
1	E	183	

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Mol	Chain	Length	Quality of chain
1	F	183	 91% 6%
2	G	183	 85% 9% 6%
2	H	183	 87% 7% 6%
2	I	183	 87% 7% 6%
2	J	183	 91% 6%
2	K	183	 89% 5% 6%
2	L	183	 86% 8% 6%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 35092 atoms, of which 16884 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 Ferritin heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	172	2861	903	1429	258	266	5	42	0	0
1	B	172	2909	915	1455	266	268	5	42	1	0
1	C	172	2883	909	1442	260	267	5	42	1	0
1	D	172	2897	914	1448	261	269	5	42	2	0
1	E	172	2861	903	1429	258	266	5	42	0	0
1	F	172	2910	919	1452	261	273	5	42	3	0

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	18	LYS	ALA	engineered mutation	UNP P02794
A	25	ARG	ASN	engineered mutation	UNP P02794
A	86	GLN	LYS	engineered mutation	UNP P02794
A	90	LYS	CYS	engineered mutation	UNP P02794
A	98	ARG	ASN	engineered mutation	UNP P02794
A	102	LYS	CYS	engineered mutation	UNP P02794
A	105	LYS	HIS	engineered mutation	UNP P02794
A	109	LYS	ASN	engineered mutation	UNP P02794
A	123	LYS	ASP	engineered mutation	UNP P02794
A	162	ARG	GLU	engineered mutation	UNP P02794
B	18	LYS	ALA	engineered mutation	UNP P02794
B	25	ARG	ASN	engineered mutation	UNP P02794
B	86	GLN	LYS	engineered mutation	UNP P02794
B	90	LYS	CYS	engineered mutation	UNP P02794
B	98	ARG	ASN	engineered mutation	UNP P02794
B	102	LYS	CYS	engineered mutation	UNP P02794
B	105	LYS	HIS	engineered mutation	UNP P02794

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Chain	Residue	Modelled	Actual	Comment	Reference
B	109	LYS	ASN	engineered mutation	UNP P02794
B	123	LYS	ASP	engineered mutation	UNP P02794
B	162	ARG	GLU	engineered mutation	UNP P02794
C	18	LYS	ALA	engineered mutation	UNP P02794
C	25	ARG	ASN	engineered mutation	UNP P02794
C	86	GLN	LYS	engineered mutation	UNP P02794
C	90	LYS	CYS	engineered mutation	UNP P02794
C	98	ARG	ASN	engineered mutation	UNP P02794
C	102	LYS	CYS	engineered mutation	UNP P02794
C	105	LYS	HIS	engineered mutation	UNP P02794
C	109	LYS	ASN	engineered mutation	UNP P02794
C	123	LYS	ASP	engineered mutation	UNP P02794
C	162	ARG	GLU	engineered mutation	UNP P02794
D	18	LYS	ALA	engineered mutation	UNP P02794
D	25	ARG	ASN	engineered mutation	UNP P02794
D	86	GLN	LYS	engineered mutation	UNP P02794
D	90	LYS	CYS	engineered mutation	UNP P02794
D	98	ARG	ASN	engineered mutation	UNP P02794
D	102	LYS	CYS	engineered mutation	UNP P02794
D	105	LYS	HIS	engineered mutation	UNP P02794
D	109	LYS	ASN	engineered mutation	UNP P02794
D	123	LYS	ASP	engineered mutation	UNP P02794
D	162	ARG	GLU	engineered mutation	UNP P02794
E	18	LYS	ALA	engineered mutation	UNP P02794
E	25	ARG	ASN	engineered mutation	UNP P02794
E	86	GLN	LYS	engineered mutation	UNP P02794
E	90	LYS	CYS	engineered mutation	UNP P02794
E	98	ARG	ASN	engineered mutation	UNP P02794
E	102	LYS	CYS	engineered mutation	UNP P02794
E	105	LYS	HIS	engineered mutation	UNP P02794
E	109	LYS	ASN	engineered mutation	UNP P02794
E	123	LYS	ASP	engineered mutation	UNP P02794
E	162	ARG	GLU	engineered mutation	UNP P02794
F	18	LYS	ALA	engineered mutation	UNP P02794
F	25	ARG	ASN	engineered mutation	UNP P02794
F	86	GLN	LYS	engineered mutation	UNP P02794
F	90	LYS	CYS	engineered mutation	UNP P02794
F	98	ARG	ASN	engineered mutation	UNP P02794
F	102	LYS	CYS	engineered mutation	UNP P02794
F	105	LYS	HIS	engineered mutation	UNP P02794
F	109	LYS	ASN	engineered mutation	UNP P02794
F	123	LYS	ASP	engineered mutation	UNP P02794

