



Full wwPDB EM Validation Report ⓘ

Dec 17, 2022 – 07:08 pm GMT

PDB ID : 6ZLQ
EMDB ID : EMD-11272
Title : Folding of an iron binding peptide in response to sedimentation is resolved using ferritin as a nano-reactor
Authors : Davidov, G.; Abelya, G.; Zalk, R.; Izbickei, B.; Shaibi, S.; Spektor, L.; Meyron Holtz, E.G.; Zarivach, R.; Frank, G.A.
Deposited on : 2020-07-01
Resolution : 3.30 Å(reported)

This is a Full wwPDB EM Validation 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

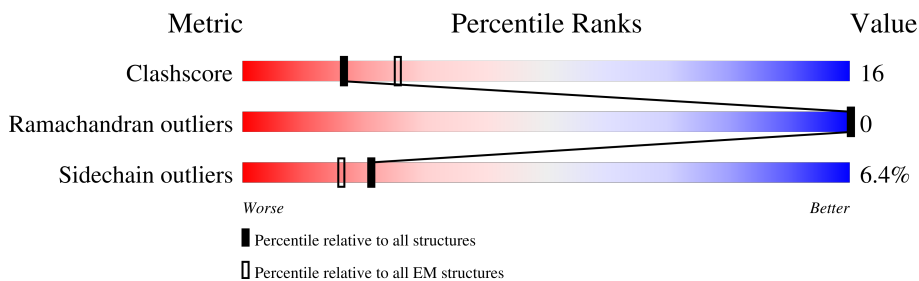
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	216	
1	B	216	
1	C	216	
1	D	216	
1	E	216	
1	F	216	
1	G	216	
1	H	216	

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Mol	Chain	Length	Quality of chain
1	I	216	 54% 25% 19%
1	J	216	 52% 25% 19%
1	K	216	 52% 27% 19%
1	L	216	 47% 32% 19%
1	M	216	 55% 25% 19%
1	N	216	 52% 27% 19%
1	O	216	 52% 25% 19%
1	P	216	 53% 26% 19%
1	Q	216	 52% 26% 19%
1	R	216	 53% 25% 19%
1	S	216	 54% 24% 19%
1	T	216	 54% 25% 19%
1	U	216	 57% 22% 19%
1	V	216	 52% 26% 19%
1	W	216	 52% 26% 19%
1	Z	216	 53% 26% 19%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 33823 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	Z	174	1406	880	253	269	4	0	0
1	A	174	1406	880	253	269	4	0	0
1	C	174	1406	880	253	269	4	0	0
1	E	174	1406	880	253	269	4	0	0
1	G	174	1406	880	253	269	4	0	0
1	H	175	1413	884	254	271	4	0	0
1	I	175	1413	884	254	271	4	0	0
1	J	174	1406	880	253	269	4	0	0
1	K	174	1406	880	253	269	4	0	0
1	L	175	1413	884	254	271	4	0	0
1	M	174	1406	880	253	269	4	0	0
1	N	175	1413	884	254	271	4	0	0
1	O	175	1413	884	254	271	4	0	0
1	P	174	1406	880	253	269	4	0	0
1	Q	175	1413	884	254	271	4	0	0
1	R	174	1406	880	253	269	4	0	0
1	S	174	1406	880	253	269	4	0	0

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Mol	Chain	Residues	Atoms				AltConf	Trace	
1	T	174	Total	C	N	O	S	0	0
			1406	880	253	269	4		
1	U	175	Total	C	N	O	S	0	0
			1413	884	254	271	4		
1	V	175	Total	C	N	O	S	0	0
			1413	884	254	271	4		
1	W	174	Total	C	N	O	S	0	0
			1406	880	253	269	4		
1	B	175	Total	C	N	O	S	0	0
			1413	884	254	271	4		
1	D	174	Total	C	N	O	S	0	0
			1406	880	253	269	4		
1	F	174	Total	C	N	O	S	0	0
			1406	880	253	269	4		

