



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 12:13 AM UTC

PDB ID : 8CPX / pdb_00008cpx
EMDB ID : EMD-16789
Title : Human apoferritin after 488 nm laser exposure in presence of rsEGFP2
Authors : Last, M.G.F.; Noteborn, W.E.M.; Sharp, T.H.
Deposited on : 2023-03-03
Resolution : 1.76 Å(reported)
Based on initial model : 6Z6U

This is a wwPDB EM 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/EMValidationReportHelp>
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:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

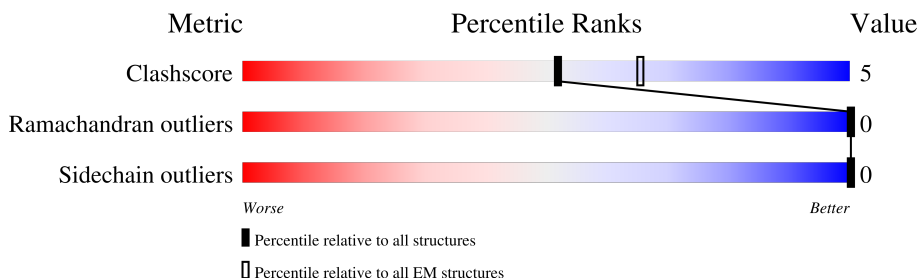
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 1.76 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)	EM structures (#Entries)
Clashscore	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	1	173	88% 12%
1	2	173	90% 10%
1	4	173	90% 10%
1	6	173	89% 11%
1	A	173	90% 10%
1	B	173	89% 11%
1	E	173	88% 12%
1	F	173	90% 10%
1	G	173	90% 10%

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Mol	Chain	Length	Quality of chain	
1	H	173		89% 11%
1	I	173		90% 10%
1	K	173		88% 12%
1	M	173		89% 11%
1	O	173		89% 11%
1	P	173		89% 11%
1	Q	173		90% 10%
1	S	173		90% 10%
1	U	173		90% 10%
1	W	173		88% 12%
1	X	173		90% 10%
1	Y	173		89% 11%
1	a	173		89% 11%
1	e	173		90% 10%
1	r	173		88% 12%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 35827 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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, N-terminally processed.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	2	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	4	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	6	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	A	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	B	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	E	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	F	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	G	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	H	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	I	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	K	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	M	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	O	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	P	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	Q	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	S	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	U	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	W	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	X	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	Y	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	a	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	e	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		
1	r	173	Total	C	N	O	S	0	0
			1420	888	249	276	7		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	86	GLN	LYS	engineered mutation	UNP P02794
2	86	GLN	LYS	engineered mutation	UNP P02794
4	86	GLN	LYS	engineered mutation	UNP P02794
6	86	GLN	LYS	engineered mutation	UNP P02794
A	86	GLN	LYS	engineered mutation	UNP P02794
B	86	GLN	LYS	engineered mutation	UNP P02794
E	86	GLN	LYS	engineered mutation	UNP P02794
F	86	GLN	LYS	engineered mutation	UNP P02794
G	86	GLN	LYS	engineered mutation	UNP P02794
H	86	GLN	LYS	engineered mutation	UNP P02794
I	86	GLN	LYS	engineered mutation	UNP P02794
K	86	GLN	LYS	engineered mutation	UNP P02794
M	86	GLN	LYS	engineered mutation	UNP P02794
O	86	GLN	LYS	engineered mutation	UNP P02794
P	86	GLN	LYS	engineered mutation	UNP P02794
Q	86	GLN	LYS	engineered mutation	UNP P02794
S	86	GLN	LYS	engineered mutation	UNP P02794
U	86	GLN	LYS	engineered mutation	UNP P02794
W	86	GLN	LYS	engineered mutation	UNP P02794
X	86	GLN	LYS	engineered mutation	UNP P02794
Y	86	GLN	LYS	engineered mutation	UNP P02794
a	86	GLN	LYS	engineered mutation	UNP P02794
e	86	GLN	LYS	engineered mutation	UNP P02794
r	86	GLN	LYS	engineered mutation	UNP P02794