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Chain	Residue	Modelled	Actual	Comment	Reference
F	162	ARG	GLU	engineered mutation	UNP P02794

- Molecule 2 is a protein called Ferritin heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
2	G	172	Total	C	H	N	O	S	42	1	0
			2796	893	1369	247	282	5			
2	H	172	Total	C	H	N	O	S	42	1	0
			2805	894	1376	250	280	5			
2	I	172	Total	C	H	N	O	S	42	0	0
			2781	888	1363	246	279	5			
2	J	172	Total	C	H	N	O	S	42	0	0
			2781	888	1363	246	279	5			
2	K	172	Total	C	H	N	O	S	42	0	0
			2781	888	1363	246	279	5			
2	L	172	Total	C	H	N	O	S	42	0	0
			2781	888	1363	246	279	5			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	86	GLN	LYS	engineered mutation	UNP P02794
G	90	GLU	CYS	engineered mutation	UNP P02794
G	102	GLU	CYS	engineered mutation	UNP P02794
G	105	GLU	HIS	engineered mutation	UNP P02794
H	86	GLN	LYS	engineered mutation	UNP P02794
H	90	GLU	CYS	engineered mutation	UNP P02794
H	102	GLU	CYS	engineered mutation	UNP P02794
H	105	GLU	HIS	engineered mutation	UNP P02794
I	86	GLN	LYS	engineered mutation	UNP P02794
I	90	GLU	CYS	engineered mutation	UNP P02794
I	102	GLU	CYS	engineered mutation	UNP P02794
I	105	GLU	HIS	engineered mutation	UNP P02794
J	86	GLN	LYS	engineered mutation	UNP P02794
J	90	GLU	CYS	engineered mutation	UNP P02794
J	102	GLU	CYS	engineered mutation	UNP P02794
J	105	GLU	HIS	engineered mutation	UNP P02794
K	86	GLN	LYS	engineered mutation	UNP P02794
K	90	GLU	CYS	engineered mutation	UNP P02794
K	102	GLU	CYS	engineered mutation	UNP P02794
K	105	GLU	HIS	engineered mutation	UNP P02794
L	86	GLN	LYS	engineered mutation	UNP P02794

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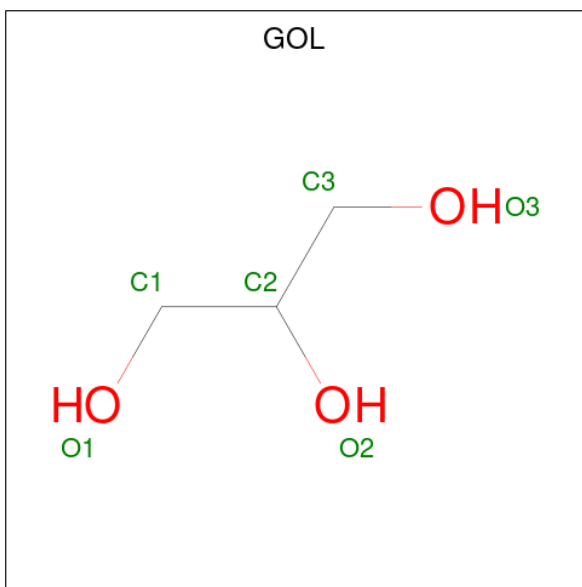
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Chain	Residue	Modelled	Actual	Comment	Reference
L	90	GLU	CYS	engineered mutation	UNP P02794
L	102	GLU	CYS	engineered mutation	UNP P02794
L	105	GLU	HIS	engineered mutation	UNP P02794

- Molecule 3 is FE (III) ION (CCD ID: FE) (formula: Fe).