There are 792 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Z	-19	MET	-	initiating methionine	UNP Q9CPX4
Z	-18	GLY	-	expression tag	UNP Q9CPX4
Z	-17	SER	-	expression tag	UNP Q9CPX4
Z	-16	SER	-	expression tag	UNP Q9CPX4
Z	-15	HIS	-	expression tag	UNP Q9CPX4
Z	-14	HIS	-	expression tag	UNP Q9CPX4
Z	-13	HIS	-	expression tag	UNP Q9CPX4
Z	-12	HIS	-	expression tag	UNP Q9CPX4
Z	-11	HIS	-	expression tag	UNP Q9CPX4
Z	-10	HIS	-	expression tag	UNP Q9CPX4
Z	-9	SER	-	expression tag	UNP Q9CPX4
Z	-8	SER	-	expression tag	UNP Q9CPX4
Z	-7	GLY	-	expression tag	UNP Q9CPX4
Z	-6	LEU	-	expression tag	UNP Q9CPX4
Z	-5	VAL	-	expression tag	UNP Q9CPX4
Z	-4	PRO	-	expression tag	UNP Q9CPX4
Z	-3	ARG	-	expression tag	UNP Q9CPX4
Z	-2	GLY	-	expression tag	UNP Q9CPX4
Z	-1	SER	-	expression tag	UNP Q9CPX4
Z	0	HIS	-	expression tag	UNP Q9CPX4
Z	184	GLY	-	expression tag	UNP Q9CPX4
Z	185	ASP	-	expression tag	UNP Q9CPX4
Z	186	ILE	-	expression tag	UNP Q9CPX4
Z	187	GLU	-	expression tag	UNP Q9CPX4
Z	188	SER	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
Z	189	ALA	-	expression tag	UNP Q9CPX4
Z	190	GLN	-	expression tag	UNP Q9CPX4
Z	191	SER	-	expression tag	UNP Q9CPX4
Z	192	ASP	-	expression tag	UNP Q9CPX4
Z	193	GLU	-	expression tag	UNP Q9CPX4
Z	194	GLU	-	expression tag	UNP Q9CPX4
Z	195	VAL	-	expression tag	UNP Q9CPX4
Z	196	GLU	-	expression tag	UNP Q9CPX4
A	-19	MET	-	initiating methionine	UNP Q9CPX4
A	-18	GLY	-	expression tag	UNP Q9CPX4
A	-17	SER	-	expression tag	UNP Q9CPX4
A	-16	SER	-	expression tag	UNP Q9CPX4
A	-15	HIS	-	expression tag	UNP Q9CPX4
A	-14	HIS	-	expression tag	UNP Q9CPX4
A	-13	HIS	-	expression tag	UNP Q9CPX4
A	-12	HIS	-	expression tag	UNP Q9CPX4
A	-11	HIS	-	expression tag	UNP Q9CPX4
A	-10	HIS	-	expression tag	UNP Q9CPX4
A	-9	SER	-	expression tag	UNP Q9CPX4
A	-8	SER	-	expression tag	UNP Q9CPX4
A	-7	GLY	-	expression tag	UNP Q9CPX4
A	-6	LEU	-	expression tag	UNP Q9CPX4
A	-5	VAL	-	expression tag	UNP Q9CPX4
A	-4	PRO	-	expression tag	UNP Q9CPX4
A	-3	ARG	-	expression tag	UNP Q9CPX4
A	-2	GLY	-	expression tag	UNP Q9CPX4
A	-1	SER	-	expression tag	UNP Q9CPX4
A	0	HIS	-	expression tag	UNP Q9CPX4
A	184	GLY	-	expression tag	UNP Q9CPX4
A	185	ASP	-	expression tag	UNP Q9CPX4
A	186	ILE	-	expression tag	UNP Q9CPX4
A	187	GLU	-	expression tag	UNP Q9CPX4
A	188	SER	-	expression tag	UNP Q9CPX4
A	189	ALA	-	expression tag	UNP Q9CPX4
A	190	GLN	-	expression tag	UNP Q9CPX4
A	191	SER	-	expression tag	UNP Q9CPX4
A	192	ASP	-	expression tag	UNP Q9CPX4
A	193	GLU	-	expression tag	UNP Q9CPX4
A	194	GLU	-	expression tag	UNP Q9CPX4
A	195	VAL	-	expression tag	UNP Q9CPX4
A	196	GLU	-	expression tag	UNP Q9CPX4
C	-19	MET	-	initiating methionine	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-18	GLY	-	expression tag	UNP Q9CPX4
C	-17	SER	-	expression tag	UNP Q9CPX4
C	-16	SER	-	expression tag	UNP Q9CPX4
C	-15	HIS	-	expression tag	UNP Q9CPX4
C	-14	HIS	-	expression tag	UNP Q9CPX4
C	-13	HIS	-	expression tag	UNP Q9CPX4
C	-12	HIS	-	expression tag	UNP Q9CPX4
C	-11	HIS	-	expression tag	UNP Q9CPX4
C	-10	HIS	-	expression tag	UNP Q9CPX4
C	-9	SER	-	expression tag	UNP Q9CPX4
C	-8	SER	-	expression tag	UNP Q9CPX4
C	-7	GLY	-	expression tag	UNP Q9CPX4
C	-6	LEU	-	expression tag	UNP Q9CPX4
C	-5	VAL	-	expression tag	UNP Q9CPX4
C	-4	PRO	-	expression tag	UNP Q9CPX4
C	-3	ARG	-	expression tag	UNP Q9CPX4
C	-2	GLY	-	expression tag	UNP Q9CPX4
C	-1	SER	-	expression tag	UNP Q9CPX4
C	0	HIS	-	expression tag	UNP Q9CPX4
C	184	GLY	-	expression tag	UNP Q9CPX4
C	185	ASP	-	expression tag	UNP Q9CPX4
C	186	ILE	-	expression tag	UNP Q9CPX4
C	187	GLU	-	expression tag	UNP Q9CPX4
C	188	SER	-	expression tag	UNP Q9CPX4
C	189	ALA	-	expression tag	UNP Q9CPX4
C	190	GLN	-	expression tag	UNP Q9CPX4
C	191	SER	-	expression tag	UNP Q9CPX4
C	192	ASP	-	expression tag	UNP Q9CPX4
C	193	GLU	-	expression tag	UNP Q9CPX4
C	194	GLU	-	expression tag	UNP Q9CPX4
C	195	VAL	-	expression tag	UNP Q9CPX4
C	196	GLU	-	expression tag	UNP Q9CPX4
E	-19	MET	-	initiating methionine	UNP Q9CPX4
E	-18	GLY	-	expression tag	UNP Q9CPX4
E	-17	SER	-	expression tag	UNP Q9CPX4
E	-16	SER	-	expression tag	UNP Q9CPX4
E	-15	HIS	-	expression tag	UNP Q9CPX4
E	-14	HIS	-	expression tag	UNP Q9CPX4
E	-13	HIS	-	expression tag	UNP Q9CPX4
E	-12	HIS	-	expression tag	UNP Q9CPX4
E	-11	HIS	-	expression tag	UNP Q9CPX4
E	-10	HIS	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-9	SER	-	expression tag	UNP Q9CPX4
E	-8	SER	-	expression tag	UNP Q9CPX4
E	-7	GLY	-	expression tag	UNP Q9CPX4
E	-6	LEU	-	expression tag	UNP Q9CPX4
E	-5	VAL	-	expression tag	UNP Q9CPX4
E	-4	PRO	-	expression tag	UNP Q9CPX4
E	-3	ARG	-	expression tag	UNP Q9CPX4
E	-2	GLY	-	expression tag	UNP Q9CPX4
E	-1	SER	-	expression tag	UNP Q9CPX4
E	0	HIS	-	expression tag	UNP Q9CPX4
E	184	GLY	-	expression tag	UNP Q9CPX4
E	185	ASP	-	expression tag	UNP Q9CPX4
E	186	ILE	-	expression tag	UNP Q9CPX4
E	187	GLU	-	expression tag	UNP Q9CPX4
E	188	SER	-	expression tag	UNP Q9CPX4
E	189	ALA	-	expression tag	UNP Q9CPX4
E	190	GLN	-	expression tag	UNP Q9CPX4
E	191	SER	-	expression tag	UNP Q9CPX4
E	192	ASP	-	expression tag	UNP Q9CPX4
E	193	GLU	-	expression tag	UNP Q9CPX4
E	194	GLU	-	expression tag	UNP Q9CPX4
E	195	VAL	-	expression tag	UNP Q9CPX4
E	196	GLU	-	expression tag	UNP Q9CPX4
G	-19	MET	-	initiating methionine	UNP Q9CPX4
G	-18	GLY	-	expression tag	UNP Q9CPX4
G	-17	SER	-	expression tag	UNP Q9CPX4
G	-16	SER	-	expression tag	UNP Q9CPX4
G	-15	HIS	-	expression tag	UNP Q9CPX4
G	-14	HIS	-	expression tag	UNP Q9CPX4
G	-13	HIS	-	expression tag	UNP Q9CPX4
G	-12	HIS	-	expression tag	UNP Q9CPX4
G	-11	HIS	-	expression tag	UNP Q9CPX4
G	-10	HIS	-	expression tag	UNP Q9CPX4
G	-9	SER	-	expression tag	UNP Q9CPX4
G	-8	SER	-	expression tag	UNP Q9CPX4
G	-7	GLY	-	expression tag	UNP Q9CPX4
G	-6	LEU	-	expression tag	UNP Q9CPX4
G	-5	VAL	-	expression tag	UNP Q9CPX4
G	-4	PRO	-	expression tag	UNP Q9CPX4
G	-3	ARG	-	expression tag	UNP Q9CPX4
G	-2	GLY	-	expression tag	UNP Q9CPX4
G	-1	SER	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
G	0	HIS	-	expression tag	UNP Q9CPX4
G	184	GLY	-	expression tag	UNP Q9CPX4
G	185	ASP	-	expression tag	UNP Q9CPX4
G	186	ILE	-	expression tag	UNP Q9CPX4
G	187	GLU	-	expression tag	UNP Q9CPX4
G	188	SER	-	expression tag	UNP Q9CPX4
G	189	ALA	-	expression tag	UNP Q9CPX4
G	190	GLN	-	expression tag	UNP Q9CPX4
G	191	SER	-	expression tag	UNP Q9CPX4
G	192	ASP	-	expression tag	UNP Q9CPX4
G	193	GLU	-	expression tag	UNP Q9CPX4
G	194	GLU	-	expression tag	UNP Q9CPX4
G	195	VAL	-	expression tag	UNP Q9CPX4
G	196	GLU	-	expression tag	UNP Q9CPX4
H	-19	MET	-	initiating methionine	UNP Q9CPX4
H	-18	GLY	-	expression tag	UNP Q9CPX4
H	-17	SER	-	expression tag	UNP Q9CPX4
H	-16	SER	-	expression tag	UNP Q9CPX4
H	-15	HIS	-	expression tag	UNP Q9CPX4
H	-14	HIS	-	expression tag	UNP Q9CPX4
H	-13	HIS	-	expression tag	UNP Q9CPX4
H	-12	HIS	-	expression tag	UNP Q9CPX4
H	-11	HIS	-	expression tag	UNP Q9CPX4
H	-10	HIS	-	expression tag	UNP Q9CPX4
H	-9	SER	-	expression tag	UNP Q9CPX4
H	-8	SER	-	expression tag	UNP Q9CPX4
H	-7	GLY	-	expression tag	UNP Q9CPX4
H	-6	LEU	-	expression tag	UNP Q9CPX4
H	-5	VAL	-	expression tag	UNP Q9CPX4
H	-4	PRO	-	expression tag	UNP Q9CPX4
H	-3	ARG	-	expression tag	UNP Q9CPX4
H	-2	GLY	-	expression tag	UNP Q9CPX4
H	-1	SER	-	expression tag	UNP Q9CPX4
H	0	HIS	-	expression tag	UNP Q9CPX4
H	184	GLY	-	expression tag	UNP Q9CPX4
H	185	ASP	-	expression tag	UNP Q9CPX4
H	186	ILE	-	expression tag	UNP Q9CPX4
H	187	GLU	-	expression tag	UNP Q9CPX4
H	188	SER	-	expression tag	UNP Q9CPX4
H	189	ALA	-	expression tag	UNP Q9CPX4
H	190	GLN	-	expression tag	UNP Q9CPX4
H	191	SER	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
H	192	ASP	-	expression tag	UNP Q9CPX4
H	193	GLU	-	expression tag	UNP Q9CPX4
H	194	GLU	-	expression tag	UNP Q9CPX4
H	195	VAL	-	expression tag	UNP Q9CPX4
H	196	GLU	-	expression tag	UNP Q9CPX4
I	-19	MET	-	initiating methionine	UNP Q9CPX4
I	-18	GLY	-	expression tag	UNP Q9CPX4
I	-17	SER	-	expression tag	UNP Q9CPX4
I	-16	SER	-	expression tag	UNP Q9CPX4
I	-15	HIS	-	expression tag	UNP Q9CPX4
I	-14	HIS	-	expression tag	UNP Q9CPX4
I	-13	HIS	-	expression tag	UNP Q9CPX4
I	-12	HIS	-	expression tag	UNP Q9CPX4
I	-11	HIS	-	expression tag	UNP Q9CPX4
I	-10	HIS	-	expression tag	UNP Q9CPX4
I	-9	SER	-	expression tag	UNP Q9CPX4
I	-8	SER	-	expression tag	UNP Q9CPX4
I	-7	GLY	-	expression tag	UNP Q9CPX4
I	-6	LEU	-	expression tag	UNP Q9CPX4
I	-5	VAL	-	expression tag	UNP Q9CPX4
I	-4	PRO	-	expression tag	UNP Q9CPX4
I	-3	ARG	-	expression tag	UNP Q9CPX4
I	-2	GLY	-	expression tag	UNP Q9CPX4
I	-1	SER	-	expression tag	UNP Q9CPX4
I	0	HIS	-	expression tag	UNP Q9CPX4
I	184	GLY	-	expression tag	UNP Q9CPX4
I	185	ASP	-	expression tag	UNP Q9CPX4
I	186	ILE	-	expression tag	UNP Q9CPX4
I	187	GLU	-	expression tag	UNP Q9CPX4
I	188	SER	-	expression tag	UNP Q9CPX4
I	189	ALA	-	expression tag	UNP Q9CPX4
I	190	GLN	-	expression tag	UNP Q9CPX4
I	191	SER	-	expression tag	UNP Q9CPX4
I	192	ASP	-	expression tag	UNP Q9CPX4
I	193	GLU	-	expression tag	UNP Q9CPX4
I	194	GLU	-	expression tag	UNP Q9CPX4
I	195	VAL	-	expression tag	UNP Q9CPX4
I	196	GLU	-	expression tag	UNP Q9CPX4
J	-19	MET	-	initiating methionine	UNP Q9CPX4
J	-18	GLY	-	expression tag	UNP Q9CPX4
J	-17	SER	-	expression tag	UNP Q9CPX4
J	-16	SER	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-15	HIS	-	expression tag	UNP Q9CPX4
J	-14	HIS	-	expression tag	UNP Q9CPX4
J	-13	HIS	-	expression tag	UNP Q9CPX4
J	-12	HIS	-	expression tag	UNP Q9CPX4
J	-11	HIS	-	expression tag	UNP Q9CPX4
J	-10	HIS	-	expression tag	UNP Q9CPX4
J	-9	SER	-	expression tag	UNP Q9CPX4
J	-8	SER	-	expression tag	UNP Q9CPX4
J	-7	GLY	-	expression tag	UNP Q9CPX4
J	-6	LEU	-	expression tag	UNP Q9CPX4
J	-5	VAL	-	expression tag	UNP Q9CPX4
J	-4	PRO	-	expression tag	UNP Q9CPX4
J	-3	ARG	-	expression tag	UNP Q9CPX4
J	-2	GLY	-	expression tag	UNP Q9CPX4
J	-1	SER	-	expression tag	UNP Q9CPX4
J	0	HIS	-	expression tag	UNP Q9CPX4
J	184	GLY	-	expression tag	UNP Q9CPX4
J	185	ASP	-	expression tag	UNP Q9CPX4
J	186	ILE	-	expression tag	UNP Q9CPX4
J	187	GLU	-	expression tag	UNP Q9CPX4
J	188	SER	-	expression tag	UNP Q9CPX4
J	189	ALA	-	expression tag	UNP Q9CPX4
J	190	GLN	-	expression tag	UNP Q9CPX4
J	191	SER	-	expression tag	UNP Q9CPX4
J	192	ASP	-	expression tag	UNP Q9CPX4
J	193	GLU	-	expression tag	UNP Q9CPX4
J	194	GLU	-	expression tag	UNP Q9CPX4
J	195	VAL	-	expression tag	UNP Q9CPX4
J	196	GLU	-	expression tag	UNP Q9CPX4
K	-19	MET	-	initiating methionine	UNP Q9CPX4
K	-18	GLY	-	expression tag	UNP Q9CPX4
K	-17	SER	-	expression tag	UNP Q9CPX4
K	-16	SER	-	expression tag	UNP Q9CPX4
K	-15	HIS	-	expression tag	UNP Q9CPX4
K	-14	HIS	-	expression tag	UNP Q9CPX4
K	-13	HIS	-	expression tag	UNP Q9CPX4
K	-12	HIS	-	expression tag	UNP Q9CPX4
K	-11	HIS	-	expression tag	UNP Q9CPX4
K	-10	HIS	-	expression tag	UNP Q9CPX4
K	-9	SER	-	expression tag	UNP Q9CPX4
K	-8	SER	-	expression tag	UNP Q9CPX4
K	-7	GLY	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
K	-6	LEU	-	expression tag	UNP Q9CPX4
K	-5	VAL	-	expression tag	UNP Q9CPX4
K	-4	PRO	-	expression tag	UNP Q9CPX4
K	-3	ARG	-	expression tag	UNP Q9CPX4
K	-2	GLY	-	expression tag	UNP Q9CPX4
K	-1	SER	-	expression tag	UNP Q9CPX4
K	0	HIS	-	expression tag	UNP Q9CPX4
K	184	GLY	-	expression tag	UNP Q9CPX4
K	185	ASP	-	expression tag	UNP Q9CPX4
K	186	ILE	-	expression tag	UNP Q9CPX4
K	187	GLU	-	expression tag	UNP Q9CPX4
K	188	SER	-	expression tag	UNP Q9CPX4
K	189	ALA	-	expression tag	UNP Q9CPX4
K	190	GLN	-	expression tag	UNP Q9CPX4
K	191	SER	-	expression tag	UNP Q9CPX4
K	192	ASP	-	expression tag	UNP Q9CPX4
K	193	GLU	-	expression tag	UNP Q9CPX4
K	194	GLU	-	expression tag	UNP Q9CPX4
K	195	VAL	-	expression tag	UNP Q9CPX4
K	196	GLU	-	expression tag	UNP Q9CPX4
L	-19	MET	-	initiating methionine	UNP Q9CPX4
L	-18	GLY	-	expression tag	UNP Q9CPX4
L	-17	SER	-	expression tag	UNP Q9CPX4
L	-16	SER	-	expression tag	UNP Q9CPX4
L	-15	HIS	-	expression tag	UNP Q9CPX4
L	-14	HIS	-	expression tag	UNP Q9CPX4
L	-13	HIS	-	expression tag	UNP Q9CPX4
L	-12	HIS	-	expression tag	UNP Q9CPX4
L	-11	HIS	-	expression tag	UNP Q9CPX4
L	-10	HIS	-	expression tag	UNP Q9CPX4
L	-9	SER	-	expression tag	UNP Q9CPX4
L	-8	SER	-	expression tag	UNP Q9CPX4
L	-7	GLY	-	expression tag	UNP Q9CPX4
L	-6	LEU	-	expression tag	UNP Q9CPX4
L	-5	VAL	-	expression tag	UNP Q9CPX4
L	-4	PRO	-	expression tag	UNP Q9CPX4
L	-3	ARG	-	expression tag	UNP Q9CPX4
L	-2	GLY	-	expression tag	UNP Q9CPX4
L	-1	SER	-	expression tag	UNP Q9CPX4
L	0	HIS	-	expression tag	UNP Q9CPX4
L	184	GLY	-	expression tag	UNP Q9CPX4
L	185	ASP	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
L	186	ILE	-	expression tag	UNP Q9CPX4
L	187	GLU	-	expression tag	UNP Q9CPX4
L	188	SER	-	expression tag	UNP Q9CPX4
L	189	ALA	-	expression tag	UNP Q9CPX4
L	190	GLN	-	expression tag	UNP Q9CPX4
L	191	SER	-	expression tag	UNP Q9CPX4
L	192	ASP	-	expression tag	UNP Q9CPX4
L	193	GLU	-	expression tag	UNP Q9CPX4
L	194	GLU	-	expression tag	UNP Q9CPX4
L	195	VAL	-	expression tag	UNP Q9CPX4
L	196	GLU	-	expression tag	UNP Q9CPX4
M	-19	MET	-	initiating methionine	UNP Q9CPX4
M	-18	GLY	-	expression tag	UNP Q9CPX4
M	-17	SER	-	expression tag	UNP Q9CPX4
M	-16	SER	-	expression tag	UNP Q9CPX4
M	-15	HIS	-	expression tag	UNP Q9CPX4
M	-14	HIS	-	expression tag	UNP Q9CPX4
M	-13	HIS	-	expression tag	UNP Q9CPX4
M	-12	HIS	-	expression tag	UNP Q9CPX4
M	-11	HIS	-	expression tag	UNP Q9CPX4
M	-10	HIS	-	expression tag	UNP Q9CPX4
M	-9	SER	-	expression tag	UNP Q9CPX4
M	-8	SER	-	expression tag	UNP Q9CPX4
M	-7	GLY	-	expression tag	UNP Q9CPX4
M	-6	LEU	-	expression tag	UNP Q9CPX4
M	-5	VAL	-	expression tag	UNP Q9CPX4
M	-4	PRO	-	expression tag	UNP Q9CPX4
M	-3	ARG	-	expression tag	UNP Q9CPX4
M	-2	GLY	-	expression tag	UNP Q9CPX4
M	-1	SER	-	expression tag	UNP Q9CPX4
M	0	HIS	-	expression tag	UNP Q9CPX4
M	184	GLY	-	expression tag	UNP Q9CPX4
M	185	ASP	-	expression tag	UNP Q9CPX4
M	186	ILE	-	expression tag	UNP Q9CPX4
M	187	GLU	-	expression tag	UNP Q9CPX4
M	188	SER	-	expression tag	UNP Q9CPX4
M	189	ALA	-	expression tag	UNP Q9CPX4
M	190	GLN	-	expression tag	UNP Q9CPX4
M	191	SER	-	expression tag	UNP Q9CPX4
M	192	ASP	-	expression tag	UNP Q9CPX4
M	193	GLU	-	expression tag	UNP Q9CPX4
M	194	GLU	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
M	195	VAL	-	expression tag	UNP Q9CPX4
M	196	GLU	-	expression tag	UNP Q9CPX4
N	-19	MET	-	initiating methionine	UNP Q9CPX4
N	-18	GLY	-	expression tag	UNP Q9CPX4
N	-17	SER	-	expression tag	UNP Q9CPX4
N	-16	SER	-	expression tag	UNP Q9CPX4
N	-15	HIS	-	expression tag	UNP Q9CPX4
N	-14	HIS	-	expression tag	UNP Q9CPX4
N	-13	HIS	-	expression tag	UNP Q9CPX4
N	-12	HIS	-	expression tag	UNP Q9CPX4
N	-11	HIS	-	expression tag	UNP Q9CPX4
N	-10	HIS	-	expression tag	UNP Q9CPX4
N	-9	SER	-	expression tag	UNP Q9CPX4
N	-8	SER	-	expression tag	UNP Q9CPX4
N	-7	GLY	-	expression tag	UNP Q9CPX4
N	-6	LEU	-	expression tag	UNP Q9CPX4
N	-5	VAL	-	expression tag	UNP Q9CPX4
N	-4	PRO	-	expression tag	UNP Q9CPX4
N	-3	ARG	-	expression tag	UNP Q9CPX4
N	-2	GLY	-	expression tag	UNP Q9CPX4
N	-1	SER	-	expression tag	UNP Q9CPX4
N	0	HIS	-	expression tag	UNP Q9CPX4
N	184	GLY	-	expression tag	UNP Q9CPX4
N	185	ASP	-	expression tag	UNP Q9CPX4
N	186	ILE	-	expression tag	UNP Q9CPX4
N	187	GLU	-	expression tag	UNP Q9CPX4
N	188	SER	-	expression tag	UNP Q9CPX4
N	189	ALA	-	expression tag	UNP Q9CPX4
N	190	GLN	-	expression tag	UNP Q9CPX4