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
2	1	1	Total 1	Na 1	0
2	2	1	Total 1	Na 1	0
2	4	1	Total 1	Na 1	0
2	6	1	Total 1	Na 1	0
2	A	1	Total 1	Na 1	0
2	B	1	Total 1	Na 1	0
2	E	1	Total 1	Na 1	0
2	F	1	Total 1	Na 1	0
2	G	1	Total 1	Na 1	0
2	H	1	Total 1	Na 1	0
2	I	1	Total 1	Na 1	0
2	K	1	Total 1	Na 1	0
2	M	1	Total 1	Na 1	0
2	O	1	Total 1	Na 1	0
2	P	1	Total 1	Na 1	0
2	Q	1	Total 1	Na 1	0
2	S	1	Total 1	Na 1	0
2	U	1	Total 1	Na 1	0
2	W	1	Total 1	Na 1	0
2	X	1	Total 1	Na 1	0
2	Y	1	Total 1	Na 1	0

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Mol	Chain	Residues	Atoms		AltConf
2	a	1	Total 1	Na 1	0
2	e	1	Total 1	Na 1	0
2	r	1	Total 1	Na 1	0

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
3	1	2	Total 2	Mg 2	0
3	2	2	Total 2	Mg 2	0
3	4	1	Total 1	Mg 1	0
3	6	2	Total 2	Mg 2	0
3	A	1	Total 1	Mg 1	0
3	B	1	Total 1	Mg 1	0
3	G	1	Total 1	Mg 1	0
3	H	2	Total 2	Mg 2	0
3	M	1	Total 1	Mg 1	0
3	O	1	Total 1	Mg 1	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		AltConf
4	1	70	Total 70	O 70	0
4	2	71	Total 71	O 71	0
4	4	71	Total 71	O 71	0
4	6	70	Total 70	O 70	0

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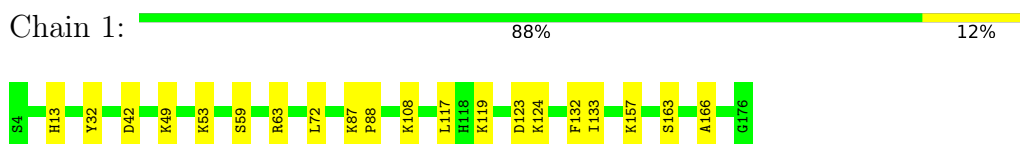
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Mol	Chain	Residues	Atoms		AltConf
4	A	72	Total 72	O 72	0
4	B	70	Total 70	O 70	0
4	E	72	Total 72	O 72	0
4	F	71	Total 71	O 71	0
4	G	71	Total 71	O 71	0
4	H	72	Total 72	O 72	0
4	I	70	Total 70	O 70	0
4	K	70	Total 70	O 70	0
4	M	72	Total 72	O 72	0
4	O	72	Total 72	O 72	0
4	P	73	Total 73	O 73	0
4	Q	70	Total 70	O 70	0
4	S	71	Total 71	O 71	0
4	U	73	Total 73	O 73	0
4	W	71	Total 71	O 71	0
4	X	72	Total 72	O 72	0
4	Y	73	Total 73	O 73	0
4	a	70	Total 70	O 70	0
4	e	71	Total 71	O 71	0
4	r	71	Total 71	O 71	0

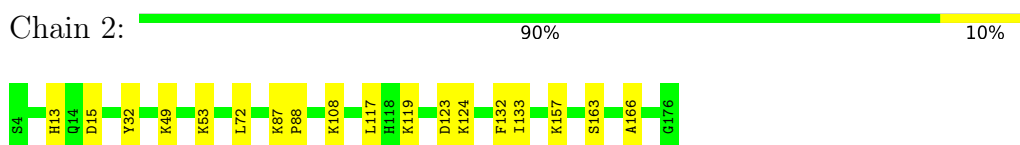
3 Residue-property plots [i](#)

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. 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. 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.