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

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	H	O	2	0
			14	3	8	3		
4	D	1	Total	C	H	O	2	0
			14	3	8	3		
4	F	1	Total	C	H	O	2	0
			14	3	8	3		
4	F	1	Total	C	H	O	2	0
			14	3	8	3		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	1	Total	Mg	0	0
			1	1		
5	J	1	Total	Mg	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	97	Total	O	0	0
			97	97		
6	B	97	Total	O	0	0
			97	97		
6	C	104	Total	O	0	0
			104	104		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	112	Total 112	O 112	0	0
6	E	113	Total 113	O 113	0	0
6	F	98	Total 98	O 98	0	0
6	G	58	Total 58	O 58	0	0
6	H	67	Total 67	O 67	0	0
6	I	51	Total 51	O 51	0	0
6	J	73	Total 73	O 73	0	0
6	K	44	Total 44	O 44	0	0
6	L	62	Total 62	O 62	0	0

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: Ferritin heavy chain

Chain A:  90% 6%



- Molecule 1: Ferritin heavy chain

Chain B:  86% 8% 6%



- Molecule 1: Ferritin heavy chain

Chain C:  92% 6%




- Molecule 1: Ferritin heavy chain

Chain D:  88% 6% 6%




- Molecule 1: Ferritin heavy chain

Chain E:  87% 7% 6%

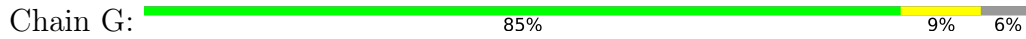


- Molecule 1: Ferritin heavy chain

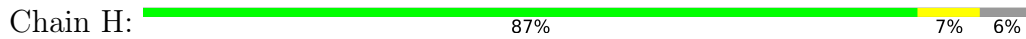
Chain F:  91% 6%



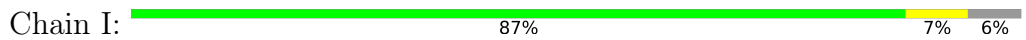
- Molecule 2: Ferritin heavy chain



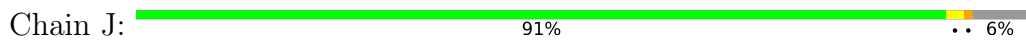
- Molecule 2: Ferritin heavy chain



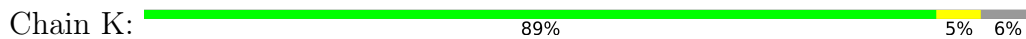
- Molecule 2: Ferritin heavy chain



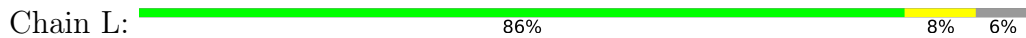
- Molecule 2: Ferritin heavy chain



- Molecule 2: Ferritin heavy chain



- Molecule 2: Ferritin heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 4	Depositor
Cell constants a, b, c, α , β , γ	127.01Å 127.01Å 175.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.77 – 1.55 59.77 – 1.55	Depositor EDS
% Data completeness (in resolution range)	97.7 (59.77-1.55) 97.5 (59.77-1.55)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.05 (at 1.55Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.218 , 0.241 0.218 , 0.240	Depositor DCC
R_{free} test set	16135 reflections (4.12%)	wwPDB-VP
Wilson B-factor (Å ²)	22.6	Xtrriage
Anisotropy	0.233	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 25.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtrriage
Estimated twinning fraction	0.216 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	35092	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.18% 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: FE, MG, GOL

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	1.05	1/1460 (0.1%)	1.29	0/1957
1	B	1.07	1/1482 (0.1%)	1.28	0/1985
1	C	1.09	0/1469	1.28	0/1968
1	D	1.00	0/1477	1.28	0/1980
1	E	1.09	0/1460	1.28	0/1957
1	F	1.04	0/1486	1.25	0/1992
2	G	1.05	0/1455	1.39	0/1960
2	H	1.06	0/1457	1.35	2/1962 (0.1%)
2	I	1.06	0/1446	1.43	2/1948 (0.1%)
2	J	1.07	0/1446	1.36	0/1948
2	K	1.05	0/1446	1.45	3/1948 (0.2%)
2	L	1.07	0/1446	1.36	1/1948 (0.1%)
All	All	1.06	2/17530 (0.0%)	1.33	8/23553 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	E	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	118	HIS	CE1-NE2	5.93	1.38	1.32
1	B	118	HIS	CE1-NE2	5.39	1.38	1.32