N	191	SER	-	expression tag	UNP Q9CPX4
N	192	ASP	-	expression tag	UNP Q9CPX4
N	193	GLU	-	expression tag	UNP Q9CPX4
N	194	GLU	-	expression tag	UNP Q9CPX4
N	195	VAL	-	expression tag	UNP Q9CPX4
N	196	GLU	-	expression tag	UNP Q9CPX4
O	-19	MET	-	initiating methionine	UNP Q9CPX4
O	-18	GLY	-	expression tag	UNP Q9CPX4
O	-17	SER	-	expression tag	UNP Q9CPX4
O	-16	SER	-	expression tag	UNP Q9CPX4
O	-15	HIS	-	expression tag	UNP Q9CPX4
O	-14	HIS	-	expression tag	UNP Q9CPX4
O	-13	HIS	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
O	-12	HIS	-	expression tag	UNP Q9CPX4
O	-11	HIS	-	expression tag	UNP Q9CPX4
O	-10	HIS	-	expression tag	UNP Q9CPX4
O	-9	SER	-	expression tag	UNP Q9CPX4
O	-8	SER	-	expression tag	UNP Q9CPX4
O	-7	GLY	-	expression tag	UNP Q9CPX4
O	-6	LEU	-	expression tag	UNP Q9CPX4
O	-5	VAL	-	expression tag	UNP Q9CPX4
O	-4	PRO	-	expression tag	UNP Q9CPX4
O	-3	ARG	-	expression tag	UNP Q9CPX4
O	-2	GLY	-	expression tag	UNP Q9CPX4
O	-1	SER	-	expression tag	UNP Q9CPX4
O	0	HIS	-	expression tag	UNP Q9CPX4
O	184	GLY	-	expression tag	UNP Q9CPX4
O	185	ASP	-	expression tag	UNP Q9CPX4
O	186	ILE	-	expression tag	UNP Q9CPX4
O	187	GLU	-	expression tag	UNP Q9CPX4
O	188	SER	-	expression tag	UNP Q9CPX4
O	189	ALA	-	expression tag	UNP Q9CPX4
O	190	GLN	-	expression tag	UNP Q9CPX4
O	191	SER	-	expression tag	UNP Q9CPX4
O	192	ASP	-	expression tag	UNP Q9CPX4
O	193	GLU	-	expression tag	UNP Q9CPX4
O	194	GLU	-	expression tag	UNP Q9CPX4
O	195	VAL	-	expression tag	UNP Q9CPX4
O	196	GLU	-	expression tag	UNP Q9CPX4
P	-19	MET	-	initiating methionine	UNP Q9CPX4
P	-18	GLY	-	expression tag	UNP Q9CPX4
P	-17	SER	-	expression tag	UNP Q9CPX4
P	-16	SER	-	expression tag	UNP Q9CPX4
P	-15	HIS	-	expression tag	UNP Q9CPX4
P	-14	HIS	-	expression tag	UNP Q9CPX4
P	-13	HIS	-	expression tag	UNP Q9CPX4
P	-12	HIS	-	expression tag	UNP Q9CPX4
P	-11	HIS	-	expression tag	UNP Q9CPX4
P	-10	HIS	-	expression tag	UNP Q9CPX4
P	-9	SER	-	expression tag	UNP Q9CPX4
P	-8	SER	-	expression tag	UNP Q9CPX4
P	-7	GLY	-	expression tag	UNP Q9CPX4
P	-6	LEU	-	expression tag	UNP Q9CPX4
P	-5	VAL	-	expression tag	UNP Q9CPX4
P	-4	PRO	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
P	-3	ARG	-	expression tag	UNP Q9CPX4
P	-2	GLY	-	expression tag	UNP Q9CPX4
P	-1	SER	-	expression tag	UNP Q9CPX4
P	0	HIS	-	expression tag	UNP Q9CPX4
P	184	GLY	-	expression tag	UNP Q9CPX4
P	185	ASP	-	expression tag	UNP Q9CPX4
P	186	ILE	-	expression tag	UNP Q9CPX4
P	187	GLU	-	expression tag	UNP Q9CPX4
P	188	SER	-	expression tag	UNP Q9CPX4
P	189	ALA	-	expression tag	UNP Q9CPX4
P	190	GLN	-	expression tag	UNP Q9CPX4
P	191	SER	-	expression tag	UNP Q9CPX4
P	192	ASP	-	expression tag	UNP Q9CPX4
P	193	GLU	-	expression tag	UNP Q9CPX4
P	194	GLU	-	expression tag	UNP Q9CPX4
P	195	VAL	-	expression tag	UNP Q9CPX4
P	196	GLU	-	expression tag	UNP Q9CPX4
Q	-19	MET	-	initiating methionine	UNP Q9CPX4
Q	-18	GLY	-	expression tag	UNP Q9CPX4
Q	-17	SER	-	expression tag	UNP Q9CPX4
Q	-16	SER	-	expression tag	UNP Q9CPX4
Q	-15	HIS	-	expression tag	UNP Q9CPX4
Q	-14	HIS	-	expression tag	UNP Q9CPX4
Q	-13	HIS	-	expression tag	UNP Q9CPX4
Q	-12	HIS	-	expression tag	UNP Q9CPX4
Q	-11	HIS	-	expression tag	UNP Q9CPX4
Q	-10	HIS	-	expression tag	UNP Q9CPX4
Q	-9	SER	-	expression tag	UNP Q9CPX4
Q	-8	SER	-	expression tag	UNP Q9CPX4
Q	-7	GLY	-	expression tag	UNP Q9CPX4
Q	-6	LEU	-	expression tag	UNP Q9CPX4
Q	-5	VAL	-	expression tag	UNP Q9CPX4
Q	-4	PRO	-	expression tag	UNP Q9CPX4
Q	-3	ARG	-	expression tag	UNP Q9CPX4
Q	-2	GLY	-	expression tag	UNP Q9CPX4
Q	-1	SER	-	expression tag	UNP Q9CPX4
Q	0	HIS	-	expression tag	UNP Q9CPX4
Q	184	GLY	-	expression tag	UNP Q9CPX4
Q	185	ASP	-	expression tag	UNP Q9CPX4
Q	186	ILE	-	expression tag	UNP Q9CPX4
Q	187	GLU	-	expression tag	UNP Q9CPX4
Q	188	SER	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	189	ALA	-	expression tag	UNP Q9CPX4
Q	190	GLN	-	expression tag	UNP Q9CPX4
Q	191	SER	-	expression tag	UNP Q9CPX4
Q	192	ASP	-	expression tag	UNP Q9CPX4
Q	193	GLU	-	expression tag	UNP Q9CPX4
Q	194	GLU	-	expression tag	UNP Q9CPX4
Q	195	VAL	-	expression tag	UNP Q9CPX4
Q	196	GLU	-	expression tag	UNP Q9CPX4
R	-19	MET	-	initiating methionine	UNP Q9CPX4
R	-18	GLY	-	expression tag	UNP Q9CPX4
R	-17	SER	-	expression tag	UNP Q9CPX4
R	-16	SER	-	expression tag	UNP Q9CPX4
R	-15	HIS	-	expression tag	UNP Q9CPX4
R	-14	HIS	-	expression tag	UNP Q9CPX4
R	-13	HIS	-	expression tag	UNP Q9CPX4
R	-12	HIS	-	expression tag	UNP Q9CPX4
R	-11	HIS	-	expression tag	UNP Q9CPX4
R	-10	HIS	-	expression tag	UNP Q9CPX4
R	-9	SER	-	expression tag	UNP Q9CPX4
R	-8	SER	-	expression tag	UNP Q9CPX4
R	-7	GLY	-	expression tag	UNP Q9CPX4
R	-6	LEU	-	expression tag	UNP Q9CPX4
R	-5	VAL	-	expression tag	UNP Q9CPX4
R	-4	PRO	-	expression tag	UNP Q9CPX4
R	-3	ARG	-	expression tag	UNP Q9CPX4
R	-2	GLY	-	expression tag	UNP Q9CPX4
R	-1	SER	-	expression tag	UNP Q9CPX4
R	0	HIS	-	expression tag	UNP Q9CPX4
R	184	GLY	-	expression tag	UNP Q9CPX4
R	185	ASP	-	expression tag	UNP Q9CPX4
R	186	ILE	-	expression tag	UNP Q9CPX4
R	187	GLU	-	expression tag	UNP Q9CPX4
R	188	SER	-	expression tag	UNP Q9CPX4
R	189	ALA	-	expression tag	UNP Q9CPX4
R	190	GLN	-	expression tag	UNP Q9CPX4
R	191	SER	-	expression tag	UNP Q9CPX4
R	192	ASP	-	expression tag	UNP Q9CPX4
R	193	GLU	-	expression tag	UNP Q9CPX4
R	194	GLU	-	expression tag	UNP Q9CPX4
R	195	VAL	-	expression tag	UNP Q9CPX4
R	196	GLU	-	expression tag	UNP Q9CPX4
S	-19	MET	-	initiating methionine	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
S	-18	GLY	-	expression tag	UNP Q9CPX4
S	-17	SER	-	expression tag	UNP Q9CPX4
S	-16	SER	-	expression tag	UNP Q9CPX4
S	-15	HIS	-	expression tag	UNP Q9CPX4
S	-14	HIS	-	expression tag	UNP Q9CPX4
S	-13	HIS	-	expression tag	UNP Q9CPX4
S	-12	HIS	-	expression tag	UNP Q9CPX4
S	-11	HIS	-	expression tag	UNP Q9CPX4
S	-10	HIS	-	expression tag	UNP Q9CPX4
S	-9	SER	-	expression tag	UNP Q9CPX4
S	-8	SER	-	expression tag	UNP Q9CPX4
S	-7	GLY	-	expression tag	UNP Q9CPX4
S	-6	LEU	-	expression tag	UNP Q9CPX4
S	-5	VAL	-	expression tag	UNP Q9CPX4
S	-4	PRO	-	expression tag	UNP Q9CPX4
S	-3	ARG	-	expression tag	UNP Q9CPX4
S	-2	GLY	-	expression tag	UNP Q9CPX4
S	-1	SER	-	expression tag	UNP Q9CPX4
S	0	HIS	-	expression tag	UNP Q9CPX4
S	184	GLY	-	expression tag	UNP Q9CPX4
S	185	ASP	-	expression tag	UNP Q9CPX4
S	186	ILE	-	expression tag	UNP Q9CPX4
S	187	GLU	-	expression tag	UNP Q9CPX4
S	188	SER	-	expression tag	UNP Q9CPX4
S	189	ALA	-	expression tag	UNP Q9CPX4
S	190	GLN	-	expression tag	UNP Q9CPX4
S	191	SER	-	expression tag	UNP Q9CPX4
S	192	ASP	-	expression tag	UNP Q9CPX4
S	193	GLU	-	expression tag	UNP Q9CPX4
S	194	GLU	-	expression tag	UNP Q9CPX4
S	195	VAL	-	expression tag	UNP Q9CPX4
S	196	GLU	-	expression tag	UNP Q9CPX4
T	-19	MET	-	initiating methionine	UNP Q9CPX4
T	-18	GLY	-	expression tag	UNP Q9CPX4
T	-17	SER	-	expression tag	UNP Q9CPX4
T	-16	SER	-	expression tag	UNP Q9CPX4
T	-15	HIS	-	expression tag	UNP Q9CPX4
T	-14	HIS	-	expression tag	UNP Q9CPX4
T	-13	HIS	-	expression tag	UNP Q9CPX4
T	-12	HIS	-	expression tag	UNP Q9CPX4
T	-11	HIS	-	expression tag	UNP Q9CPX4
T	-10	HIS	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
T	-9	SER	-	expression tag	UNP Q9CPX4
T	-8	SER	-	expression tag	UNP Q9CPX4
T	-7	GLY	-	expression tag	UNP Q9CPX4
T	-6	LEU	-	expression tag	UNP Q9CPX4
T	-5	VAL	-	expression tag	UNP Q9CPX4
T	-4	PRO	-	expression tag	UNP Q9CPX4
T	-3	ARG	-	expression tag	UNP Q9CPX4
T	-2	GLY	-	expression tag	UNP Q9CPX4
T	-1	SER	-	expression tag	UNP Q9CPX4
T	0	HIS	-	expression tag	UNP Q9CPX4
T	184	GLY	-	expression tag	UNP Q9CPX4
T	185	ASP	-	expression tag	UNP Q9CPX4
T	186	ILE	-	expression tag	UNP Q9CPX4
T	187	GLU	-	expression tag	UNP Q9CPX4
T	188	SER	-	expression tag	UNP Q9CPX4
T	189	ALA	-	expression tag	UNP Q9CPX4
T	190	GLN	-	expression tag	UNP Q9CPX4
T	191	SER	-	expression tag	UNP Q9CPX4
T	192	ASP	-	expression tag	UNP Q9CPX4
T	193	GLU	-	expression tag	UNP Q9CPX4
T	194	GLU	-	expression tag	UNP Q9CPX4
T	195	VAL	-	expression tag	UNP Q9CPX4
T	196	GLU	-	expression tag	UNP Q9CPX4
U	-19	MET	-	initiating methionine	UNP Q9CPX4
U	-18	GLY	-	expression tag	UNP Q9CPX4
U	-17	SER	-	expression tag	UNP Q9CPX4
U	-16	SER	-	expression tag	UNP Q9CPX4
U	-15	HIS	-	expression tag	UNP Q9CPX4
U	-14	HIS	-	expression tag	UNP Q9CPX4
U	-13	HIS	-	expression tag	UNP Q9CPX4
U	-12	HIS	-	expression tag	UNP Q9CPX4
U	-11	HIS	-	expression tag	UNP Q9CPX4
U	-10	HIS	-	expression tag	UNP Q9CPX4
U	-9	SER	-	expression tag	UNP Q9CPX4
U	-8	SER	-	expression tag	UNP Q9CPX4
U	-7	GLY	-	expression tag	UNP Q9CPX4
U	-6	LEU	-	expression tag	UNP Q9CPX4
U	-5	VAL	-	expression tag	UNP Q9CPX4
U	-4	PRO	-	expression tag	UNP Q9CPX4
U	-3	ARG	-	expression tag	UNP Q9CPX4
U	-2	GLY	-	expression tag	UNP Q9CPX4
U	-1	SER	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
U	0	HIS	-	expression tag	UNP Q9CPX4
U	184	GLY	-	expression tag	UNP Q9CPX4
U	185	ASP	-	expression tag	UNP Q9CPX4
U	186	ILE	-	expression tag	UNP Q9CPX4
U	187	GLU	-	expression tag	UNP Q9CPX4
U	188	SER	-	expression tag	UNP Q9CPX4
U	189	ALA	-	expression tag	UNP Q9CPX4
U	190	GLN	-	expression tag	UNP Q9CPX4
U	191	SER	-	expression tag	UNP Q9CPX4
U	192	ASP	-	expression tag	UNP Q9CPX4
U	193	GLU	-	expression tag	UNP Q9CPX4
U	194	GLU	-	expression tag	UNP Q9CPX4
U	195	VAL	-	expression tag	UNP Q9CPX4
U	196	GLU	-	expression tag	UNP Q9CPX4
V	-19	MET	-	initiating methionine	UNP Q9CPX4
V	-18	GLY	-	expression tag	UNP Q9CPX4
V	-17	SER	-	expression tag	UNP Q9CPX4
V	-16	SER	-	expression tag	UNP Q9CPX4
V	-15	HIS	-	expression tag	UNP Q9CPX4
V	-14	HIS	-	expression tag	UNP Q9CPX4
V	-13	HIS	-	expression tag	UNP Q9CPX4
V	-12	HIS	-	expression tag	UNP Q9CPX4
V	-11	HIS	-	expression tag	UNP Q9CPX4
V	-10	HIS	-	expression tag	UNP Q9CPX4
V	-9	SER	-	expression tag	UNP Q9CPX4
V	-8	SER	-	expression tag	UNP Q9CPX4
V	-7	GLY	-	expression tag	UNP Q9CPX4
V	-6	LEU	-	expression tag	UNP Q9CPX4
V	-5	VAL	-	expression tag	UNP Q9CPX4
V	-4	PRO	-	expression tag	UNP Q9CPX4
V	-3	ARG	-	expression tag	UNP Q9CPX4
V	-2	GLY	-	expression tag	UNP Q9CPX4
V	-1	SER	-	expression tag	UNP Q9CPX4
V	0	HIS	-	expression tag	UNP Q9CPX4
V	184	GLY	-	expression tag	UNP Q9CPX4
V	185	ASP	-	expression tag	UNP Q9CPX4
V	186	ILE	-	expression tag	UNP Q9CPX4
V	187	GLU	-	expression tag	UNP Q9CPX4
V	188	SER	-	expression tag	UNP Q9CPX4
V	189	ALA	-	expression tag	UNP Q9CPX4
V	190	GLN	-	expression tag	UNP Q9CPX4
V	191	SER	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
V	192	ASP	-	expression tag	UNP Q9CPX4
V	193	GLU	-	expression tag	UNP Q9CPX4
V	194	GLU	-	expression tag	UNP Q9CPX4
V	195	VAL	-	expression tag	UNP Q9CPX4
V	196	GLU	-	expression tag	UNP Q9CPX4
W	-19	MET	-	initiating methionine	UNP Q9CPX4
W	-18	GLY	-	expression tag	UNP Q9CPX4
W	-17	SER	-	expression tag	UNP Q9CPX4
W	-16	SER	-	expression tag	UNP Q9CPX4
W	-15	HIS	-	expression tag	UNP Q9CPX4
W	-14	HIS	-	expression tag	UNP Q9CPX4
W	-13	HIS	-	expression tag	UNP Q9CPX4
W	-12	HIS	-	expression tag	UNP Q9CPX4
W	-11	HIS	-	expression tag	UNP Q9CPX4
W	-10	HIS	-	expression tag	UNP Q9CPX4
W	-9	SER	-	expression tag	UNP Q9CPX4
W	-8	SER	-	expression tag	UNP Q9CPX4
W	-7	GLY	-	expression tag	UNP Q9CPX4
W	-6	LEU	-	expression tag	UNP Q9CPX4
W	-5	VAL	-	expression tag	UNP Q9CPX4
W	-4	PRO	-	expression tag	UNP Q9CPX4
W	-3	ARG	-	expression tag	UNP Q9CPX4
W	-2	GLY	-	expression tag	UNP Q9CPX4
W	-1	SER	-	expression tag	UNP Q9CPX4
W	0	HIS	-	expression tag	UNP Q9CPX4
W	184	GLY	-	expression tag	UNP Q9CPX4
W	185	ASP	-	expression tag	UNP Q9CPX4
W	186	ILE	-	expression tag	UNP Q9CPX4
W	187	GLU	-	expression tag	UNP Q9CPX4
W	188	SER	-	expression tag	UNP Q9CPX4
W	189	ALA	-	expression tag	UNP Q9CPX4
W	190	GLN	-	expression tag	UNP Q9CPX4
W	191	SER	-	expression tag	UNP Q9CPX4
W	192	ASP	-	expression tag	UNP Q9CPX4
W	193	GLU	-	expression tag	UNP Q9CPX4
W	194	GLU	-	expression tag	UNP Q9CPX4
W	195	VAL	-	expression tag	UNP Q9CPX4
W	196	GLU	-	expression tag	UNP Q9CPX4
B	-19	MET	-	initiating methionine	UNP Q9CPX4
B	-18	GLY	-	expression tag	UNP Q9CPX4
B	-17	SER	-	expression tag	UNP Q9CPX4
B	-16	SER	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	HIS	-	expression tag	UNP Q9CPX4
B	-14	HIS	-	expression tag	UNP Q9CPX4
B	-13	HIS	-	expression tag	UNP Q9CPX4
B	-12	HIS	-	expression tag	UNP Q9CPX4
B	-11	HIS	-	expression tag	UNP Q9CPX4
B	-10	HIS	-	expression tag	UNP Q9CPX4
B	-9	SER	-	expression tag	UNP Q9CPX4
B	-8	SER	-	expression tag	UNP Q9CPX4
B	-7	GLY	-	expression tag	UNP Q9CPX4
B	-6	LEU	-	expression tag	UNP Q9CPX4
B	-5	VAL	-	expression tag	UNP Q9CPX4
B	-4	PRO	-	expression tag	UNP Q9CPX4
B	-3	ARG	-	expression tag	UNP Q9CPX4
B	-2	GLY	-	expression tag	UNP Q9CPX4
B	-1	SER	-	expression tag	UNP Q9CPX4
B	0	HIS	-	expression tag	UNP Q9CPX4
B	184	GLY	-	expression tag	UNP Q9CPX4
B	185	ASP	-	expression tag	UNP Q9CPX4
B	186	ILE	-	expression tag	UNP Q9CPX4
B	187	GLU	-	expression tag	UNP Q9CPX4
B	188	SER	-	expression tag	UNP Q9CPX4
B	189	ALA	-	expression tag	UNP Q9CPX4
B	190	GLN	-	expression tag	UNP Q9CPX4
B	191	SER	-	expression tag	UNP Q9CPX4
B	192	ASP	-	expression tag	UNP Q9CPX4
B	193	GLU	-	expression tag	UNP Q9CPX4
B	194	GLU	-	expression tag	UNP Q9CPX4
B	195	VAL	-	expression tag	UNP Q9CPX4
B	196	GLU	-	expression tag	UNP Q9CPX4
D	-19	MET	-	initiating methionine	UNP Q9CPX4
D	-18	GLY	-	expression tag	UNP Q9CPX4
D	-17	SER	-	expression tag	UNP Q9CPX4
D	-16	SER	-	expression tag	UNP Q9CPX4
D	-15	HIS	-	expression tag	UNP Q9CPX4
D	-14	HIS	-	expression tag	UNP Q9CPX4
D	-13	HIS	-	expression tag	UNP Q9CPX4
D	-12	HIS	-	expression tag	UNP Q9CPX4
D	-11	HIS	-	expression tag	UNP Q9CPX4
D	-10	HIS	-	expression tag	UNP Q9CPX4
D	-9	SER	-	expression tag	UNP Q9CPX4
D	-8	SER	-	expression tag	UNP Q9CPX4
D	-7	GLY	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-6	LEU	-	expression tag	UNP Q9CPX4
D	-5	VAL	-	expression tag	UNP Q9CPX4
D	-4	PRO	-	expression tag	UNP Q9CPX4
D	-3	ARG	-	expression tag	UNP Q9CPX4
D	-2	GLY	-	expression tag	UNP Q9CPX4
D	-1	SER	-	expression tag	UNP Q9CPX4
D	0	HIS	-	expression tag	UNP Q9CPX4
D	184	GLY	-	expression tag	UNP Q9CPX4
D	185	ASP	-	expression tag	UNP Q9CPX4
D	186	ILE	-	expression tag	UNP Q9CPX4
D	187	GLU	-	expression tag	UNP Q9CPX4
D	188	SER	-	expression tag	UNP Q9CPX4
D	189	ALA	-	expression tag	UNP Q9CPX4
D	190	GLN	-	expression tag	UNP Q9CPX4
D	191	SER	-	expression tag	UNP Q9CPX4
D	192	ASP	-	expression tag	UNP Q9CPX4
D	193	GLU	-	expression tag	UNP Q9CPX4
D	194	GLU	-	expression tag	UNP Q9CPX4
D	195	VAL	-	expression tag	UNP Q9CPX4
D	196	GLU	-	expression tag	UNP Q9CPX4
F	-19	MET	-	initiating methionine	UNP Q9CPX4
F	-18	GLY	-	expression tag	UNP Q9CPX4
F	-17	SER	-	expression tag	UNP Q9CPX4
F	-16	SER	-	expression tag	UNP Q9CPX4
F	-15	HIS	-	expression tag	UNP Q9CPX4
F	-14	HIS	-	expression tag	UNP Q9CPX4
F	-13	HIS	-	expression tag	UNP Q9CPX4
F	-12	HIS	-	expression tag	UNP Q9CPX4
F	-11	HIS	-	expression tag	UNP Q9CPX4
F	-10	HIS	-	expression tag	UNP Q9CPX4
F	-9	SER	-	expression tag	UNP Q9CPX4
F	-8	SER	-	expression tag	UNP Q9CPX4
F	-7	GLY	-	expression tag	UNP Q9CPX4
F	-6	LEU	-	expression tag	UNP Q9CPX4
F	-5	VAL	-	expression tag	UNP Q9CPX4
F	-4	PRO	-	expression tag	UNP Q9CPX4
F	-3	ARG	-	expression tag	UNP Q9CPX4
F	-2	GLY	-	expression tag	UNP Q9CPX4
F	-1	SER	-	expression tag	UNP Q9CPX4
F	0	HIS	-	expression tag	UNP Q9CPX4
F	184	GLY	-	expression tag	UNP Q9CPX4
F	185	ASP	-	expression tag	UNP Q9CPX4