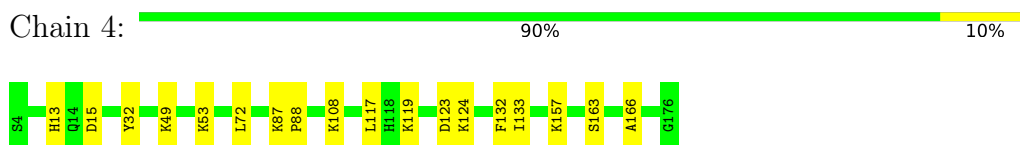
- Molecule 1: Ferritin heavy chain, N-terminally processed



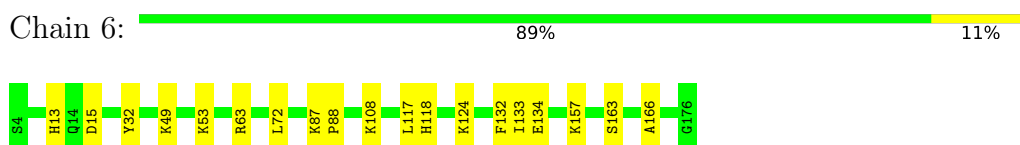
- Molecule 1: Ferritin heavy chain, N-terminally processed



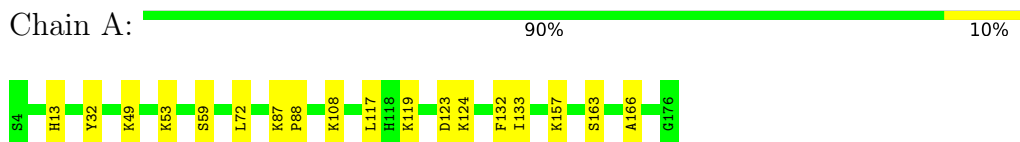
- Molecule 1: Ferritin heavy chain, N-terminally processed



- Molecule 1: Ferritin heavy chain, N-terminally processed



- Molecule 1: Ferritin heavy chain, N-terminally processed



- Molecule 1: Ferritin heavy chain, N-terminally processed





- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain E: 88% 12%



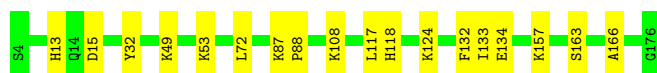
- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain F: 90% 10%



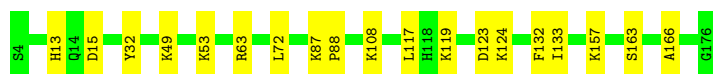
- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain G: 90% 10%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain H: 89% 11%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain I: 90% 10%



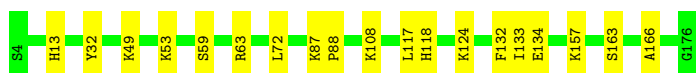
- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain K: 88% 12%



- Molecule 1: Ferritin heavy chain, N-terminally processed

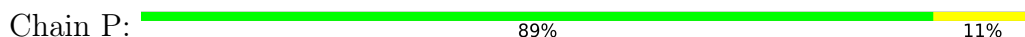
Chain M: 89% 11%



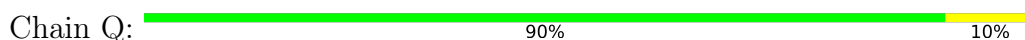
- Molecule 1: Ferritin heavy chain, N-terminally processed



- Molecule 1: Ferritin heavy chain, N-terminally processed



- Molecule 1: Ferritin heavy chain, N-terminally processed



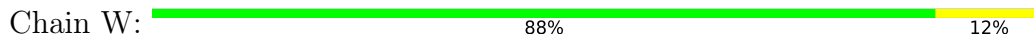
- Molecule 1: Ferritin heavy chain, N-terminally processed