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	150	ASP	CA-CB-CG	5.44	118.04	112.60
2	L	91	ASP	N-CA-C	-5.22	107.04	113.41
2	K	36	SER	CA-C-N	5.21	127.21	120.44
2	K	36	SER	C-N-CA	5.21	127.21	120.44
2	H	164	GLY	CA-C-N	5.17	127.16	120.44

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	163	SER	Peptide

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	1432	1429	1419	6	0
1	B	1454	1455	1444	11	0
1	C	1441	1442	1431	3	1
1	D	1449	1448	1437	11	0
1	E	1432	1429	1419	8	0
1	F	1458	1452	1439	9	0
2	G	1427	1369	1358	11	0
2	H	1429	1376	1365	14	0
2	I	1418	1363	1353	16	0
2	J	1418	1363	1353	5	0
2	K	1418	1363	1353	6	0
2	L	1418	1363	1353	10	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
3	I	1	0	0	0	0
3	J	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	1	0	0	0	0
3	L	1	0	0	0	0
4	B	6	8	8	0	0
4	D	6	8	8	0	0
4	F	12	16	16	0	1
5	H	1	0	0	0	0
5	J	1	0	0	0	0
6	A	97	0	0	2	0
6	B	97	0	0	0	0
6	C	104	0	0	1	0
6	D	112	0	0	2	0
6	E	113	0	0	1	0
6	F	98	0	0	1	0
6	G	58	0	0	2	0
6	H	67	0	0	2	0
6	I	51	0	0	0	0
6	J	73	0	0	0	0
6	K	44	0	0	0	0
6	L	62	0	0	2	0
All	All	18208	16884	16756	86	1

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 3.

The worst 5 of 86 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)
2:G:163:SER:O	6:G:301:HOH:O	1.68	1.10
2:H:174:THR:HG23	2:I:168:TYR:OH	1.72	0.89
2:H:153:THR:HG21	2:I:44:ASP:O	1.74	0.87
1:A:86:GLN:OE1	2:G:22:ARG:HD3	1.75	0.87
2:J:60:HIS:O	2:J:63:ARG:HG3	1.76	0.84

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:71:LYS:HZ3	4:F:201:GOL:HO2[3_755]	1.31	0.29

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	170/183 (93%)	167 (98%)	3 (2%)	0	100	100
1	B	172/183 (94%)	169 (98%)	3 (2%)	0	100	100
1	C	171/183 (93%)	167 (98%)	4 (2%)	0	100	100
1	D	172/183 (94%)	169 (98%)	3 (2%)	0	100	100
1	E	170/183 (93%)	166 (98%)	3 (2%)	1 (1%)	21	6
1	F	173/183 (94%)	171 (99%)	2 (1%)	0	100	100
2	G	171/183 (93%)	168 (98%)	3 (2%)	0	100	100
2	H	171/183 (93%)	168 (98%)	3 (2%)	0	100	100
2	I	170/183 (93%)	168 (99%)	2 (1%)	0	100	100
2	J	170/183 (93%)	166 (98%)	4 (2%)	0	100	100
2	K	170/183 (93%)	167 (98%)	3 (2%)	0	100	100
2	L	170/183 (93%)	167 (98%)	3 (2%)	0	100	100
All	All	2050/2196 (93%)	2013 (98%)	36 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	165	LEU

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	154/164 (94%)	154 (100%)	0	100	100
1	B	156/164 (95%)	156 (100%)	0	100	100
1	C	155/164 (94%)	155 (100%)	0	100	100
1	D	156/164 (95%)	154 (99%)	2 (1%)	61	36
1	E	154/164 (94%)	153 (99%)	1 (1%)	78	64
1	F	157/164 (96%)	156 (99%)	1 (1%)	78	64
2	G	154/163 (94%)	153 (99%)	1 (1%)	78	64
2	H	154/163 (94%)	153 (99%)	1 (1%)	78	64
2	I	153/163 (94%)	153 (100%)	0	100	100
2	J	153/163 (94%)	152 (99%)	1 (1%)	76	59
2	K	153/163 (94%)	153 (100%)	0	100	100
2	L	153/163 (94%)	152 (99%)	1 (1%)	76	59
All	All	1852/1962 (94%)	1844 (100%)	8 (0%)	84	73