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Chain	Residue	Modelled	Actual	Comment	Reference
F	186	ILE	-	expression tag	UNP Q9CPX4
F	187	GLU	-	expression tag	UNP Q9CPX4
F	188	SER	-	expression tag	UNP Q9CPX4
F	189	ALA	-	expression tag	UNP Q9CPX4
F	190	GLN	-	expression tag	UNP Q9CPX4
F	191	SER	-	expression tag	UNP Q9CPX4
F	192	ASP	-	expression tag	UNP Q9CPX4
F	193	GLU	-	expression tag	UNP Q9CPX4
F	194	GLU	-	expression tag	UNP Q9CPX4
F	195	VAL	-	expression tag	UNP Q9CPX4
F	196	GLU	-	expression tag	UNP Q9CPX4

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
2	A	1	Total Fe 1 1	0
2	C	1	Total Fe 1 1	0
2	H	1	Total Fe 1 1	0
2	I	2	Total Fe 2 2	0
2	J	1	Total Fe 1 1	0
2	O	1	Total Fe 1 1	0
2	Q	1	Total Fe 1 1	0
2	R	1	Total Fe 1 1	0
2	S	1	Total Fe 1 1	0
2	U	1	Total Fe 1 1	0
2	V	1	Total Fe 1 1	0
2	B	1	Total Fe 1 1	0
2	D	2	Total Fe 2 2	0

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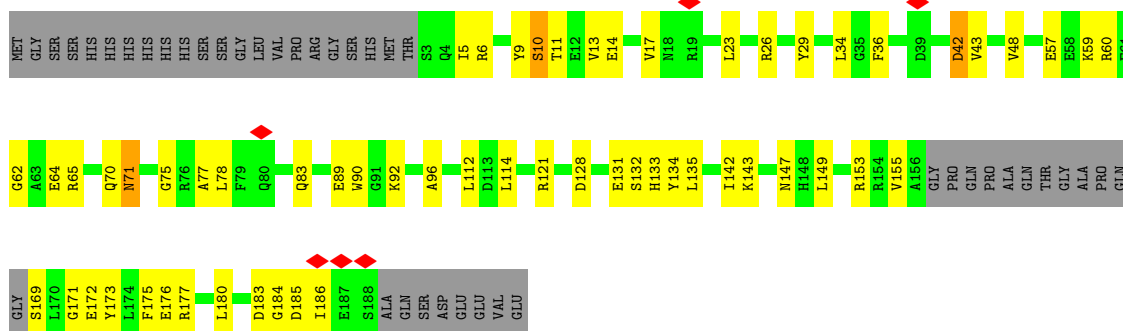
Mol	Chain	Residues	Atoms		AltConf
2	F	1	Total 1	Fe 1	0

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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

Chain Z: 




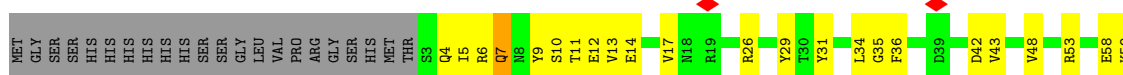
- Molecule 1: Ferritin

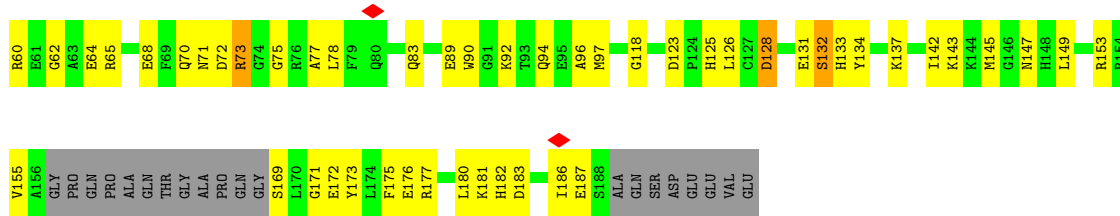
Chain A: 



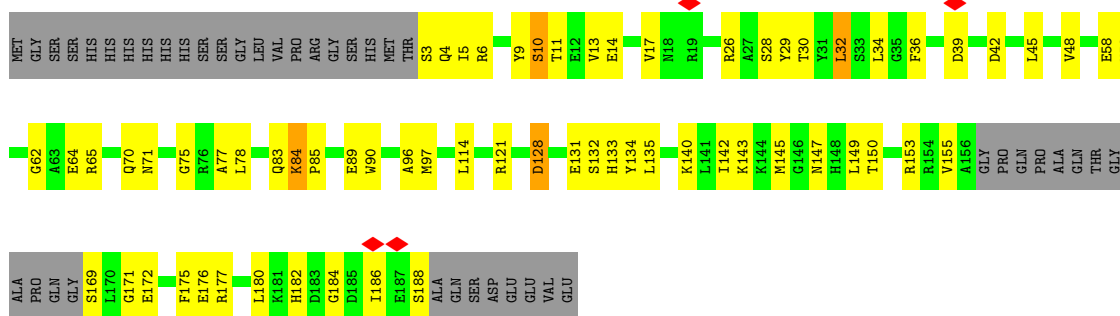
- Molecule 1: Ferritin

Chain C: 