- Molecule 1: Ferritin heavy chain, N-terminally processed

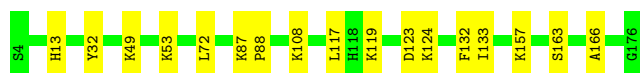


- Molecule 1: Ferritin heavy chain, N-terminally processed



- Molecule 1: Ferritin heavy chain, N-terminally processed





- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain Y: 89% 11%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain a: 89% 11%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain e: 90% 10%



- Molecule 1: Ferritin heavy chain, N-terminally processed

Chain r: 88% 12%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	97000	Depositor
Resolution determination method	DIFFRACTION PATTERN/LAYERLINES	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor

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: CSX, MG, NA

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	1	0.23	0/1441	0.47	0/1940
1	2	0.22	0/1441	0.47	0/1940
1	4	0.22	0/1441	0.47	0/1940
1	6	0.22	0/1441	0.47	0/1940
1	A	0.22	0/1441	0.47	0/1940
1	B	0.22	0/1441	0.47	0/1940
1	E	0.22	0/1441	0.47	0/1940
1	F	0.22	0/1441	0.47	0/1940
1	G	0.22	0/1441	0.46	0/1940
1	H	0.22	0/1441	0.47	0/1940
1	I	0.22	0/1441	0.47	0/1940
1	K	0.22	0/1441	0.47	0/1940
1	M	0.22	0/1441	0.47	0/1940
1	O	0.22	0/1441	0.48	0/1940
1	P	0.22	0/1441	0.47	0/1940
1	Q	0.22	0/1441	0.47	0/1940
1	S	0.22	0/1441	0.47	0/1940
1	U	0.22	0/1441	0.47	0/1940
1	W	0.22	0/1441	0.47	0/1940
1	X	0.22	0/1441	0.47	0/1940
1	Y	0.22	0/1441	0.48	0/1940
1	a	0.22	0/1441	0.47	0/1940
1	e	0.22	0/1441	0.47	0/1940
1	r	0.22	0/1441	0.47	0/1940
All	All	0.22	0/34584	0.47	0/46560

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 ⓘ

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	1	1420	0	1356	16	0
1	2	1420	0	1356	14	0
1	4	1420	0	1356	14	0
1	6	1420	0	1356	18	0
1	A	1420	0	1356	15	0
1	B	1420	0	1356	15	0
1	E	1420	0	1356	16	0
1	F	1420	0	1356	16	0
1	G	1420	0	1356	15	0
1	H	1420	0	1356	17	0
1	I	1420	0	1356	14	0
1	K	1420	0	1356	16	0
1	M	1420	0	1356	16	0
1	O	1420	0	1356	16	0
1	P	1420	0	1356	16	0
1	Q	1420	0	1356	14	0
1	S	1420	0	1356	15	0
1	U	1420	0	1356	14	0
1	W	1420	0	1356	17	0
1	X	1420	0	1356	14	0
1	Y	1420	0	1356	17	0
1	a	1420	0	1356	15	0
1	e	1420	0	1356	13	0
1	r	1420	0	1356	17	0
2	1	1	0	0	0	0
2	2	1	0	0	0	0
2	4	1	0	0	0	0
2	6	1	0	0	0	0
2	A	1	0	0	0	0
2	B	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	K	1	0	0	0	0
2	M	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	O	1	0	0	0	0
2	P	1	0	0	0	0
2	Q	1	0	0	0	0
2	S	1	0	0	0	0
2	U	1	0	0	0	0
2	W	1	0	0	0	0
2	X	1	0	0	0	0
2	Y	1	0	0	0	0
2	a	1	0	0	0	0
2	e	1	0	0	0	0
2	r	1	0	0	0	0
3	1	2	0	0	0	0
3	2	2	0	0	0	0
3	4	1	0	0	0	0
3	6	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	G	1	0	0	0	0
3	H	2	0	0	0	0
3	M	1	0	0	0	0
3	O	1	0	0	0	0
4	1	70	0	0	3	0
4	2	71	0	0	2	0
4	4	71	0	0	2	0
4	6	70	0	0	2	0
4	A	72	0	0	2	0
4	B	70	0	0	2	0
4	E	72	0	0	2	0
4	F	71	0	0	2	0
4	G	71	0	0	2	0
4	H	72	0	0	2	0
4	I	70	0	0	2	0
4	K	70	0	0	2	0
4	M	72	0	0	2	0
4	O	72	0	0	2	0
4	P	73	0	0	2	0
4	Q	70	0	0	3	0
4	S	71	0	0	2	0
4	U	73	0	0	2	0
4	W	71	0	0	3	0
4	X	72	0	0	2	0
4	Y	73	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	a	70	0	0	2	0
4	e	71	0	0	2	0
4	r	71	0	0	2	0
All	All	35827	0	32544	358	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.