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	L	49	LYS
2	J	63	ARG
2	G	61	GLU
1	F	114	LEU
2	H	162	GLU

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

Mol	Chain	Res	Type
2	H	112	GLN
2	I	50	ASN
2	L	50	ASN
2	J	173	HIS
2	L	7	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 14 are monoatomic - leaving 4 for Mogul analysis.

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	$\# Z > 2$
4	GOL	B	201	-	5,5,5	0.15	0	5,5,5	0.49	0
4	GOL	F	202	-	5,5,5	0.23	0	5,5,5	0.34	0
4	GOL	D	201	-	5,5,5	0.23	0	5,5,5	0.50	0
4	GOL	F	201	-	5,5,5	0.18	0	5,5,5	0.46	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
4	GOL	B	201	-	-	2/4/4/4	-
4	GOL	F	202	-	-	0/4/4/4	-
4	GOL	D	201	-	-	1/4/4/4	-
4	GOL	F	201	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	201	GOL	C1-C2-C3-O3
4	B	201	GOL	O2-C2-C3-O3
4	D	201	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	201	GOL	0	1

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	172/183 (93%)	-1.19	0 100 100	16, 21, 33, 59	0
1	B	172/183 (93%)	-1.17	0 100 100	8, 21, 34, 58	1 (0%)
1	C	172/183 (93%)	-1.23	0 100 100	11, 20, 34, 54	1 (0%)
1	D	172/183 (93%)	-1.18	0 100 100	10, 20, 32, 70	2 (1%)
1	E	172/183 (93%)	-1.20	0 100 100	16, 20, 35, 73	0
1	F	172/183 (93%)	-1.17	0 100 100	9, 20, 34, 58	3 (1%)
2	G	172/183 (93%)	-0.94	0 100 100	17, 29, 40, 46	1 (0%)
2	H	172/183 (93%)	-1.02	0 100 100	15, 26, 39, 57	1 (0%)
2	I	172/183 (93%)	-1.02	0 100 100	20, 27, 36, 44	0
2	J	172/183 (93%)	-1.03	0 100 100	20, 26, 36, 42	0
2	K	172/183 (93%)	-0.87	0 100 100	24, 30, 42, 56	0
2	L	172/183 (93%)	-0.97	0 100 100	22, 28, 40, 54	0
All	All	2064/2196 (93%)	-1.08	0 100 100	8, 25, 38, 73	9 (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
4	GOL	B	201	6/6	0.99	0.04	31,36,38,38	2
4	GOL	D	201	6/6	0.99	0.04	28,30,32,32	2
4	GOL	F	201	6/6	0.99	0.04	30,32,34,34	2
4	GOL	F	202	6/6	0.99	0.04	27,29,32,32	2
5	MG	J	202	1/1	0.99	0.02	31,31,31,31	0
3	FE	F	203	1/1	1.00	0.02	24,24,24,24	0
3	FE	G	201	1/1	1.00	0.02	33,33,33,33	0
3	FE	H	201	1/1	1.00	0.03	30,30,30,30	0
3	FE	I	201	1/1	1.00	0.02	29,29,29,29	0
3	FE	J	201	1/1	1.00	0.03	31,31,31,31	0
3	FE	K	201	1/1	1.00	0.03	37,37,37,37	0
3	FE	L	201	1/1	1.00	0.03	31,31,31,31	0
3	FE	A	201	1/1	1.00	0.02	25,25,25,25	0
3	FE	B	202	1/1	1.00	0.03	24,24,24,24	0
3	FE	C	201	1/1	1.00	0.02	23,23,23,23	0
3	FE	D	202	1/1	1.00	0.02	24,24,24,24	0
5	MG	H	202	1/1	1.00	0.01	27,27,27,27	0
3	FE	E	201	1/1	1.00	0.03	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.