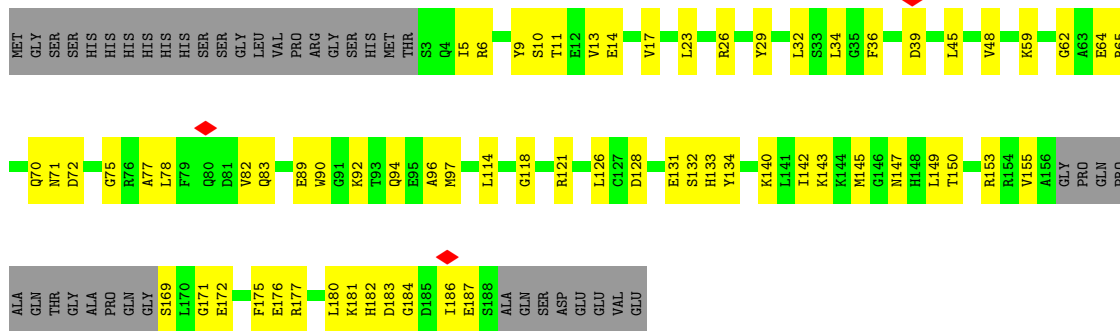




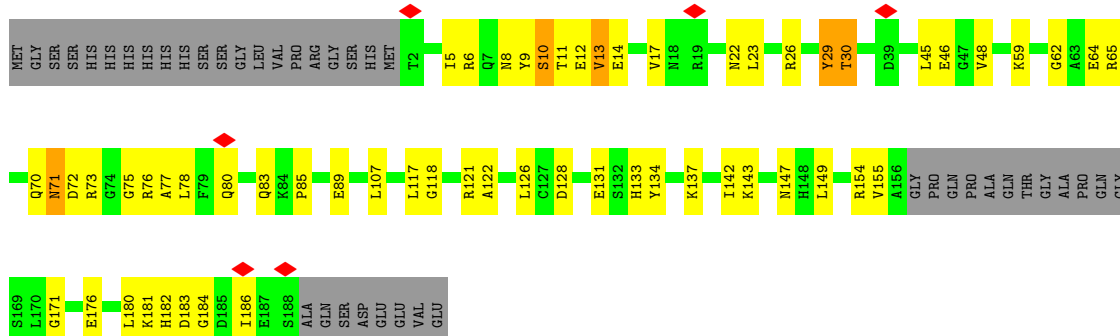
• Molecule 1: Ferritin



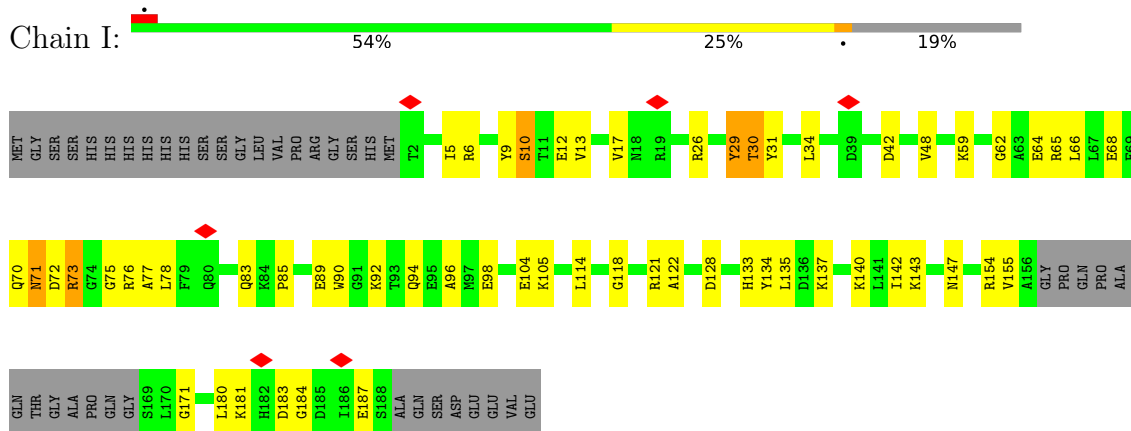
• Molecule 1: Ferritin



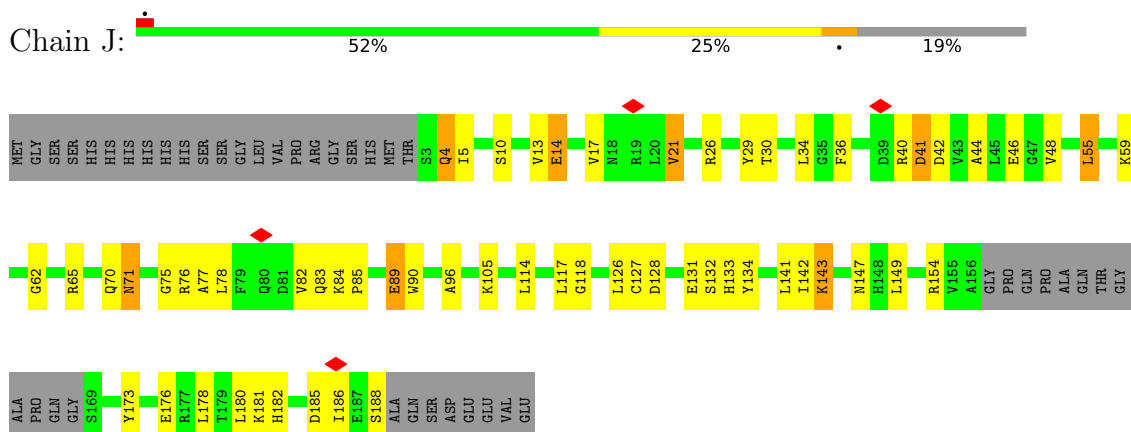
• Molecule 1: Ferritin



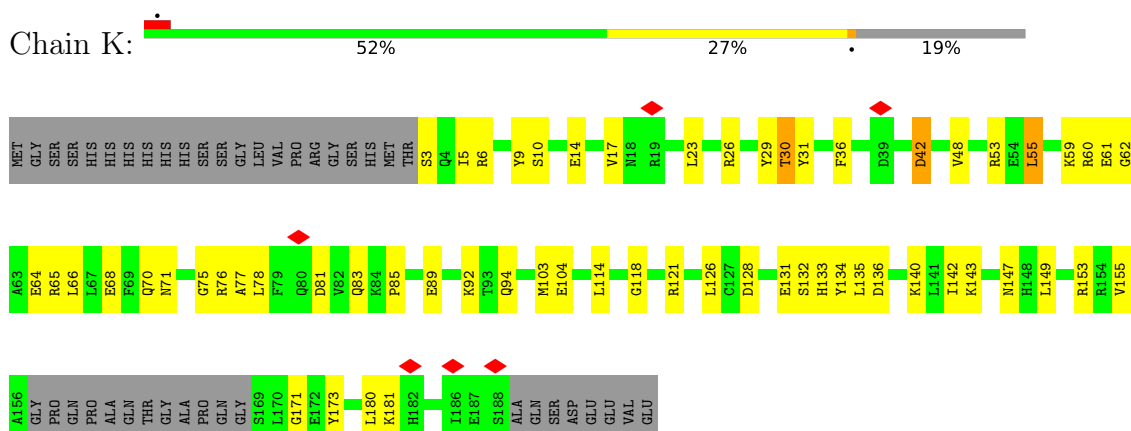
• Molecule 1: Ferritin



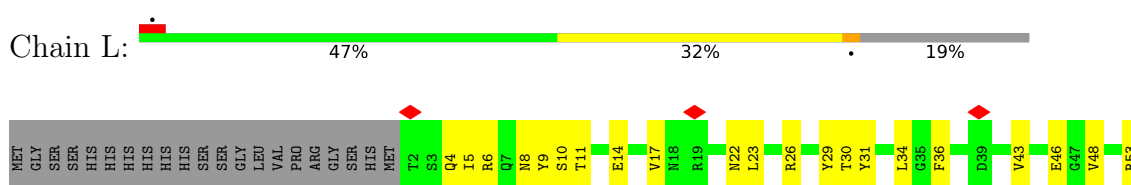
• Molecule 1: Ferritin

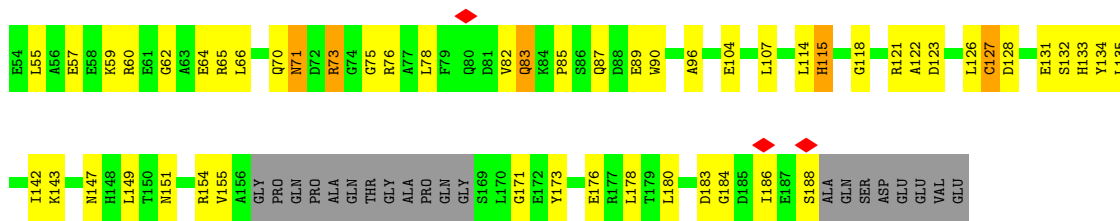


• Molecule 1: Ferritin

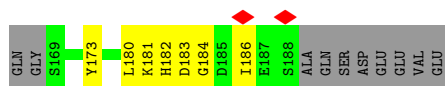


• Molecule 1: Ferritin

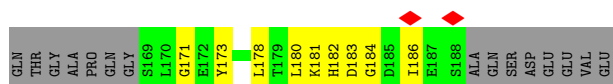
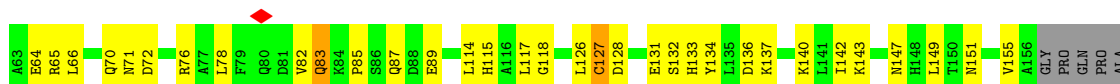




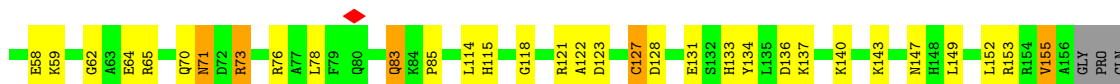
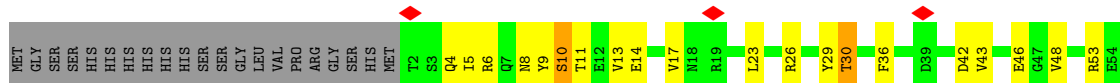
• Molecule 1: Ferritin



• Molecule 1: Ferritin

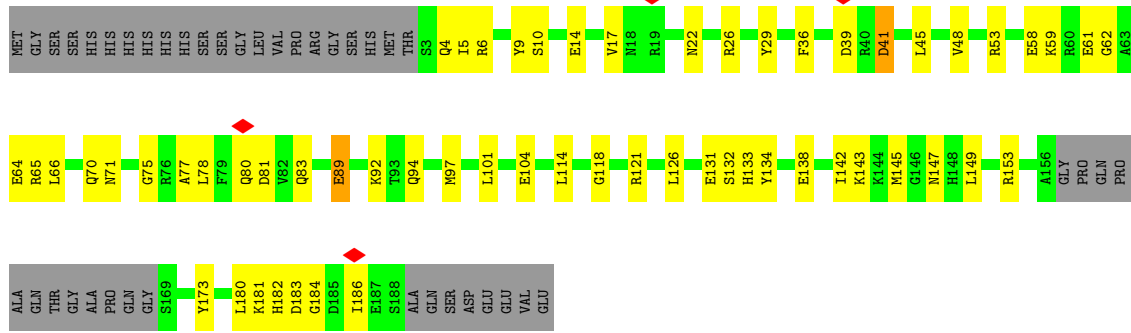


• Molecule 1: Ferritin



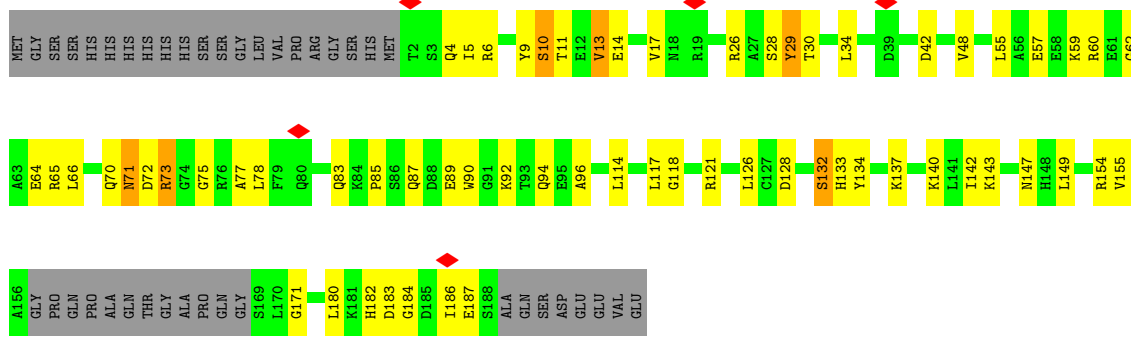
• Molecule 1: Ferritin

Chain P: 53% 26% 19%



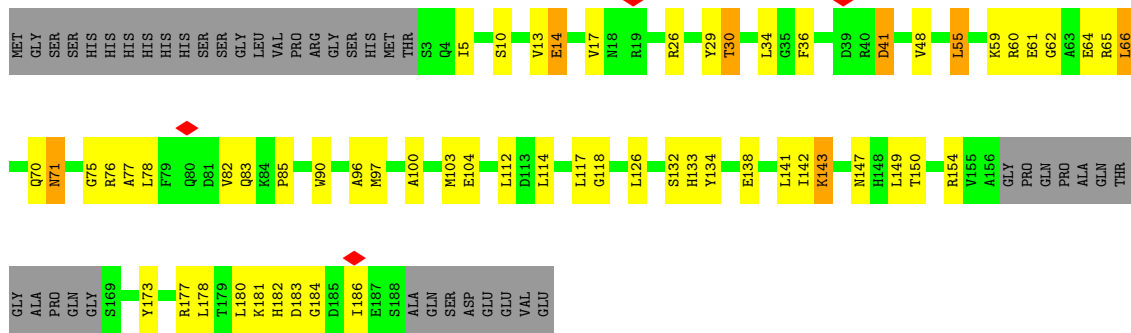
• Molecule 1: Ferritin

Chain Q: 52% 26% 19%



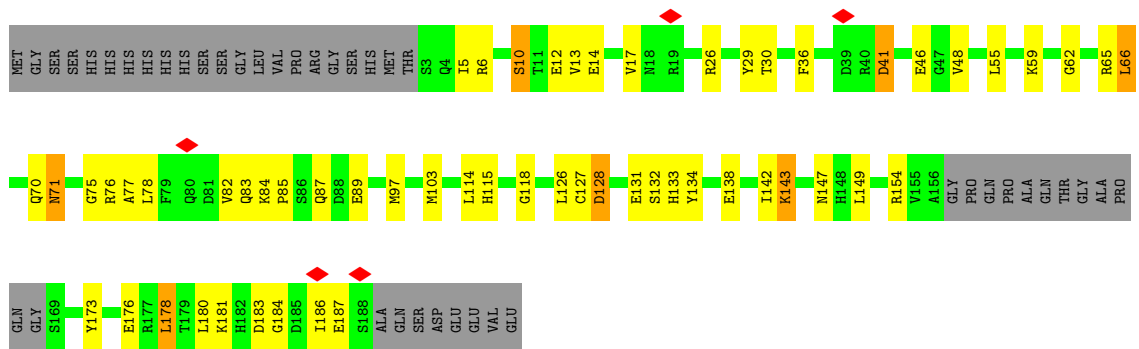
• Molecule 1: Ferritin

Chain R: 53% 25% 19%

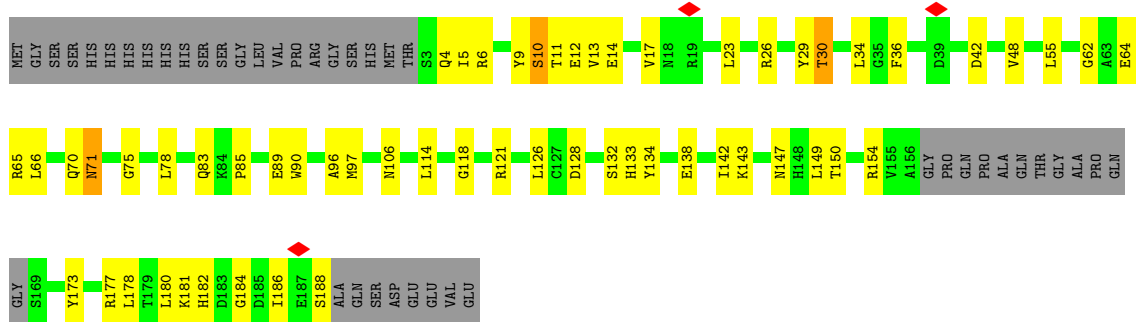


• Molecule 1: Ferritin

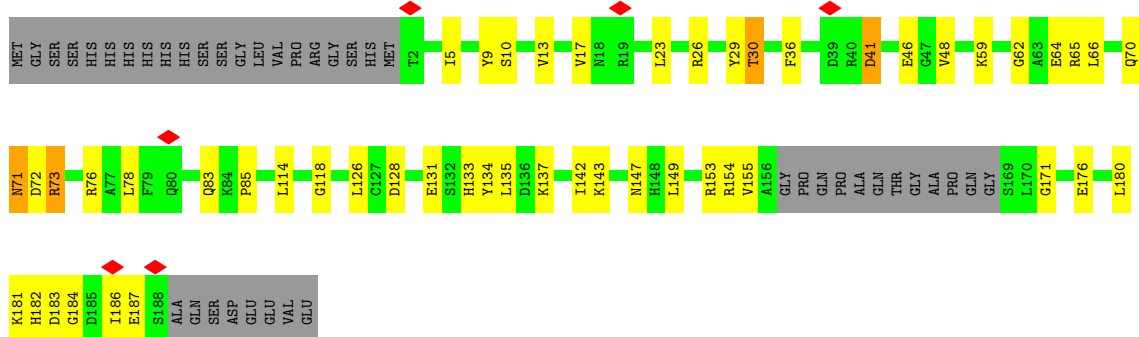
Chain S: 54% 24% 19%



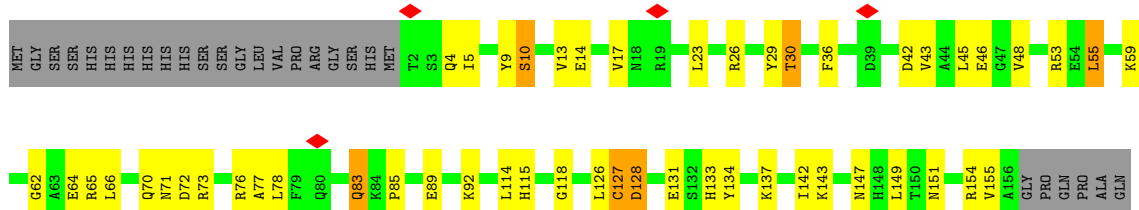
• Molecule 1: Ferritin

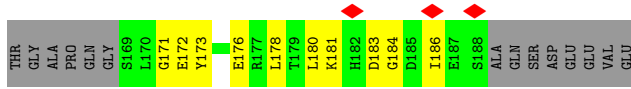


• Molecule 1: Ferritin

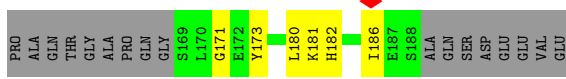
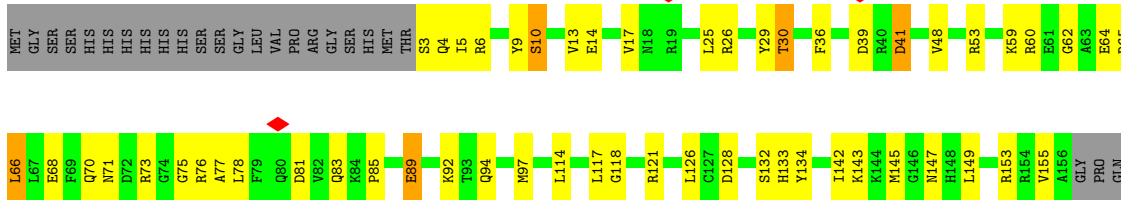


• Molecule 1: Ferritin

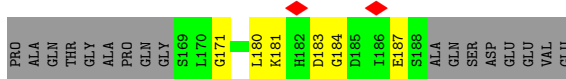
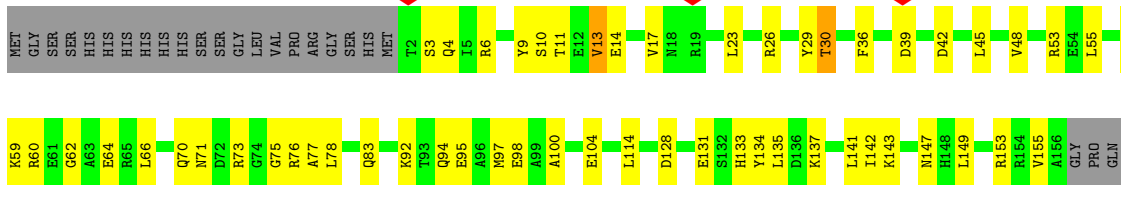




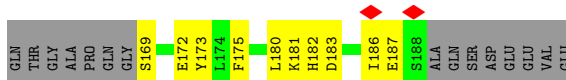
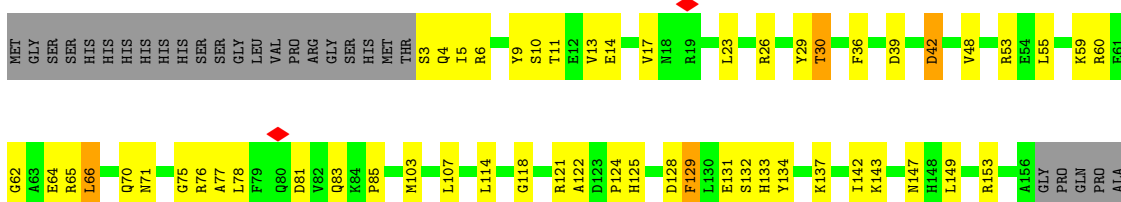
• Molecule 1: Ferritin



• Molecule 1: Ferritin

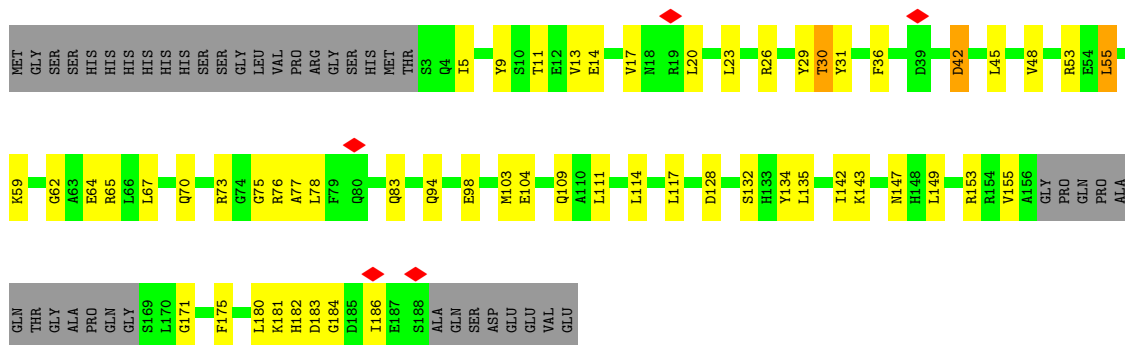


• Molecule 1: Ferritin



• Molecule 1: Ferritin





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	201772	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	80	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.088	Depositor
Minimum map value	-0.031	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0134	Depositor
Map size (\AA)	281.6, 281.6, 281.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FE

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	0.44	0/1429	0.46	0/1919
1	B	0.44	0/1436	0.46	0/1929
1	C	0.44	0/1429	0.45	0/1919
1	D	0.44	0/1429	0.47	0/1919
1	E	0.44	0/1429	0.45	0/1919
1	F	0.44	0/1429	0.46	0/1919
1	G	0.44	0/1429	0.46	0/1919
1	H	0.43	0/1436	0.46	0/1929
1	I	0.43	0/1436	0.46	0/1929
1	J	0.44	0/1429	0.46	0/1919
1	K	0.44	0/1429	0.45	0/1919
1	L	0.44	0/1436	0.47	0/1929
1	M	0.44	0/1429	0.45	0/1919
1	N	0.44	0/1436	0.47	0/1929
1	O	0.44	0/1436	0.46	0/1929
1	P	0.44	0/1429	0.45	0/1919
1	Q	0.43	0/1436	0.46	0/1929
1	R	0.44	0/1429	0.46	0/1919
1	S	0.43	0/1429	0.45	0/1919
1	T	0.44	0/1429	0.46	0/1919
1	U	0.43	0/1436	0.45	0/1929
1	V	0.45	0/1436	0.47	0/1929
1	W	0.44	0/1429	0.45	0/1919
1	Z	0.44	0/1429	0.45	0/1919
All	All	0.44	0/34359	0.46	0/46146

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	A	1406	0	1367	51	0
1	B	1413	0	1373	45	0
1	C	1406	0	1366	59	0
1	D	1406	0	1367	50	0
1	E	1406	0	1366	49	0
1	F	1406	0	1366	44	0
1	G	1406	0	1367	52	0
1	H	1413	0	1374	48	0
1	I	1413	0	1373	47	0
1	J	1406	0	1366	49	0
1	K	1406	0	1366	48	0
1	L	1413	0	1374	68	0
1	M	1406	0	1366	47	0
1	N	1413	0	1374	53	0
1	O	1413	0	1374	57	0
1	P	1406	0	1366	47	0
1	Q	1413	0	1374	49	0
1	R	1406	0	1366	50	0
1	S	1406	0	1366	51	0
1	T	1406	0	1366	46	0
1	U	1413	0	1374	40	0
1	V	1413	0	1374	56	0
1	W	1406	0	1366	49	0
1	Z	1406	0	1367	46	0
2	A	1	0	0	1	0
2	B	1	0	0	1	0
2	C	1	0	0	1	0
2	D	2	0	0	0	0
2	F	1	0	0	1	0
2	H	1	0	0	0	0
2	I	2	0	0	1	0
2	J	1	0	0	1	0
2	O	1	0	0	1	0
2	Q	1	0	0	1	0
2	R	1	0	0	0	0
2	S	1	0	0	1	0
2	U	1	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	V	1	0	0	1	0
All	All	33823	0	32858	1041	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 16.