The worst 5 of 358 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:P:13:HIS:HD2	1:P:15:ASP:H	1.38	0.72
1:H:13:HIS:HD2	1:H:15:ASP:H	1.38	0.72
1:e:13:HIS:HD2	1:e:15:ASP:H	1.38	0.71
1:E:13:HIS:HD2	1:E:15:ASP:H	1.38	0.71
1:U:13:HIS:HD2	1:U:15:ASP:H	1.38	0.70

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 PDB entries followed by that with respect to all EM entries.

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	1	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	2	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	4	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	6	170/173 (98%)	169 (99%)	1 (1%)	0	100	100
1	A	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	B	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	E	170/173 (98%)	168 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	G	170/173 (98%)	169 (99%)	1 (1%)	0	100	100
1	H	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	I	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	K	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	M	170/173 (98%)	169 (99%)	1 (1%)	0	100	100
1	O	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	P	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	Q	170/173 (98%)	169 (99%)	1 (1%)	0	100	100
1	S	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	U	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	W	170/173 (98%)	169 (99%)	1 (1%)	0	100	100
1	X	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	Y	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	a	170/173 (98%)	169 (99%)	1 (1%)	0	100	100
1	e	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
1	r	170/173 (98%)	168 (99%)	2 (1%)	0	100	100
All	All	4080/4152 (98%)	4038 (99%)	42 (1%)	0	100	100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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	1	153/153 (100%)	153 (100%)	0	100	100
1	2	153/153 (100%)	153 (100%)	0	100	100
1	4	153/153 (100%)	153 (100%)	0	100	100
1	6	153/153 (100%)	153 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	153/153 (100%)	153 (100%)	0	100	100
1	B	153/153 (100%)	153 (100%)	0	100	100
1	E	153/153 (100%)	153 (100%)	0	100	100
1	F	153/153 (100%)	153 (100%)	0	100	100
1	G	153/153 (100%)	153 (100%)	0	100	100
1	H	153/153 (100%)	153 (100%)	0	100	100
1	I	153/153 (100%)	153 (100%)	0	100	100
1	K	153/153 (100%)	153 (100%)	0	100	100
1	M	153/153 (100%)	153 (100%)	0	100	100
1	O	153/153 (100%)	153 (100%)	0	100	100
1	P	153/153 (100%)	153 (100%)	0	100	100
1	Q	153/153 (100%)	153 (100%)	0	100	100
1	S	153/153 (100%)	153 (100%)	0	100	100
1	U	153/153 (100%)	153 (100%)	0	100	100
1	W	153/153 (100%)	153 (100%)	0	100	100
1	X	153/153 (100%)	153 (100%)	0	100	100
1	Y	153/153 (100%)	153 (100%)	0	100	100
1	a	153/153 (100%)	153 (100%)	0	100	100
1	e	153/153 (100%)	153 (100%)	0	100	100
1	r	153/153 (100%)	153 (100%)	0	100	100
All	All	3672/3672 (100%)	3672 (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. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	13	HIS
1	r	136	HIS
1	P	13	HIS
1	r	112	GLN
1	Y	136	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