All (1041) 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:D:183:ASP:O	1:D:187:GLU:HB2	1.73	0.86
1:L:115:HIS:NE2	1:L:131:GLU:OE2	2.15	0.79
1:C:142:ILE:HG22	1:N:5:ILE:HG22	1.65	0.78
1:Z:142:ILE:HG22	1:L:5:ILE:HG22	1.67	0.77
1:S:30:THR:OG1	1:S:103:MET:SD	2.44	0.76
1:D:133:HIS:O	1:D:137:LYS:NZ	2.18	0.76
1:T:26:ARG:HE	1:T:83:GLN:HB2	1.51	0.76
1:W:39:ASP:OD2	1:W:53:ARG:NH1	2.20	0.75
1:S:26:ARG:HE	1:S:83:GLN:HB3	1.53	0.74
1:H:133:HIS:O	1:H:137:LYS:NZ	2.19	0.73
1:B:133:HIS:O	1:B:137:LYS:NZ	2.18	0.73
1:U:9:TYR:OH	1:U:70:GLN:NE2	2.21	0.73
1:F:17:VAL:HG12	1:F:114:LEU:HD21	1.71	0.73
1:I:133:HIS:O	1:I:137:LYS:NZ	2.19	0.73
1:N:115:HIS:HE2	1:N:127:CYS:HG	1.37	0.72
1:B:26:ARG:HE	1:B:83:GLN:HB2	1.54	0.72
1:A:62:GLY:O	1:A:134:TYR:OH	2.06	0.72
1:C:133:HIS:O	1:C:137:LYS:NZ	2.18	0.71
1:K:5:ILE:HG22	1:U:142:ILE:HG22	1.72	0.71
1:Z:173:TYR:HB2	1:V:154:ARG:HD2	1.72	0.71
1:F:62:GLY:O	1:F:134:TYR:OH	2.07	0.71
1:C:5:ILE:HG22	1:F:142:ILE:HG22	1.70	0.71
1:O:133:HIS:O	1:O:137:LYS:NZ	2.19	0.71
1:Q:62:GLY:O	1:Q:134:TYR:OH	2.08	0.71
1:C:173:TYR:HB2	1:L:154:ARG:HD2	1.71	0.70
1:C:43:VAL:O	1:L:154:ARG:NH2	2.24	0.70
1:E:62:GLY:O	1:E:134:TYR:OH	2.10	0.69
1:L:62:GLY:O	1:L:134:TYR:OH	2.10	0.69
1:T:184:GLY:O	1:T:188:SER:OG	2.10	0.69
1:B:17:VAL:HG12	1:B:114:LEU:HD21	1.74	0.69
1:A:26:ARG:HE	1:A:83:GLN:HB2	1.56	0.69
1:U:41:ASP:OD2	1:U:41:ASP:N	2.24	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:143:LYS:O	1:D:147:ASN:ND2	2.25	0.69
1:P:62:GLY:O	1:P:134:TYR:OH	2.11	0.69
1:R:41:ASP:OD1	1:R:41:ASP:N	2.24	0.69
1:G:62:GLY:O	1:G:134:TYR:OH	2.09	0.69
1:R:132:SER:HG	1:R:133:HIS:HD1	1.40	0.69
1:B:62:GLY:O	1:B:134:TYR:OH	2.11	0.69
1:Z:143:LYS:O	1:Z:147:ASN:ND2	2.26	0.69
1:T:62:GLY:O	1:T:134:TYR:OH	2.10	0.69
1:E:143:LYS:O	1:E:147:ASN:ND2	2.25	0.68
1:J:62:GLY:O	1:J:134:TYR:OH	2.10	0.68
1:N:62:GLY:O	1:N:134:TYR:OH	2.10	0.68
1:O:43:VAL:O	1:Q:154:ARG:NH2	2.26	0.68
1:T:14:GLU:HG3	1:T:70:GLN:HE22	1.58	0.68
1:O:143:LYS:O	1:O:147:ASN:ND2	2.25	0.68
1:T:132:SER:HG	1:T:133:HIS:HD1	1.41	0.68
1:R:62:GLY:O	1:R:134:TYR:OH	2.11	0.68
1:U:62:GLY:O	1:U:134:TYR:OH	2.11	0.68
1:S:41:ASP:N	1:S:41:ASP:OD1	2.26	0.68
1:I:62:GLY:O	1:I:134:TYR:OH	2.11	0.68
1:H:154:ARG:NH2	1:V:43:VAL:O	2.26	0.68
1:L:143:LYS:O	1:L:147:ASN:ND2	2.26	0.68
1:S:62:GLY:O	1:S:134:TYR:OH	2.11	0.68
1:W:41:ASP:OD2	1:W:41:ASP:N	2.23	0.68
1:Z:43:VAL:O	1:V:154:ARG:NH2	2.27	0.67
1:I:143:LYS:O	1:I:147:ASN:ND2	2.26	0.67
1:Q:64:GLU:HG3	1:R:36:PHE:HZ	1.59	0.67
1:D:17:VAL:HG12	1:D:114:LEU:HD21	1.76	0.67
1:Z:62:GLY:O	1:Z:134:TYR:OH	2.11	0.67
1:H:62:GLY:O	1:H:134:TYR:OH	2.11	0.67
1:O:115:HIS:HE2	1:O:127:CYS:HG	1.42	0.67
1:P:26:ARG:HE	1:P:83:GLN:HB2	1.59	0.67
1:H:26:ARG:HE	1:H:83:GLN:HG2	1.58	0.67
1:P:6:ARG:NH2	1:P:14:GLU:OE1	2.26	0.67
1:I:154:ARG:NH2	1:N:43:VAL:O	2.27	0.67
1:T:132:SER:OG	1:T:133:HIS:ND1	2.27	0.67
1:U:133:HIS:O	1:U:137:LYS:NZ	2.19	0.67
1:A:143:LYS:O	1:A:147:ASN:ND2	2.27	0.67
1:J:17:VAL:HG12	1:J:114:LEU:HD21	1.77	0.67
1:L:184:GLY:O	1:L:188:SER:OG	2.12	0.67
1:D:26:ARG:HE	1:D:83:GLN:HB2	1.60	0.67
1:O:62:GLY:O	1:O:134:TYR:OH	2.13	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:143:LYS:O	1:G:147:ASN:ND2	2.27	0.67
1:K:62:GLY:O	1:K:134:TYR:OH	2.13	0.66
1:S:132:SER:OG	1:S:133:HIS:ND1	2.26	0.66
1:F:143:LYS:O	1:F:147:ASN:ND2	2.27	0.66
1:C:62:GLY:O	1:C:134:TYR:OH	2.13	0.66
1:V:155:VAL:HG22	1:V:171:GLY:HA3	1.76	0.66
1:J:41:ASP:OD1	1:J:41:ASP:N	2.24	0.66
1:L:43:VAL:O	1:U:154:ARG:NH2	2.28	0.66
1:S:143:LYS:O	1:S:147:ASN:ND2	2.29	0.66
1:V:62:GLY:O	1:V:134:TYR:OH	2.14	0.66
1:W:143:LYS:O	1:W:147:ASN:ND2	2.27	0.66
1:L:155:VAL:HG22	1:L:171:GLY:HA3	1.76	0.66
1:O:17:VAL:HG12	1:O:114:LEU:HD21	1.78	0.66
1:N:155:VAL:HG22	1:N:171:GLY:HA3	1.78	0.66
1:P:41:ASP:OD2	1:P:41:ASP:N	2.25	0.66
1:T:17:VAL:HG12	1:T:114:LEU:HD21	1.77	0.66
1:I:183:ASP:OD1	1:I:184:GLY:N	2.27	0.66
1:C:143:LYS:O	1:C:147:ASN:ND2	2.29	0.66
1:M:62:GLY:O	1:M:134:TYR:OH	2.12	0.66
1:M:143:LYS:O	1:M:147:ASN:ND2	2.29	0.66
1:J:143:LYS:O	1:J:147:ASN:ND2	2.28	0.65
1:K:143:LYS:O	1:K:147:ASN:ND2	2.28	0.65
1:O:173:TYR:HB2	1:Q:154:ARG:HD2	1.77	0.65
1:P:143:LYS:O	1:P:147:ASN:ND2	2.28	0.65
1:W:26:ARG:HE	1:W:83:GLN:HB2	1.61	0.65
1:Q:133:HIS:O	1:Q:137:LYS:NZ	2.19	0.65
1:E:17:VAL:HG12	1:E:114:LEU:HD21	1.79	0.65
1:I:26:ARG:HE	1:I:83:GLN:HB2	1.61	0.65
1:V:115:HIS:NE2	1:V:127:CYS:SG	2.69	0.65
1:R:30:THR:OG1	1:R:103:MET:SD	2.51	0.65
1:H:154:ARG:HD2	1:V:173:TYR:HB2	1.78	0.65
1:Q:13:VAL:HG13	1:Q:117:LEU:HD22	1.79	0.65
1:J:132:SER:OG	1:J:133:HIS:ND1	2.26	0.65
1:V:133:HIS:O	1:V:137:LYS:NZ	2.23	0.65
1:V:143:LYS:O	1:V:147:ASN:ND2	2.29	0.65
1:D:62:GLY:O	1:D:134:TYR:OH	2.13	0.65
1:P:5:ILE:HG22	1:Q:142:ILE:HG22	1.79	0.65
1:C:34:LEU:HD11	1:C:96:ALA:HB1	1.79	0.64
1:W:62:GLY:O	1:W:134:TYR:OH	2.13	0.64
1:I:154:ARG:HD2	1:N:173:TYR:HB2	1.79	0.64
1:M:6:ARG:NH2	1:M:14:GLU:OE1	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:17:VAL:HG12	1:U:114:LEU:HD21	1.79	0.64
1:G:17:VAL:HG12	1:G:114:LEU:HD21	1.79	0.64
1:G:34:LEU:HD11	1:G:96:ALA:HB1	1.80	0.64
1:M:26:ARG:HE	1:M:83:GLN:HB2	1.61	0.64
1:M:89:GLU:OE2	1:N:76:ARG:NH1	2.31	0.64
1:R:143:LYS:O	1:R:147:ASN:ND2	2.29	0.64
1:U:143:LYS:O	1:U:147:ASN:ND2	2.31	0.64
1:W:6:ARG:NH2	1:W:14:GLU:OE1	2.31	0.64
1:Z:70:GLN:HE21	1:Z:75:GLY:HA3	1.62	0.64
1:H:143:LYS:O	1:H:147:ASN:ND2	2.31	0.64
1:L:173:TYR:HB2	1:U:154:ARG:HD2	1.81	0.63
1:K:26:ARG:HE	1:K:83:GLN:HB2	1.62	0.63
1:A:17:VAL:HG12	1:A:114:LEU:HD21	1.79	0.63
1:L:115:HIS:CD2	1:D:124:PRO:HB3	2.34	0.63
1:B:143:LYS:O	1:B:147:ASN:ND2	2.30	0.63
1:G:26:ARG:HD3	1:G:83:GLN:HB3	1.80	0.63
1:H:89:GLU:OE2	1:S:76:ARG:NH1	2.32	0.63
1:E:34:LEU:HD11	1:E:96:ALA:HB1	1.81	0.63
1:I:34:LEU:HD11	1:I:96:ALA:HB1	1.81	0.63
1:T:143:LYS:O	1:T:147:ASN:ND2	2.29	0.63
1:N:143:LYS:O	1:N:147:ASN:ND2	2.31	0.63
1:R:132:SER:OG	1:R:133:HIS:ND1	2.26	0.62
1:I:17:VAL:HG12	1:I:114:LEU:HD21	1.79	0.62
1:Z:26:ARG:HE	1:Z:83:GLN:HB3	1.63	0.62
1:E:184:GLY:O	1:E:188:SER:OG	2.14	0.62
1:H:142:ILE:HG22	1:W:5:ILE:HG22	1.82	0.62
1:G:183:ASP:OD1	1:G:184:GLY:N	2.33	0.62
1:A:133:HIS:O	1:A:137:LYS:NZ	2.20	0.62
1:T:34:LEU:HD11	1:T:96:ALA:HB1	1.82	0.62
1:V:26:ARG:HD2	1:V:83:GLN:HG3	1.82	0.62
1:V:89:GLU:OE2	1:W:76:ARG:NE	2.33	0.62
1:V:17:VAL:HG12	1:V:114:LEU:HD21	1.81	0.61
1:W:10:SER:HB2	1:W:121:ARG:HH21	1.65	0.61
1:P:17:VAL:HG12	1:P:114:LEU:HD21	1.82	0.61
1:S:6:ARG:NH2	1:S:14:GLU:OE1	2.34	0.61
1:P:183:ASP:OD1	1:P:184:GLY:N	2.34	0.61
1:Z:70:GLN:NE2	1:Z:75:GLY:HA3	2.16	0.61
1:I:142:ILE:HG22	1:M:5:ILE:HG22	1.81	0.61
1:E:70:GLN:HG2	1:E:77:ALA:HB2	1.81	0.61
1:R:183:ASP:OD1	1:R:184:GLY:N	2.33	0.61
1:I:89:GLU:OE2	1:J:76:ARG:NH1	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:26:ARG:HE	1:J:83:GLN:HB3	1.65	0.61
1:G:183:ASP:O	1:G:187:GLU:N	2.34	0.61
1:I:72:ASP:HA	1:T:143:LYS:HD3	1.82	0.60
1:Q:143:LYS:O	1:Q:147:ASN:ND2	2.34	0.60
1:S:17:VAL:HG12	1:S:114:LEU:HD21	1.83	0.60
1:L:34:LEU:HD11	1:L:96:ALA:HB1	1.83	0.60
1:F:26:ARG:O	1:F:30:THR:HG22	2.01	0.60
1:L:6:ARG:NH1	1:L:9:TYR:O	2.35	0.60
1:O:183:ASP:OD1	1:O:184:GLY:N	2.34	0.60
1:F:183:ASP:OD1	1:F:184:GLY:N	2.35	0.60
1:J:34:LEU:HD11	1:J:96:ALA:HB1	1.82	0.60
1:O:115:HIS:NE2	1:O:127:CYS:SG	2.72	0.60
1:N:133:HIS:O	1:N:137:LYS:NZ	2.25	0.60
1:T:89:GLU:OE2	1:U:76:ARG:NE	2.35	0.60
1:B:183:ASP:O	1:B:187:GLU:N	2.30	0.60
1:J:5:ILE:HG22	1:P:142:ILE:HG22	1.84	0.60
1:Z:34:LEU:HD11	1:Z:96:ALA:HB1	1.84	0.60
1:O:26:ARG:HD2	1:O:83:GLN:HG3	1.82	0.60
1:H:183:ASP:OD2	1:H:184:GLY:N	2.34	0.59
1:O:8:ASN:O	1:O:121:ARG:NH2	2.36	0.59
1:M:17:VAL:HG12	1:M:114:LEU:HD21	1.82	0.59
1:H:76:ARG:NH1	1:S:89:GLU:OE1	2.36	0.59
1:E:153:ARG:NH2	1:O:4:GLN:OE1	2.36	0.59
1:G:153:ARG:NH2	1:V:4:GLN:OE1	2.36	0.59
1:A:30:THR:HG22	1:A:85:PRO:HA	1.85	0.59
1:U:26:ARG:HE	1:U:83:GLN:HB2	1.66	0.59
1:A:34:LEU:HD11	1:A:96:ALA:HB1	1.85	0.59
1:G:131:GLU:OE1	1:V:127:CYS:HB3	2.03	0.59
1:W:3:SER:OG	1:W:4:GLN:N	2.35	0.59
1:N:17:VAL:HG12	1:N:114:LEU:HD21	1.84	0.59
1:R:17:VAL:HG12	1:R:114:LEU:HD21	1.83	0.59
1:G:36:PHE:HZ	1:B:64:GLU:HG2	1.68	0.59
1:M:36:PHE:O	1:N:71:ASN:ND2	2.36	0.58
1:S:132:SER:HG	1:S:133:HIS:HD1	1.45	0.58
1:I:183:ASP:O	1:I:187:GLU:N	2.36	0.58
1:K:6:ARG:NH2	1:K:14:GLU:OE1	2.30	0.58
1:C:70:GLN:HG2	1:C:77:ALA:HB2	1.84	0.58
1:M:70:GLN:NE2	1:M:75:GLY:HA3	2.19	0.58
1:K:142:ILE:HG22	1:S:5:ILE:HG22	1.86	0.58
1:B:183:ASP:OD1	1:B:184:GLY:N	2.37	0.58
1:A:5:ILE:HG22	1:V:142:ILE:HG22	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:10:SER:OG	1:C:11:THR:N	2.34	0.57
1:E:5:ILE:HG22	1:B:142:ILE:HG22	1.85	0.57
1:J:17:VAL:O	1:J:21:VAL:HG12	2.04	0.57
1:K:70:GLN:NE2	1:K:75:GLY:HA3	2.20	0.57
1:K:81:ASP:HB2	1:L:83:GLN:HA	1.86	0.57
1:L:8:ASN:O	1:L:121:ARG:NH2	2.37	0.57
1:A:142:ILE:HG22	1:G:5:ILE:HG22	1.86	0.57
1:Q:34:LEU:HD11	1:Q:96:ALA:HB1	1.84	0.57
1:N:151:ASN:O	1:N:155:VAL:HG12	2.04	0.57
1:E:131:GLU:OE1	1:O:127:CYS:HB3	2.04	0.57
1:R:34:LEU:HD11	1:R:96:ALA:HB1	1.86	0.57
1:J:143:LYS:HD3	1:Q:72:ASP:HA	1.85	0.57
1:P:9:TYR:HE2	1:P:70:GLN:HE22	1.52	0.57
1:Q:26:ARG:HE	1:Q:83:GLN:HB2	1.69	0.57
1:N:183:ASP:OD1	1:N:184:GLY:N	2.38	0.57
1:Z:5:ILE:HG22	1:D:142:ILE:HG22	1.87	0.57
1:I:5:ILE:HB	1:T:142:ILE:HG22	1.87	0.57
1:H:17:VAL:HG21	1:H:70:GLN:HE22	1.69	0.56
1:R:5:ILE:HG22	1:W:142:ILE:HG22	1.87	0.56
1:H:72:ASP:HA	1:R:143:LYS:HD3	1.86	0.56
1:J:14:GLU:HG2	1:J:70:GLN:HE22	1.69	0.56
1:O:76:ARG:NH1	1:P:89:GLU:OE2	2.37	0.56
1:M:183:ASP:OD2	1:M:184:GLY:N	2.39	0.56
1:N:13:VAL:HG23	1:N:114:LEU:HD11	1.86	0.56
1:D:128:ASP:HA	1:D:131:GLU:HB2	1.88	0.56
1:E:9:TYR:OH	1:E:70:GLN:NE2	2.32	0.56
1:Q:183:ASP:OD2	1:Q:184:GLY:N	2.39	0.56
1:Z:153:ARG:NH2	1:L:4:GLN:OE1	2.38	0.56
1:C:153:ARG:NH2	1:N:4:GLN:OE1	2.38	0.56
1:H:5:ILE:HG12	1:S:41:ASP:OD2	2.06	0.56
1:M:81:ASP:HB2	1:N:83:GLN:HA	1.87	0.56
1:P:39:ASP:OD2	1:P:53:ARG:NH1	2.31	0.56
1:P:70:GLN:NE2	1:P:75:GLY:HA3	2.21	0.56
1:A:30:THR:OG1	1:A:103:MET:SD	2.54	0.56
1:E:64:GLU:OE1	1:F:53:ARG:NH1	2.38	0.56
1:G:65:ARG:HD3	1:G:133:HIS:CD2	2.40	0.56
1:G:70:GLN:NE2	1:G:75:GLY:HA3	2.21	0.55
1:A:70:GLN:HG2	1:A:77:ALA:HB2	1.87	0.55
1:H:10:SER:OG	1:H:12:GLU:OE1	2.21	0.55
1:L:142:ILE:HG22	1:D:5:ILE:HG22	1.88	0.55
1:D:65:ARG:HH21	1:D:137:LYS:HZ2	1.55	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:65:ARG:HD3	1:E:133:HIS:CD2	2.42	0.55
1:V:76:ARG:NH1	1:W:89:GLU:OE2	2.38	0.55
1:G:9:TYR:HE2	1:G:70:GLN:HE22	1.55	0.55
1:F:94:GLN:O	1:F:98:GLU:HG3	2.06	0.55
1:H:64:GLU:HG2	1:S:36:PHE:HZ	1.72	0.55
1:E:3:SER:OG	1:E:4:GLN:N	2.39	0.55
1:C:83:GLN:HA	1:D:81:ASP:HB2	1.89	0.55
1:Q:65:ARG:HD3	1:Q:133:HIS:CD2	2.41	0.55
1:M:10:SER:HB2	1:M:121:ARG:HH21	1.72	0.54
1:M:142:ILE:HG22	1:T:5:ILE:HB	1.88	0.54
1:O:131:GLU:HB3	1:B:128:ASP:HB3	1.88	0.54
1:S:26:ARG:O	1:S:30:THR:HG23	2.07	0.54
1:B:39:ASP:OD2	1:B:53:ARG:NH2	2.38	0.54
1:Q:5:ILE:HG12	1:R:41:ASP:OD2	2.08	0.54
1:K:131:GLU:HB3	1:S:128:ASP:HB2	1.88	0.54
1:L:11:THR:HA	1:L:14:GLU:HB3	1.89	0.54
1:O:6:ARG:NH1	1:O:9:TYR:O	2.40	0.54
1:C:10:SER:OG	1:C:12:GLU:OE1	2.22	0.54
1:G:36:PHE:CZ	1:B:64:GLU:HG2	2.42	0.54
1:J:41:ASP:O	1:T:150:THR:OG1	2.21	0.54
1:O:65:ARG:HD3	1:O:133:HIS:ND1	2.23	0.54
1:D:70:GLN:HG2	1:D:77:ALA:HB2	1.89	0.54
1:K:17:VAL:HG12	1:K:114:LEU:HD21	1.90	0.54
1:W:17:VAL:HG12	1:W:114:LEU:HD21	1.90	0.54
1:K:89:GLU:OE1	1:L:76:ARG:NE	2.41	0.54
1:C:7:GLN:HE22	1:F:109:GLN:HG2	1.72	0.54
1:M:9:TYR:HE2	1:M:70:GLN:HE22	1.56	0.54
1:Q:6:ARG:NH1	1:Q:9:TYR:O	2.41	0.54
1:V:71:ASN:ND2	1:W:36:PHE:O	2.40	0.54
1:O:11:THR:HA	1:O:14:GLU:HB3	1.88	0.54
1:R:14:GLU:HG2	1:R:70:GLN:HE22	1.72	0.54
1:R:26:ARG:HE	1:R:83:GLN:HB3	1.73	0.54
1:H:6:ARG:NH1	1:H:9:TYR:O	2.40	0.53
1:I:94:GLN:O	1:I:98:GLU:HG3	2.07	0.53
1:K:60:ARG:NH2	1:L:57:GLU:OE2	2.40	0.53
1:L:65:ARG:HB3	1:L:134:TYR:OH	2.08	0.53
1:O:10:SER:HB3	1:O:121:ARG:HE	1.73	0.53
1:C:89:GLU:OE2	1:D:76:ARG:NE	2.42	0.53
1:O:5:ILE:HG12	1:P:41:ASP:OD1	2.07	0.53
1:L:115:HIS:O	1:L:115:HIS:ND1	2.41	0.53
1:F:31:TYR:OH	1:F:104:GLU:OE2	2.19	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:6:ARG:NH1	1:E:9:TYR:O	2.41	0.53
1:E:34:LEU:HD13	1:E:90:TRP:CD2	2.44	0.53
1:L:118:GLY:HA3	1:L:126:LEU:HD23	1.90	0.53
1:N:142:ILE:HG22	1:F:5:ILE:HG22	1.90	0.53
1:Z:70:GLN:HG2	1:Z:77:ALA:HB2	1.90	0.53
1:Z:131:GLU:OE1	1:L:127:CYS:HB3	2.08	0.53
1:J:13:VAL:HG23	1:J:114:LEU:HD11	1.91	0.53
1:L:17:VAL:HG12	1:L:114:LEU:HD21	1.89	0.53
1:L:26:ARG:HG2	1:L:82:VAL:HG13	1.89	0.53
1:L:183:ASP:OD1	1:L:184:GLY:N	2.42	0.53
1:N:26:ARG:HG2	1:N:82:VAL:HG13	1.90	0.53
1:C:10:SER:HB3	1:C:13:VAL:HG13	1.91	0.52
1:V:151:ASN:O	1:V:155:VAL:HG12	2.09	0.52
1:T:65:ARG:HD3	1:T:133:HIS:CD2	2.44	0.52
1:V:183:ASP:OD2	1:V:184:GLY:N	2.42	0.52
1:R:13:VAL:HG23	1:R:114:LEU:HD11	1.90	0.52
1:F:20:LEU:HD21	1:F:111:LEU:HD12	1.90	0.52
1:K:70:GLN:HG2	1:K:77:ALA:HB2	1.92	0.52
1:S:142:ILE:HG22	1:U:5:ILE:HG22	1.90	0.52
1:O:10:SER:HB3	1:O:121:ARG:NE	2.25	0.52
1:H:5:ILE:HB	1:R:142:ILE:HG22	1.90	0.52
1:C:60:ARG:HD2	1:D:60:ARG:CZ	2.40	0.52
1:K:65:ARG:HD3	1:K:133:HIS:CD2	2.45	0.52
1:O:121:ARG:HG2	1:O:121:ARG:O	2.10	0.52
1:B:26:ARG:O	1:B:30:THR:HG22	2.10	0.52
1:N:65:ARG:HB3	1:N:134:TYR:OH	2.09	0.52
1:Q:64:GLU:HG3	1:R:36:PHE:CZ	2.43	0.52
1:F:13:VAL:HG23	1:F:114:LEU:HD11	1.92	0.52
1:Q:121:ARG:HH11	1:Q:121:ARG:HG2	1.75	0.52
1:G:11:THR:HA	1:G:14:GLU:HB3	1.91	0.51
1:O:121:ARG:NH1	1:O:123:ASP:HB2	2.25	0.51
1:A:97:MET:HG2	1:A:149:LEU:HG	1.92	0.51
1:C:31:TYR:O	1:C:35:GLY:N	2.44	0.51
1:G:34:LEU:HD13	1:G:90:TRP:CD2	2.45	0.51
1:M:182:HIS:O	1:M:186:ILE:HG12	2.10	0.51
1:O:36:PHE:HZ	1:P:64:GLU:HG2	1.75	0.51
1:N:131:GLU:HB3	1:F:128:ASP:HB2	1.92	0.51
1:C:11:THR:HA	1:C:14:GLU:HB3	1.92	0.51
1:C:143:LYS:HD3	1:N:72:ASP:HA	1.92	0.51
1:C:182:HIS:O	1:C:186:ILE:HG12	2.10	0.51
1:I:64:GLU:HG2	1:J:36:PHE:HZ	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:118:GLY:HA3	1:C:126:LEU:HD23	1.92	0.51
1:G:6:ARG:NH1	1:G:9:TYR:O	2.43	0.51
1:I:121:ARG:HG2	1:I:121:ARG:HH11	1.75	0.51
1:Q:71:ASN:OD1	1:Q:71:ASN:N	2.43	0.51
1:S:10:SER:OG	1:S:12:GLU:OE2	2.22	0.51
1:J:65:ARG:HD3	1:J:133:HIS:CD2	2.45	0.51
1:K:30:THR:OG1	1:K:103:MET:SD	2.58	0.51
1:R:34:LEU:HD13	1:R:90:TRP:CD2	2.46	0.51
1:T:34:LEU:HD13	1:T:90:TRP:CD2	2.46	0.51
1:D:121:ARG:HG2	1:D:121:ARG:HH11	1.75	0.51
1:C:34:LEU:HD13	1:C:90:TRP:CD2	2.46	0.51
1:G:89:GLU:OE1	1:B:76:ARG:NE	2.44	0.51
1:G:121:ARG:HG2	1:G:121:ARG:HH21	1.76	0.51
1:L:151:ASN:O	1:L:155:VAL:HG12	2.11	0.51
1:O:36:PHE:CZ	1:P:64:GLU:HG2	2.45	0.51
1:U:183:ASP:OD1	1:U:184:GLY:N	2.44	0.51
1:F:182:HIS:O	1:F:186:ILE:HG12	2.11	0.51
1:L:34:LEU:HD13	1:L:90:TRP:CD2	2.46	0.51
1:M:76:ARG:NH1	1:N:89:GLU:OE2	2.44	0.51
1:J:34:LEU:HD13	1:J:90:TRP:CD2	2.46	0.51
1:Q:34:LEU:HD13	1:Q:90:TRP:CD2	2.46	0.51
1:R:65:ARG:HD3	1:R:133:HIS:CD2	2.45	0.51
1:E:26:ARG:NH1	1:E:83:GLN:HB3	2.26	0.51
1:G:143:LYS:HD3	1:V:72:ASP:HA	1.93	0.51
1:N:115:HIS:NE2	1:N:127:CYS:SG	2.78	0.51
1:O:71:ASN:OD1	1:O:71:ASN:N	2.44	0.51
1:F:26:ARG:HH11	1:F:83:GLN:HB2	1.76	0.51
1:F:70:GLN:HG2	1:F:77:ALA:HB2	1.93	0.51
1:H:121:ARG:HG2	1:H:121:ARG:HH11	1.76	0.50
1:J:182:HIS:O	1:J:186:ILE:HG12	2.12	0.50
1:L:121:ARG:O	1:L:121:ARG:HG2	2.11	0.50
1:V:155:VAL:O	1:V:155:VAL:HG13	2.11	0.50
1:I:34:LEU:HD13	1:I:90:TRP:CD2	2.47	0.50
1:L:71:ASN:OD1	1:L:71:ASN:N	2.44	0.50
1:S:183:ASP:OD1	1:S:184:GLY:N	2.45	0.50
1:W:65:ARG:HD3	1:W:133:HIS:CD2	2.46	0.50
1:J:142:ILE:HG22	1:Q:5:ILE:HB	1.92	0.50
1:B:48:VAL:HG22	1:B:180:LEU:HD12	1.93	0.50
1:A:6:ARG:NH1	1:A:9:TYR:O	2.44	0.50
1:S:14:GLU:HG3	1:S:70:GLN:HE22	1.76	0.50
1:S:65:ARG:HD3	1:S:133:HIS:CD2	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:182:HIS:O	1:N:186:ILE:HG12	2.12	0.50
1:V:83:GLN:HA	1:W:81:ASP:HB2	1.92	0.50
1:W:70:GLN:NE2	1:W:75:GLY:HA3	2.26	0.50
1:G:150:THR:OG1	1:W:41:ASP:O	2.17	0.50
1:Z:17:VAL:HG12	1:Z:114:LEU:HD21	1.92	0.50
1:Z:65:ARG:HD3	1:Z:133:HIS:CD2	2.47	0.50
1:A:34:LEU:HD13	1:A:90:TRP:CD2	2.46	0.50
1:E:13:VAL:HG11	1:E:121:ARG:HH21	1.77	0.50
1:G:13:VAL:HG11	1:G:121:ARG:HH11	1.76	0.50
1:U:118:GLY:HA3	1:U:126:LEU:HD23	1.94	0.50
1:A:13:VAL:HG11	1:A:121:ARG:HH11	1.77	0.49
1:A:182:HIS:O	1:A:186:ILE:HG12	2.11	0.49
1:L:155:VAL:O	1:L:155:VAL:HG13	2.12	0.49
1:Q:87:GLN:NE2	1:Q:89:GLU:O	2.45	0.49
1:D:6:ARG:NH1	1:D:9:TYR:O	2.45	0.49
1:E:11:THR:HA	1:E:14:GLU:HB3	1.94	0.49
1:M:118:GLY:HA3	1:M:126:LEU:HD23	1.94	0.49
1:O:83:GLN:HA	1:P:81:ASP:HB2	1.93	0.49
1:P:65:ARG:HD3	1:P:133:HIS:CD2	2.47	0.49
1:V:36:PHE:CZ	1:W:64:GLU:HG2	2.47	0.49
1:S:118:GLY:HA3	1:S:126:LEU:HD23	1.92	0.49
1:T:118:GLY:HA3	1:T:126:LEU:HD23	1.94	0.49
1:U:17:VAL:HG21	1:U:70:GLN:HE21	1.77	0.49
1:H:71:ASN:OD1	1:H:71:ASN:N	2.45	0.49
1:K:76:ARG:NH1	1:L:89:GLU:OE2	2.45	0.49
1:M:64:GLU:HG2	1:N:36:PHE:CZ	2.47	0.49
1:S:143:LYS:HD3	1:U:72:ASP:HA	1.92	0.49
1:Z:143:LYS:NZ	1:Z:147:ASN:HD21	2.10	0.49
1:I:6:ARG:NH1	1:I:9:TYR:O	2.45	0.49
1:Q:118:GLY:HA3	1:Q:126:LEU:HD23	1.95	0.49
1:W:9:TYR:HE2	1:W:70:GLN:HE22	1.58	0.49
1:W:48:VAL:HG22	1:W:180:LEU:HD12	1.93	0.49
1:W:182:HIS:O	1:W:186:ILE:HG12	2.12	0.49
1:A:132:SER:OG	1:A:133:HIS:HD2	1.96	0.49
1:C:73:ARG:NH1	1:C:123:ASP:OD2	2.35	0.49
1:G:118:GLY:HA3	1:G:126:LEU:HD23	1.95	0.49
1:M:30:THR:OG1	1:M:103:MET:SD	2.58	0.49
1:S:183:ASP:O	1:S:187:GLU:N	2.40	0.49
1:T:36:PHE:CZ	1:U:64:GLU:HG2	2.47	0.49
1:C:65:ARG:HD3	1:C:133:HIS:HD2	1.76	0.49
2:C:201:FE:FE	2:F:201:FE:FE	0.98	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:201:FE:FE	2:Q:201:FE:FE	0.99	0.49
1:N:22:ASN:O	1:N:26:ARG:HG3	2.12	0.49
1:Z:34:LEU:HD13	1:Z:90:TRP:CD2	2.48	0.49
1:H:11:THR:HA	1:H:14:GLU:HB3	1.94	0.49
1:G:143:LYS:NZ	1:G:147:ASN:HD21	2.11	0.49
1:L:22:ASN:O	1:L:26:ARG:HG3	2.12	0.49
1:M:65:ARG:HD3	1:M:133:HIS:CD2	2.47	0.49
1:Q:92:LYS:HD2	1:Q:94:GLN:HB3	1.95	0.49
1:A:143:LYS:NZ	1:A:147:ASN:HD21	2.11	0.48
1:R:10:SER:OG	1:R:13:VAL:HG12	2.13	0.48
1:F:143:LYS:NZ	1:F:147:ASN:HD21	2.10	0.48
2:I:201:FE:FE	2:I:202:FE:FE	0.99	0.48
1:S:71:ASN:OD1	1:S:71:ASN:N	2.46	0.48
1:V:13:VAL:HG23	1:V:114:LEU:HD11	1.95	0.48
1:V:64:GLU:HG2	1:W:36:PHE:HZ	1.79	0.48
1:B:11:THR:HA	1:B:14:GLU:HB3	1.95	0.48
1:E:143:LYS:NZ	1:E:147:ASN:HD21	2.10	0.48
1:I:76:ARG:NH1	1:J:89:GLU:OE2	2.46	0.48
1:I:155:VAL:HB	1:I:171:GLY:HA3	1.96	0.48
1:Q:48:VAL:HG22	1:Q:180:LEU:HD12	1.95	0.48
1:R:134:TYR:O	1:R:138:GLU:HG2	2.13	0.48
2:S:201:FE:FE	2:U:201:FE:FE	0.99	0.48
1:D:3:SER:OG	1:D:4:GLN:N	2.45	0.48
1:V:48:VAL:HG22	1:V:180:LEU:HD12	1.95	0.48
1:Z:71:ASN:OD1	1:Z:71:ASN:N	2.46	0.48
1:G:65:ARG:HB3	1:G:134:TYR:OH	2.14	0.48
1:O:58:GLU:OE1	1:O:59:LYS:NZ	2.38	0.48
1:A:93:THR:HG22	1:A:152:LEU:HD11	1.96	0.48
1:K:128:ASP:HB2	1:U:131:GLU:HB3	1.94	0.48
1:D:70:GLN:OE1	1:D:75:GLY:HA3	2.14	0.48
1:H:155:VAL:HB	1:H:171:GLY:HA3	1.96	0.48
1:J:71:ASN:OD1	1:J:71:ASN:N	2.47	0.48
1:V:36:PHE:O	1:W:71:ASN:ND2	2.47	0.48
1:W:65:ARG:HA	1:W:68:GLU:HG2	1.96	0.48
1:D:182:HIS:O	1:D:186:ILE:HG12	2.13	0.48
1:Z:9:TYR:HE2	1:Z:70:GLN:HE22	1.60	0.48
1:E:150:THR:OG1	1:P:41:ASP:O	2.19	0.48
1:L:10:SER:HB3	1:L:121:ARG:HE	1.79	0.48
1:O:118:GLY:O	1:O:122:ALA:N	2.47	0.48
1:P:48:VAL:HG22	1:P:180:LEU:HD12	1.96	0.48
1:P:59:LYS:HA	1:P:59:LYS:HD3	1.63	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:48:VAL:HG22	1:R:180:LEU:HD12	1.96	0.48
1:W:118:GLY:HA3	1:W:126:LEU:HD23	1.95	0.48
1:B:70:GLN:OE1	1:B:75:GLY:HA3	2.14	0.48
1:Z:11:THR:HA	1:Z:14:GLU:HB3	1.95	0.48
1:I:71:ASN:OD1	1:I:71:ASN:N	2.45	0.48
1:M:64:GLU:CD	1:N:53:ARG:HH21	2.17	0.48
1:O:143:LYS:NZ	1:O:147:ASN:HD21	2.12	0.48
1:R:118:GLY:HA3	1:R:126:LEU:HD23	1.96	0.48
1:S:132:SER:OG	1:S:133:HIS:N	2.47	0.48
1:T:71:ASN:OD1	1:T:71:ASN:N	2.46	0.48
1:H:182:HIS:O	1:H:186:ILE:HG12	2.13	0.47
1:N:13:VAL:HB	1:N:117:LEU:HD22	1.96	0.47
1:O:152:LEU:O	1:O:155:VAL:HG12	2.13	0.47
1:P:149:LEU:HA	1:P:149:LEU:HD23	1.68	0.47
1:S:48:VAL:HG22	1:S:180:LEU:HD12	1.96	0.47
1:S:70:GLN:HG2	1:S:77:ALA:HB2	1.96	0.47
1:U:71:ASN:N	1:U:71:ASN:OD1	2.46	0.47
1:V:36:PHE:HZ	1:W:64:GLU:HG2	1.79	0.47
1:A:48:VAL:HG22	1:A:180:LEU:HD12	1.96	0.47
1:N:30:THR:HA	1:N:85:PRO:HB3	1.95	0.47
1:Q:183:ASP:O	1:Q:187:GLU:N	2.46	0.47
1:U:13:VAL:HG23	1:U:114:LEU:HD11	1.95	0.47
1:V:17:VAL:HG21	1:V:70:GLN:NE2	2.29	0.47
1:B:143:LYS:NZ	1:B:147:ASN:HD21	2.11	0.47
1:P:118:GLY:HA3	1:P:126:LEU:HD23	1.96	0.47
1:Q:155:VAL:HB	1:Q:171:GLY:HA3	1.96	0.47
1:B:149:LEU:O	1:B:153:ARG:HG3	2.15	0.47
1:D:48:VAL:HG22	1:D:180:LEU:HD12	1.96	0.47
1:J:118:GLY:HA3	1:J:126:LEU:HD23	1.95	0.47
1:K:64:GLU:CD	1:L:53:ARG:HH21	2.16	0.47
1:N:17:VAL:HG21	1:N:70:GLN:NE2	2.29	0.47
1:O:65:ARG:HB3	1:O:134:TYR:OH	2.14	0.47
1:S:13:VAL:HG23	1:S:114:LEU:HD11	1.97	0.47
1:C:128:ASP:O	1:C:132:SER:HB3	2.15	0.47
1:C:143:LYS:NZ	1:C:147:ASN:HD21	2.12	0.47
1:E:182:HIS:O	1:E:186:ILE:HG12	2.15	0.47
1:L:48:VAL:HG22	1:L:180:LEU:HD12	1.97	0.47
1:O:181:LYS:HD2	1:O:181:LYS:HA	1.77	0.47
1:D:143:LYS:NZ	1:D:147:ASN:HD21	2.12	0.47
1:F:70:GLN:OE1	1:F:75:GLY:HA3	2.14	0.47
1:I:143:LYS:NZ	1:I:147:ASN:HD21	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:118:GLY:HA3	1:K:126:LEU:HD23	1.97	0.47
1:L:143:LYS:NZ	1:L:147:ASN:HD21	2.12	0.47
1:Q:89:GLU:OE2	1:R:76:ARG:NH1	2.47	0.47
1:R:132:SER:OG	1:R:133:HIS:N	2.47	0.47
1:T:48:VAL:HG22	1:T:180:LEU:HD12	1.97	0.47
1:V:55:LEU:HD13	1:V:55:LEU:HA	1.71	0.47
1:W:143:LYS:NZ	1:W:147:ASN:HD21	2.13	0.47
1:A:71:ASN:N	1:A:71:ASN:OD1	2.48	0.47
1:A:149:LEU:HD23	1:A:149:LEU:HA	1.74	0.47
1:C:177:ARG:HG2	1:L:178:LEU:HB3	1.96	0.47
1:E:48:VAL:HG22	1:E:180:LEU:HD12	1.97	0.47
1:E:121:ARG:HH11	1:E:121:ARG:HG2	1.79	0.47
1:H:59:LYS:HD3	1:H:59:LYS:HA	1.64	0.47
1:M:17:VAL:HG21	1:M:70:GLN:OE1	2.15	0.47
1:N:10:SER:OG	1:N:13:VAL:HG12	2.14	0.47
1:O:70:GLN:O	1:O:73:ARG:N	2.48	0.47
1:B:3:SER:HB3	1:B:6:ARG:HB2	1.95	0.47
1:Z:177:ARG:HG2	1:V:178:LEU:HB3	1.97	0.47
1:J:132:SER:OG	1:J:133:HIS:N	2.48	0.47
1:K:143:LYS:NZ	1:K:147:ASN:HD21	2.13	0.47
1:M:23:LEU:HD12	1:M:23:LEU:HA	1.69	0.47
1:R:30:THR:HA	1:R:85:PRO:HB3	1.96	0.47
1:T:132:SER:OG	1:T:133:HIS:N	2.47	0.47
1:D:11:THR:HA	1:D:14:GLU:HB3	1.96	0.47
1:G:64:GLU:HG2	1:B:36:PHE:HZ	1.80	0.47
1:K:17:VAL:HG21	1:K:70:GLN:OE1	2.14	0.47
1:L:180:LEU:HD23	1:L:180:LEU:HA	1.79	0.47
1:M:64:GLU:HG2	1:N:36:PHE:HZ	1.80	0.47
1:O:48:VAL:HG22	1:O:180:LEU:HD12	1.96	0.47
1:R:150:THR:OG1	1:S:41:ASP:O	2.21	0.47
1:U:155:VAL:HB	1:U:171:GLY:HA3	1.97	0.47
1:E:177:ARG:HG2	1:N:178:LEU:HB3	1.97	0.47
1:N:9:TYR:OH	1:N:70:GLN:NE2	2.45	0.47
1:O:136:ASP:OD1	1:O:140:LYS:NZ	2.44	0.47
1:W:10:SER:HB2	1:W:121:ARG:NH2	2.30	0.47
1:C:65:ARG:HD3	1:C:133:HIS:CD2	2.50	0.46
1:E:65:ARG:HB3	1:E:134:TYR:OH	2.14	0.46
1:K:9:TYR:HE2	1:K:70:GLN:HE22	1.61	0.46
1:M:48:VAL:HG22	1:M:180:LEU:HD12	1.97	0.46
1:O:13:VAL:HG11	1:O:121:ARG:NH1	2.30	0.46
1:U:143:LYS:NZ	1:U:147:ASN:HD21	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:30:THR:HA	1:D:85:PRO:HB3	1.96	0.46
1:C:7:GLN:HE21	1:C:7:GLN:HB2	1.54	0.46
1:E:169:SER:HB2	1:E:172:GLU:HB3	1.97	0.46
1:K:180:LEU:HA	1:K:180:LEU:HD23	1.79	0.46
1:K:181:LYS:HD2	1:K:181:LYS:HA	1.72	0.46
1:L:121:ARG:NH1	1:L:123:ASP:HB2	2.30	0.46
1:N:26:ARG:O	1:N:30:THR:HG22	2.16	0.46
1:Q:17:VAL:HG21	1:Q:70:GLN:NE2	2.30	0.46
1:Q:132:SER:HG	1:Q:133:HIS:CE1	2.30	0.46
1:T:10:SER:HB2	1:T:121:ARG:NH2	2.30	0.46
1:T:134:TYR:O	1:T:138:GLU:HG2	2.15	0.46
1:W:13:VAL:HG13	1:W:117:LEU:HD22	1.96	0.46
1:B:70:GLN:HG2	1:B:77:ALA:HB2	1.97	0.46
1:E:30:THR:HA	1:E:85:PRO:HB3	1.96	0.46
1:J:48:VAL:HG22	1:J:180:LEU:HD12	1.97	0.46
1:J:180:LEU:HD23	1:J:180:LEU:HA	1.80	0.46
1:K:23:LEU:HD12	1:K:23:LEU:HA	1.69	0.46
1:M:149:LEU:HD23	1:M:149:LEU:HA	1.70	0.46
1:V:10:SER:OG	1:V:13:VAL:HG12	2.15	0.46
1:A:11:THR:HA	1:A:14:GLU:HB3	1.96	0.46
1:C:58:GLU:OE2	1:C:59:LYS:NZ	2.40	0.46
1:C:59:LYS:HD3	1:C:59:LYS:HA	1.65	0.46
1:E:59:LYS:HA	1:E:59:LYS:HD3	1.70	0.46
1:L:183:ASP:HA	1:L:186:ILE:HG13	1.98	0.46
1:V:30:THR:HA	1:V:85:PRO:HB3	1.96	0.46
1:V:118:GLY:HA3	1:V:126:LEU:HD23	1.97	0.46
1:Z:131:GLU:HB3	1:L:128:ASP:HB2	1.98	0.46
1:A:70:GLN:OE1	1:A:75:GLY:HA3	2.16	0.46
1:G:142:ILE:HG22	1:V:5:ILE:HB	1.98	0.46
1:H:180:LEU:HD23	1:H:180:LEU:HA	1.80	0.46
1:L:30:THR:HA	1:L:85:PRO:HB3	1.96	0.46
1:Q:17:VAL:HG12	1:Q:114:LEU:HD21	1.96	0.46
1:U:59:LYS:HA	1:U:59:LYS:HD3	1.67	0.46
1:Z:92:LYS:HD2	1:Z:172:GLU:OE2	2.15	0.46
1:I:59:LYS:HA	1:I:59:LYS:HD3	1.68	0.46
1:K:30:THR:HA	1:K:85:PRO:HB3	1.97	0.46
1:O:30:THR:HA	1:O:85:PRO:HB3	1.97	0.46
1:O:53:ARG:HH21	1:P:64:GLU:CD	2.19	0.46
1:S:115:HIS:NE2	1:S:127:CYS:SG	2.89	0.46
1:T:6:ARG:NH1	1:T:9:TYR:O	2.49	0.46
1:U:48:VAL:HG22	1:U:180:LEU:HD12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:10:SER:OG	1:Z:11:THR:N	2.47	0.46
1:L:23:LEU:HD12	1:L:23:LEU:HA	1.71	0.46
1:N:48:VAL:HG22	1:N:180:LEU:HD12	1.97	0.46
1:P:22:ASN:ND2	1:P:80:GLN:O	2.49	0.46
1:P:143:LYS:NZ	1:P:147:ASN:HD21	2.13	0.46
1:T:64:GLU:HG2	1:U:36:PHE:HZ	1.81	0.46
1:W:17:VAL:HG21	1:W:70:GLN:OE1	2.16	0.46
1:F:48:VAL:HG22	1:F:180:LEU:HD12	1.97	0.46
1:L:26:ARG:O	1:L:30:THR:HG22	2.16	0.46
1:T:30:THR:HA	1:T:85:PRO:HB3	1.98	0.46
1:V:180:LEU:HD23	1:V:180:LEU:HA	1.79	0.46
1:W:30:THR:HA	1:W:85:PRO:HB3	1.98	0.46
1:F:17:VAL:HG21	1:F:70:GLN:NE2	2.31	0.46
1:Z:149:LEU:HD23	1:Z:149:LEU:HA	1.77	0.46
1:C:48:VAL:HG22	1:C:180:LEU:HD12	1.98	0.46
1:G:177:ARG:HG2	1:O:178:LEU:HB3	1.97	0.46
1:K:48:VAL:HG22	1:K:180:LEU:HD12	1.97	0.46
1:R:71:ASN:N	1:R:71:ASN:OD1	2.45	0.46
1:S:59:LYS:HD3	1:S:59:LYS:HA	1.65	0.46
1:S:70:GLN:NE2	1:S:75:GLY:HA3	2.31	0.46
1:A:13:VAL:HG23	1:A:114:LEU:HD11	1.97	0.46
1:A:26:ARG:O	1:A:30:THR:HG23	2.16	0.46
1:H:131:GLU:HB3	1:W:128:ASP:HB2	1.97	0.46
1:P:17:VAL:HG21	1:P:70:GLN:OE1	2.16	0.46
1:K:59:LYS:HA	1:K:59:LYS:HD3	1.67	0.45
1:K:70:GLN:HE21	1:K:75:GLY:HA3	1.80	0.45
1:P:70:GLN:HE21	1:P:75:GLY:HA3	1.80	0.45
1:U:23:LEU:HA	1:U:23:LEU:HD12	1.68	0.45
1:V:26:ARG:O	1:V:30:THR:HG22	2.16	0.45
1:V:143:LYS:NZ	1:V:147:ASN:HD21	2.13	0.45
1:B:149:LEU:HD23	1:B:149:LEU:HA	1.73	0.45
1:A:55:LEU:HD21	1:A:141:LEU:HD11	1.98	0.45
1:I:92:LYS:HD2	1:I:94:GLN:HB3	1.98	0.45
1:K:65:ARG:HA	1:K:68:GLU:HG2	1.98	0.45
1:E:89:GLU:OE1	1:F:76:ARG:NE	2.49	0.45
1:N:115:HIS:CE1	1:N:127:CYS:HG	2.33	0.45
1:Q:17:VAL:HG21	1:Q:70:GLN:HE22	1.81	0.45
1:V:149:LEU:HD23	1:V:149:LEU:HA	1.71	0.45
1:V:181:LYS:HD2	1:V:181:LYS:HA	1.75	0.45
1:B:97:MET:HG2	1:B:149:LEU:HG	1.98	0.45
1:G:23:LEU:HD12	1:G:23:LEU:HA	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:10:SER:HB3	1:L:121:ARG:NE	2.32	0.45
1:M:143:LYS:NZ	1:M:147:ASN:HD21	2.13	0.45
1:M:180:LEU:HD23	1:M:180:LEU:HA	1.79	0.45
1:O:26:ARG:O	1:O:30:THR:HG22	2.17	0.45
1:Q:143:LYS:NZ	1:Q:147:ASN:HD21	2.14	0.45
1:D:181:LYS:HD2	1:D:181:LYS:HA	1.67	0.45
1:F:59:LYS:HD3	1:F:59:LYS:HA	1.68	0.45
1:H:48:VAL:HG22	1:H:180:LEU:HD12	1.99	0.45
1:K:3:SER:O	1:K:3:SER:OG	2.29	0.45
1:Q:59:LYS:HA	1:Q:59:LYS:HD3	1.67	0.45
1:R:149:LEU:HD23	1:R:149:LEU:HA	1.72	0.45
1:U:149:LEU:O	1:U:153:ARG:HG3	2.16	0.45
1:D:59:LYS:HA	1:D:59:LYS:HD3	1.63	0.45
1:A:59:LYS:HD3	1:A:59:LYS:HA	1.66	0.45
1:G:17:VAL:HG21	1:G:70:GLN:OE1	2.17	0.45
1:G:48:VAL:HG22	1:G:180:LEU:HD12	1.99	0.45
1:N:143:LYS:NZ	1:N:147:ASN:HD21	2.14	0.45
1:P:181:LYS:HD2	1:P:181:LYS:HA	1.76	0.45
1:Q:11:THR:HA	1:Q:14:GLU:HB3	1.98	0.45
1:R:181:LYS:HD2	1:R:181:LYS:HA	1.74	0.45
1:U:26:ARG:NH2	1:U:83:GLN:OE1	2.39	0.45
1:B:58:GLU:OE2	1:B:59:LYS:NZ	2.34	0.45
1:A:30:THR:HA	1:A:85:PRO:HB3	1.97	0.45
1:A:121:ARG:HG2	1:A:121:ARG:HH21	1.80	0.45
1:I:13:VAL:HG11	1:I:121:ARG:HH21	1.82	0.45
1:M:31:TYR:OH	1:M:104:GLU:OE2	2.18	0.45
1:S:154:ARG:HD2	1:T:173:TYR:HB2	1.99	0.45
1:F:111:LEU:HD21	1:F:134:TYR:HB3	1.98	0.45
1:G:64:GLU:HG2	1:B:36:PHE:CZ	2.52	0.45
1:G:70:GLN:HG2	1:G:77:ALA:HB2	1.99	0.45
1:I:31:TYR:OH	1:I:104:GLU:OE2	2.25	0.45
1:M:59:LYS:HA	1:M:59:LYS:HD3	1.67	0.45
1:P:10:SER:HB2	1:P:121:ARG:NH2	2.32	0.45
1:B:155:VAL:HB	1:B:171:GLY:HA3	1.98	0.45
1:Z:48:VAL:HG22	1:Z:180:LEU:HD12	1.99	0.45
1:I:48:VAL:HG22	1:I:180:LEU:HD12	1.99	0.45
1:L:17:VAL:HG21	1:L:70:GLN:NE2	2.32	0.45
1:Q:30:THR:HA	1:Q:85:PRO:HB3	1.98	0.45
1:Q:149:LEU:HA	1:Q:149:LEU:HD23	1.69	0.45
1:T:10:SER:HB2	1:T:121:ARG:HH21	1.81	0.45
1:A:181:LYS:HD2	1:A:181:LYS:HA	1.69	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:53:ARG:NH2	1:D:64:GLU:OE2	2.50	0.45
1:G:45:LEU:HD23	1:G:45:LEU:HA	1.80	0.45
1:G:131:GLU:HB3	1:V:128:ASP:HB2	1.99	0.45
1:J:65:ARG:HB3	1:J:134:TYR:OH	2.17	0.45
1:H:30:THR:HA	1:H:85:PRO:HB3	1.99	0.44
1:J:178:LEU:HD13	1:T:178:LEU:HD13	1.98	0.44
1:L:149:LEU:HD23	1:L:149:LEU:HA	1.72	0.44
1:D:71:ASN:N	1:D:71:ASN:OD1	2.49	0.44
1:A:42:ASP:OD1	1:A:42:ASP:N	2.49	0.44
1:L:57:GLU:CD	1:L:60:ARG:HE	2.21	0.44
2:O:201:FE:FE	2:B:201:FE:FE	1.00	0.44
1:P:149:LEU:O	1:P:153:ARG:HG3	2.18	0.44
1:B:92:LYS:H	1:B:95:GLU:CD	2.20	0.44
1:F:9:TYR:OH	1:F:70:GLN:NE2	2.45	0.44
1:Z:59:LYS:HA	1:Z:59:LYS:HD3	1.69	0.44
1:Z:64:GLU:HG2	1:A:36:PHE:CZ	2.52	0.44