24 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CSX	A	90	1	3,6,7	0.83	0	1,6,8	1.43	0
1	CSX	O	90	1	3,6,7	0.82	0	1,6,8	1.38	0
1	CSX	Y	90	1	3,6,7	0.81	0	1,6,8	1.39	0
1	CSX	K	90	1	3,6,7	0.84	0	1,6,8	1.38	0
1	CSX	e	90	1	3,6,7	0.82	0	1,6,8	1.45	0
1	CSX	r	90	1	3,6,7	0.84	0	1,6,8	1.40	0
1	CSX	I	90	1	3,6,7	0.83	0	1,6,8	1.37	0
1	CSX	E	90	1	3,6,7	0.83	0	1,6,8	1.46	0
1	CSX	a	90	1	3,6,7	0.85	0	1,6,8	1.38	0
1	CSX	F	90	1	3,6,7	0.84	0	1,6,8	1.34	0
1	CSX	2	90	1	3,6,7	0.83	0	1,6,8	1.38	0
1	CSX	Q	90	1	3,6,7	0.82	0	1,6,8	1.43	0
1	CSX	4	90	1	3,6,7	0.83	0	1,6,8	1.45	0
1	CSX	S	90	1	3,6,7	0.82	0	1,6,8	1.39	0
1	CSX	1	90	1	3,6,7	0.84	0	1,6,8	1.44	0
1	CSX	G	90	1	3,6,7	0.82	0	1,6,8	1.40	0
1	CSX	U	90	1	3,6,7	0.84	0	1,6,8	1.38	0
1	CSX	H	90	1	3,6,7	0.83	0	1,6,8	1.43	0
1	CSX	P	90	1	3,6,7	0.83	0	1,6,8	1.44	0
1	CSX	6	90	1	3,6,7	0.83	0	1,6,8	1.38	0
1	CSX	W	90	1	3,6,7	0.84	0	1,6,8	1.38	0
1	CSX	X	90	1	3,6,7	0.84	0	1,6,8	1.36	0
1	CSX	M	90	1	3,6,7	0.83	0	1,6,8	1.36	0
1	CSX	B	90	1	3,6,7	0.81	0	1,6,8	1.45	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
1	CSX	A	90	1	-	0/2/5/7	-
1	CSX	O	90	1	-	0/2/5/7	-
1	CSX	Y	90	1	-	0/2/5/7	-
1	CSX	K	90	1	-	0/2/5/7	-
1	CSX	e	90	1	-	0/2/5/7	-
1	CSX	r	90	1	-	0/2/5/7	-
1	CSX	I	90	1	-	0/2/5/7	-
1	CSX	E	90	1	-	0/2/5/7	-
1	CSX	a	90	1	-	0/2/5/7	-
1	CSX	F	90	1	-	0/2/5/7	-
1	CSX	2	90	1	-	0/2/5/7	-
1	CSX	Q	90	1	-	0/2/5/7	-
1	CSX	4	90	1	-	0/2/5/7	-
1	CSX	S	90	1	-	0/2/5/7	-
1	CSX	1	90	1	-	0/2/5/7	-
1	CSX	G	90	1	-	0/2/5/7	-
1	CSX	U	90	1	-	0/2/5/7	-
1	CSX	H	90	1	-	0/2/5/7	-
1	CSX	P	90	1	-	0/2/5/7	-
1	CSX	6	90	1	-	0/2/5/7	-
1	CSX	W	90	1	-	0/2/5/7	-
1	CSX	X	90	1	-	0/2/5/7	-
1	CSX	M	90	1	-	0/2/5/7	-
1	CSX	B	90	1	-	0/2/5/7	-

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.

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 38 ligands modelled in this entry, 38 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Map visualisation

This section contains visualisations of the EMDB entry EMD-16789. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

This section was not generated. No masks/segmentation were deposited.

7 Map analysis ⓘ

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.