1:Z:183:ASP:HA	1:Z:186:ILE:HB	1.99	0.44
1:H:26:ARG:O	1:H:30:THR:HG22	2.18	0.44
1:J:84:LYS:HG3	1:J:85:PRO:HD2	1.99	0.44
1:J:173:TYR:HB2	1:T:154:ARG:HD2	2.00	0.44
1:Q:70:GLN:HG2	1:Q:77:ALA:HB2	1.99	0.44
1:S:181:LYS:HD2	1:S:181:LYS:HA	1.75	0.44
1:T:70:GLN:NE2	1:T:75:GLY:HA3	2.31	0.44
1:B:100:ALA:O	1:B:104:GLU:N	2.48	0.44
1:A:94:GLN:O	1:A:98:GLU:HG3	2.18	0.44
1:J:105:LYS:HE2	1:J:105:LYS:HB3	1.85	0.44
1:P:101:LEU:HD12	1:P:149:LEU:HD12	2.00	0.44
1:P:182:HIS:O	1:P:186:ILE:HG12	2.18	0.44
1:U:26:ARG:O	1:U:30:THR:HG22	2.17	0.44
1:A:92:LYS:H	1:A:95:GLU:CD	2.21	0.44
1:G:71:ASN:ND2	1:B:36:PHE:O	2.50	0.44
1:J:149:LEU:HD23	1:J:149:LEU:HA	1.78	0.44
1:N:149:LEU:HA	1:N:149:LEU:HD23	1.73	0.44
1:O:4:GLN:H	1:O:4:GLN:HG2	1.59	0.44
1:T:182:HIS:O	1:T:186:ILE:HG12	2.17	0.44
1:W:66:LEU:HD13	1:W:66:LEU:HA	1.84	0.44
1:F:181:LYS:HD2	1:F:181:LYS:HA	1.76	0.44
2:A:201:FE:FE	2:V:201:FE:FE	1.00	0.44
1:E:175:PHE:HA	1:P:173:TYR:OH	2.18	0.44
1:I:118:GLY:O	1:I:122:ALA:N	2.51	0.44
1:J:70:GLN:NE2	1:J:75:GLY:HA3	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:92:LYS:HD2	1:P:94:GLN:HB3	2.00	0.44
1:Q:182:HIS:O	1:Q:186:ILE:HG12	2.18	0.44
1:R:59:LYS:HD3	1:R:59:LYS:HA	1.68	0.44
1:U:30:THR:HA	1:U:85:PRO:HB3	2.00	0.44
1:V:9:TYR:OH	1:V:70:GLN:NE2	2.44	0.44
1:V:45:LEU:HD23	1:V:45:LEU:HA	1.83	0.44
1:W:149:LEU:O	1:W:153:ARG:HG3	2.18	0.44
1:C:64:GLU:O	1:C:68:GLU:HG2	2.17	0.44
1:H:45:LEU:HD23	1:H:45:LEU:HA	1.83	0.44
1:I:30:THR:HA	1:I:85:PRO:HB3	2.00	0.44
1:L:31:TYR:OH	1:L:104:GLU:OE2	2.23	0.44
1:N:60:ARG:HD2	1:N:60:ARG:C	2.38	0.44
1:R:55:LEU:HD21	1:R:141:LEU:HD11	2.00	0.44
1:V:59:LYS:HA	1:V:59:LYS:HD3	1.67	0.44
1:V:70:GLN:O	1:V:73:ARG:N	2.50	0.44
1:Z:183:ASP:OD1	1:Z:184:GLY:N	2.51	0.44
1:H:181:LYS:HD2	1:H:181:LYS:HA	1.76	0.44
1:M:30:THR:HA	1:M:85:PRO:HB3	1.98	0.44
1:O:36:PHE:O	1:P:71:ASN:ND2	2.51	0.44
1:P:45:LEU:HD23	1:P:45:LEU:HA	1.83	0.44
1:F:45:LEU:HD23	1:F:45:LEU:HA	1.81	0.44
1:Z:180:LEU:HA	1:Z:180:LEU:HD23	1.83	0.43
1:A:17:VAL:HG21	1:A:70:GLN:NE2	2.33	0.43
1:A:55:LEU:HD13	1:A:55:LEU:HA	1.89	0.43
1:A:115:HIS:NE2	1:A:127:CYS:SG	2.91	0.43
1:H:13:VAL:HG13	1:H:117:LEU:HD22	1.99	0.43
1:H:23:LEU:HD23	1:H:107:LEU:HD13	2.00	0.43
1:K:149:LEU:O	1:K:153:ARG:HG3	2.18	0.43
1:S:30:THR:HA	1:S:85:PRO:HB3	1.99	0.43
1:Z:57:GLU:HG2	1:Z:60:ARG:HH21	1.82	0.43
1:C:169:SER:HB2	1:C:172:GLU:HB3	2.01	0.43
1:E:97:MET:SD	1:E:145:MET:HG2	2.58	0.43
1:E:128:ASP:HB2	1:B:131:GLU:HG2	2.00	0.43
1:G:155:VAL:HB	1:G:171:GLY:HA3	1.99	0.43
1:J:13:VAL:HB	1:J:117:LEU:HD22	1.99	0.43
1:Q:65:ARG:HB3	1:Q:134:TYR:OH	2.17	0.43
1:B:17:VAL:HG21	1:B:70:GLN:NE2	2.33	0.43
1:D:66:LEU:HD13	1:D:66:LEU:HA	1.86	0.43
1:A:100:ALA:O	1:A:104:GLU:N	2.44	0.43
1:C:92:LYS:HD2	1:C:94:GLN:HB3	2.00	0.43
1:G:169:SER:HB2	1:G:172:GLU:HB3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:26:ARG:NE	1:H:83:GLN:HG2	2.29	0.43
1:N:23:LEU:HA	1:N:23:LEU:HD12	1.73	0.43
1:A:134:TYR:O	1:A:138:GLU:HG2	2.18	0.43
1:C:73:ARG:NH2	1:C:125:HIS:HB3	2.33	0.43
1:G:59:LYS:HD3	1:G:59:LYS:HA	1.67	0.43
1:M:181:LYS:HD2	1:M:181:LYS:HA	1.74	0.43
1:R:70:GLN:NE2	1:R:75:GLY:HA3	2.33	0.43
1:S:149:LEU:HD23	1:S:149:LEU:HA	1.76	0.43
1:S:180:LEU:HD23	1:S:180:LEU:HA	1.78	0.43
1:W:70:GLN:HG2	1:W:77:ALA:HB2	2.01	0.43
1:D:26:ARG:HH21	1:D:83:GLN:NE2	2.16	0.43
1:Z:175:PHE:HA	1:K:173:TYR:OH	2.19	0.43
1:G:97:MET:HG2	1:G:149:LEU:HG	2.01	0.43
1:G:182:HIS:O	1:G:186:ILE:HG12	2.19	0.43
1:I:10:SER:OG	1:I:12:GLU:OE2	2.23	0.43
1:I:180:LEU:HD23	1:I:180:LEU:HA	1.80	0.43
1:J:59:LYS:HD3	1:J:59:LYS:HA	1.65	0.43
1:S:30:THR:HG22	1:S:85:PRO:HA	2.00	0.43
1:W:181:LYS:HD2	1:W:181:LYS:HA	1.73	0.43
1:D:10:SER:OG	1:D:13:VAL:HG12	2.18	0.43
1:D:23:LEU:HA	1:D:23:LEU:HD12	1.68	0.43
1:Z:6:ARG:NH1	1:Z:9:TYR:O	2.51	0.43
1:Z:36:PHE:CE2	1:A:64:GLU:HG2	2.54	0.43
1:E:71:ASN:ND2	1:F:36:PHE:O	2.52	0.43
1:L:70:GLN:OE1	1:L:75:GLY:HA3	2.19	0.43
1:O:182:HIS:O	1:O:186:ILE:HG12	2.18	0.43
1:T:10:SER:HB3	1:T:13:VAL:HG12	2.00	0.43
1:D:39:ASP:OD2	1:D:53:ARG:NH2	2.52	0.43
1:D:169:SER:HB2	1:D:172:GLU:HB2	1.99	0.43
1:F:149:LEU:O	1:F:153:ARG:HG3	2.19	0.43
1:Z:10:SER:HB2	1:Z:121:ARG:NH1	2.33	0.43
1:C:71:ASN:ND2	1:D:36:PHE:O	2.51	0.43
1:C:155:VAL:HB	1:C:171:GLY:HA3	2.01	0.43
1:J:30:THR:HA	1:J:85:PRO:HB3	1.99	0.43
1:K:10:SER:HB2	1:K:121:ARG:HH21	1.82	0.43
1:K:53:ARG:NH2	1:L:64:GLU:OE2	2.51	0.43
1:M:131:GLU:HB3	1:T:128:ASP:HB2	2.00	0.43
1:N:87:GLN:NE2	1:N:89:GLU:O	2.51	0.43
1:P:70:GLN:HG2	1:P:77:ALA:HB2	2.01	0.43
1:R:70:GLN:HG2	1:R:77:ALA:HB2	2.01	0.43
1:R:182:HIS:O	1:R:186:ILE:HG12	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:183:ASP:O	1:U:187:GLU:N	2.41	0.43
1:V:92:LYS:HB3	1:V:172:GLU:OE2	2.18	0.43
1:B:23:LEU:HA	1:B:23:LEU:HD12	1.76	0.43
1:Z:65:ARG:HB3	1:Z:134:TYR:OH	2.18	0.43
1:A:131:GLU:HB3	1:G:128:ASP:HB2	2.00	0.43
1:C:175:PHE:HA	1:M:173:TYR:OH	2.19	0.43
1:E:58:GLU:OE2	1:E:59:LYS:NZ	2.41	0.43
1:E:83:GLN:NE2	1:E:84:LYS:O	2.51	0.43
1:G:140:LYS:HE2	1:G:140:LYS:HB2	1.67	0.43
1:H:118:GLY:O	1:H:122:ALA:N	2.51	0.43
1:I:121:ARG:HG2	1:I:121:ARG:NH1	2.32	0.43
1:P:10:SER:HB2	1:P:121:ARG:HH21	1.83	0.43
1:B:45:LEU:HD23	1:B:45:LEU:HA	1.81	0.43
1:D:173:TYR:OH	1:F:175:PHE:HA	2.19	0.43
1:Z:155:VAL:HB	1:Z:171:GLY:HA3	2.00	0.43
1:E:84:LYS:HB2	1:E:85:PRO:HD2	2.01	0.43
1:G:175:PHE:HA	1:W:173:TYR:OH	2.18	0.43
1:H:121:ARG:HG2	1:H:121:ARG:NH1	2.33	0.43
1:H:149:LEU:HD23	1:H:149:LEU:HA	1.73	0.43
1:I:140:LYS:HB2	1:I:140:LYS:HE2	1.69	0.43
1:O:23:LEU:HD12	1:O:23:LEU:HA	1.74	0.43
1:T:10:SER:OG	1:T:12:GLU:N	2.50	0.43
1:C:6:ARG:NH1	1:C:9:TYR:O	2.51	0.43
1:C:64:GLU:HG2	1:D:36:PHE:CE2	2.52	0.43
1:H:22:ASN:ND2	1:H:80:GLN:O	2.52	0.43
1:L:4:GLN:H	1:L:4:GLN:HG2	1.60	0.43
1:Q:13:VAL:HG21	1:Q:121:ARG:HH21	1.84	0.43
1:F:155:VAL:HB	1:F:171:GLY:HA3	2.00	0.43
1:A:128:ASP:HB2	1:V:131:GLU:HB3	2.00	0.42
1:C:36:PHE:CZ	1:D:64:GLU:HG2	2.54	0.42
1:J:185:ASP:O	1:J:188:SER:OG	2.36	0.42
1:R:178:LEU:HD13	1:S:178:LEU:HD13	2.01	0.42
1:T:177:ARG:HA	1:T:177:ARG:HD3	1.49	0.42
1:V:65:ARG:HD3	1:V:133:HIS:ND1	2.34	0.42
1:F:65:ARG:HB3	1:F:134:TYR:OH	2.19	0.42
1:H:143:LYS:NZ	1:H:147:ASN:HD21	2.16	0.42
1:I:65:ARG:HD3	1:I:133:HIS:ND1	2.34	0.42
1:I:73:ARG:HD3	1:I:73:ARG:HA	1.88	0.42
1:L:70:GLN:O	1:L:73:ARG:N	2.51	0.42
1:M:149:LEU:O	1:M:153:ARG:HG3	2.19	0.42
1:S:183:ASP:HA	1:S:186:ILE:HB	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:13:VAL:HG23	1:T:114:LEU:HD11	1.99	0.42
1:U:147:ASN:N	1:U:147:ASN:HD22	2.17	0.42
1:D:149:LEU:O	1:D:153:ARG:HG3	2.19	0.42
1:Z:112:LEU:HD13	1:L:8:ASN:HD22	1.84	0.42
1:A:118:GLY:HA3	1:A:126:LEU:HD23	2.00	0.42
1:H:118:GLY:HA3	1:H:126:LEU:HD23	2.01	0.42
1:M:10:SER:HB2	1:M:121:ARG:NH2	2.33	0.42
1:M:53:ARG:NH2	1:N:64:GLU:OE2	2.52	0.42
1:M:147:ASN:HD22	1:M:147:ASN:H	1.66	0.42
1:Q:70:GLN:OE1	1:Q:75:GLY:HA3	2.19	0.42
1:W:26:ARG:HH21	1:W:83:GLN:NE2	2.17	0.42
1:D:42:ASP:OD1	1:D:42:ASP:N	2.49	0.42
1:K:71:ASN:ND2	1:L:36:PHE:O	2.52	0.42
1:N:155:VAL:O	1:N:155:VAL:HG13	2.19	0.42
1:R:154:ARG:HD2	1:S:173:TYR:HB2	2.00	0.42
1:U:65:ARG:HD3	1:U:133:HIS:ND1	2.35	0.42
1:U:73:ARG:HD3	1:U:73:ARG:HA	1.87	0.42
1:Z:135:LEU:HD23	1:Z:135:LEU:HA	1.94	0.42
1:E:10:SER:OG	1:E:13:VAL:HG12	2.19	0.42
1:K:92:LYS:HD2	1:K:94:GLN:HB3	2.00	0.42
1:L:135:LEU:HD23	1:L:135:LEU:HA	1.91	0.42
1:M:70:GLN:HG2	1:M:77:ALA:HB2	2.02	0.42
1:N:132:SER:OG	1:N:133:HIS:HD2	2.03	0.42
1:N:181:LYS:HD2	1:N:181:LYS:HA	1.78	0.42
1:O:180:LEU:HA	1:O:180:LEU:HD23	1.79	0.42
1:R:97:MET:HG2	1:R:149:LEU:HG	2.01	0.42
1:W:92:LYS:HD2	1:W:94:GLN:HB3	2.00	0.42
1:A:10:SER:OG	1:A:13:VAL:HG12	2.19	0.42
1:H:70:GLN:OE1	1:H:75:GLY:HA3	2.19	0.42
1:I:181:LYS:HD2	1:I:181:LYS:HA	1.83	0.42
1:O:73:ARG:HD3	1:O:73:ARG:HA	1.87	0.42
1:O:149:LEU:HD23	1:O:149:LEU:HA	1.77	0.42
1:Q:180:LEU:HA	1:Q:180:LEU:HD23	1.78	0.42
1:V:70:GLN:HG2	1:V:77:ALA:HB2	2.02	0.42
1:V:183:ASP:HA	1:V:186:ILE:HD12	2.01	0.42
1:D:132:SER:OG	1:D:133:HIS:HD2	2.01	0.42
1:F:180:LEU:HD23	1:F:180:LEU:HA	1.80	0.42
1:C:65:ARG:HB3	1:C:134:TYR:OH	2.19	0.42
1:I:70:GLN:OE1	1:I:75:GLY:HA3	2.20	0.42
1:J:127:CYS:O	1:J:131:GLU:HB2	2.20	0.42
1:K:55:LEU:HA	1:K:55:LEU:HD13	1.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:149:LEU:HD23	1:K:149:LEU:HA	1.71	0.42
1:L:87:GLN:NE2	1:L:89:GLU:O	2.53	0.42
1:L:118:GLY:O	1:L:122:ALA:N	2.52	0.42
1:L:132:SER:OG	1:L:133:HIS:HD2	2.02	0.42
1:N:180:LEU:HA	1:N:180:LEU:HD23	1.80	0.42
1:R:66:LEU:HD13	1:R:66:LEU:HA	1.85	0.42
1:T:4:GLN:H	1:T:4:GLN:HG2	1.64	0.42
1:W:60:ARG:O	1:W:60:ARG:HG2	2.20	0.42
1:D:17:VAL:HG21	1:D:70:GLN:NE2	2.35	0.42
1:F:135:LEU:HD23	1:F:135:LEU:HA	1.90	0.42
1:E:70:GLN:OE1	1:E:75:GLY:HA3	2.19	0.42
1:G:70:GLN:HE21	1:G:75:GLY:HA3	1.84	0.42
1:G:149:LEU:HD23	1:G:149:LEU:HA	1.75	0.42
1:J:143:LYS:NZ	1:J:147:ASN:HD21	2.18	0.42
1:J:178:LEU:HD12	1:J:178:LEU:HA	1.79	0.42
1:M:10:SER:HB2	1:M:121:ARG:HE	1.84	0.42
1:M:36:PHE:HZ	1:N:64:GLU:HG2	1.82	0.42
1:T:97:MET:HG2	1:T:149:LEU:HG	2.01	0.42
1:V:4:GLN:H	1:V:4:GLN:HG2	1.60	0.42
1:V:73:ARG:HA	1:V:73:ARG:HD2	1.89	0.42
1:Z:23:LEU:HD12	1:Z:23:LEU:HA	1.94	0.42
1:A:149:LEU:O	1:A:153:ARG:HG3	2.19	0.42
1:C:131:GLU:OE1	1:N:127:CYS:HB3	2.19	0.42
1:G:97:MET:SD	1:G:145:MET:HG2	2.60	0.42
1:J:55:LEU:HD13	1:J:55:LEU:HA	1.92	0.42
1:K:155:VAL:HB	1:K:171:GLY:HA3	2.02	0.42
1:L:128:ASP:O	1:L:132:SER:HB3	2.20	0.42
1:N:118:GLY:HA3	1:N:126:LEU:HD23	2.02	0.42
1:Q:70:GLN:O	1:Q:73:ARG:N	2.53	0.42
1:B:92:LYS:HA	1:B:92:LYS:HD3	1.63	0.42
1:Z:42:ASP:OD1	1:Z:42:ASP:N	2.52	0.42
1:A:180:LEU:HA	1:A:180:LEU:HD23	1.78	0.42
1:E:36:PHE:CZ	1:F:64:GLU:HG2	2.54	0.42
1:F:11:THR:HA	1:F:14:GLU:HB3	2.02	0.42
1:C:17:VAL:HG21	1:C:70:GLN:HE22	1.86	0.41
1:G:92:LYS:HD2	1:G:94:GLN:HB3	2.02	0.41
1:G:181:LYS:HD2	1:G:181:LYS:HA	1.74	0.41
1:H:65:ARG:HD3	1:H:133:HIS:ND1	2.35	0.41
1:H:70:GLN:HG2	1:H:77:ALA:HB2	2.02	0.41
1:H:147:ASN:N	1:H:147:ASN:HD22	2.18	0.41
1:I:29:TYR:CE2	1:J:82:VAL:HG23	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:65:ARG:HA	1:I:68:GLU:HG2	2.01	0.41
1:J:55:LEU:HD21	1:J:141:LEU:HD11	2.02	0.41
1:J:128:ASP:HB2	1:P:131:GLU:HB3	2.02	0.41
1:K:31:TYR:OH	1:K:104:GLU:OE2	2.18	0.41
1:S:66:LEU:HD13	1:S:66:LEU:HA	1.84	0.41
1:S:115:HIS:ND1	1:S:115:HIS:O	2.52	0.41
1:T:23:LEU:HA	1:T:23:LEU:HD12	1.68	0.41
1:T:149:LEU:HD23	1:T:149:LEU:HA	1.75	0.41
1:B:94:GLN:O	1:B:98:GLU:HG3	2.19	0.41
1:C:97:MET:HG2	1:C:149:LEU:HG	2.01	0.41
1:E:26:ARG:HH11	1:E:83:GLN:HB3	1.85	0.41
1:E:36:PHE:CE2	1:F:64:GLU:HG2	2.55	0.41
1:E:149:LEU:HD23	1:E:149:LEU:HA	1.76	0.41
1:J:4:GLN:NE2	1:J:4:GLN:H	2.18	0.41
1:M:26:ARG:HH21	1:M:83:GLN:NE2	2.18	0.41
1:R:100:ALA:O	1:R:104:GLU:N	2.51	0.41
1:S:84:LYS:HG3	1:S:85:PRO:HD2	2.01	0.41
1:V:23:LEU:HD12	1:V:23:LEU:HA	1.73	0.41
1:W:59:LYS:HA	1:W:59:LYS:HD3	1.88	0.41
1:A:73:ARG:HD3	1:A:73:ARG:HA	1.96	0.41
1:C:97:MET:SD	1:C:145:MET:HG2	2.60	0.41
1:E:32:LEU:HD12	1:E:36:PHE:HD2	1.84	0.41
1:E:155:VAL:HB	1:E:171:GLY:HA3	2.02	0.41
1:K:10:SER:HB2	1:K:121:ARG:NH2	2.35	0.41
1:P:58:GLU:O	1:P:61:GLU:HG2	2.20	0.41
1:Q:57:GLU:OE1	1:Q:60:ARG:NH1	2.46	0.41
1:V:53:ARG:HH21	1:W:64:GLU:CD	2.23	0.41
1:W:155:VAL:HB	1:W:171:GLY:HA3	2.02	0.41
1:B:9:TYR:OH	1:B:70:GLN:NE2	2.48	0.41
1:D:13:VAL:HG23	1:D:114:LEU:HD11	2.01	0.41
1:H:13:VAL:HG21	1:H:121:ARG:HH21	1.84	0.41
1:K:36:PHE:HZ	1:L:64:GLU:HG2	1.84	0.41
1:R:143:LYS:NZ	1:R:147:ASN:HD21	2.18	0.41
1:W:97:MET:SD	1:W:145:MET:HG2	2.61	0.41
1:W:149:LEU:HD23	1:W:149:LEU:HA	1.69	0.41
1:F:13:VAL:HB	1:F:117:LEU:HD22	2.01	0.41
1:F:103:MET:HB2	1:F:103:MET:HE3	1.78	0.41
1:A:66:LEU:HD13	1:A:66:LEU:HA	1.85	0.41
1:E:45:LEU:HD23	1:E:45:LEU:HA	1.80	0.41
1:E:140:LYS:HE3	1:E:140:LYS:HB2	1.76	0.41
1:I:105:LYS:HE2	1:I:105:LYS:HB3	1.87	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:154:ARG:HD2	1:R:173:TYR:HB2	2.02	0.41
1:O:83:GLN:HG3	1:O:83:GLN:H	1.72	0.41
1:S:127:CYS:O	1:S:131:GLU:HB2	2.19	0.41
1:T:143:LYS:NZ	1:T:147:ASN:HD21	2.18	0.41
1:D:118:GLY:O	1:D:122:ALA:N	2.53	0.41
1:F:42:ASP:OD1	1:F:42:ASP:N	2.51	0.41
1:F:67:LEU:HA	1:F:67:LEU:HD23	1.82	0.41
1:H:17:VAL:HG21	1:H:70:GLN:NE2	2.33	0.41
1:I:70:GLN:O	1:I:73:ARG:N	2.53	0.41
1:M:71:ASN:ND2	1:N:36:PHE:O	2.53	0.41
1:O:153:ARG:HH22	1:B:4:GLN:NE2	2.19	0.41
1:P:147:ASN:HD22	1:P:147:ASN:H	1.68	0.41
1:R:61:GLU:HA	1:R:64:GLU:HG2	2.02	0.41
1:U:182:HIS:O	1:U:186:ILE:HG12	2.21	0.41
1:V:46:GLU:N	1:V:176:GLU:OE2	2.53	0.41
1:W:180:LEU:HD23	1:W:180:LEU:HA	1.76	0.41
1:B:71:ASN:OD1	1:B:71:ASN:N	2.53	0.41
1:D:65:ARG:HB3	1:D:134:TYR:OH	2.20	0.41
1:F:55:LEU:HD13	1:F:55:LEU:HA	1.72	0.41
1:C:26:ARG:HE	1:C:83:GLN:HG3	1.85	0.41
1:I:13:VAL:HG23	1:I:114:LEU:HD11	2.03	0.41
1:N:4:GLN:H	1:N:4:GLN:HG2	1.56	0.41
1:N:136:ASP:OD1	1:N:140:LYS:NZ	2.45	0.41
1:P:97:MET:SD	1:P:145:MET:HG2	2.61	0.41
1:R:177:ARG:HD3	1:R:177:ARG:HA	1.49	0.41
1:V:73:ARG:HH11	1:V:73:ARG:HG2	1.85	0.41
1:B:135:LEU:HD23	1:B:135:LEU:HA	1.92	0.41
1:D:125:HIS:O	1:D:129:PHE:HB3	2.21	0.41
1:A:173:TYR:OH	1:D:175:PHE:HA	2.20	0.41
1:C:132:SER:OG	1:C:133:HIS:ND1	2.39	0.41
1:J:181:LYS:HD2	1:J:181:LYS:HA	1.75	0.41
1:K:135:LEU:HD23	1:K:135:LEU:HA	1.92	0.41
1:O:9:TYR:OH	1:O:70:GLN:NE2	2.51	0.41
1:O:64:GLU:HG3	1:P:36:PHE:CZ	2.55	0.41
1:Z:10:SER:HB3	1:Z:13:VAL:HG12	2.03	0.41
1:C:17:VAL:HG21	1:C:70:GLN:NE2	2.36	0.41
1:C:70:GLN:OE1	1:C:75:GLY:HA3	2.20	0.41
1:H:8:ASN:HD22	1:R:112:LEU:HD13	1.86	0.41
1:J:70:GLN:HG2	1:J:77:ALA:HB2	2.03	0.41
1:K:42:ASP:OD2	1:K:42:ASP:N	2.54	0.41
1:M:10:SER:OG	1:M:12:GLU:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:70:GLN:HE21	1:M:75:GLY:HA3	1.86	0.41
1:O:55:LEU:HD13	1:O:55:LEU:HA	1.71	0.41
1:Q:140:LYS:HE3	1:Q:140:LYS:HB2	1.88	0.41
1:R:13:VAL:HB	1:R:117:LEU:HD22	2.03	0.41
1:R:104:GLU:HG3	1:R:142:ILE:HG12	2.02	0.41
1:S:97:MET:HG2	1:S:149:LEU:HG	2.02	0.41
1:T:11:THR:HA	1:T:14:GLU:HB3	2.03	0.41
1:U:181:LYS:HD2	1:U:181:LYS:HA	1.74	0.41
1:D:30:THR:OG1	1:D:103:MET:SD	2.75	0.41
1:F:149:LEU:HD23	1:F:149:LEU:HA	1.75	0.41
1:C:181:LYS:HD2	1:C:181:LYS:HA	1.73	0.41
1:G:149:LEU:O	1:G:153:ARG:HG3	2.21	0.41
1:L:59:LYS:HA	1:L:59:LYS:HD3	1.70	0.41
1:O:46:GLU:N	1:O:176:GLU:OE2	2.53	0.41
1:Q:29:TYR:CE1	1:R:82:VAL:HG23	2.56	0.41
1:W:25:LEU:HD23	1:W:25:LEU:HA	1.88	0.41
1:C:64:GLU:HG2	1:D:36:PHE:HE2	1.86	0.40
1:H:46:GLU:N	1:H:176:GLU:OE2	2.55	0.40
1:J:40:ARG:O	1:J:44:ALA:N	2.48	0.40
1:P:104:GLU:HG3	1:P:142:ILE:HG12	2.03	0.40
1:P:138:GLU:O	1:P:142:ILE:HG13	2.21	0.40
1:Q:10:SER:OG	1:Q:11:THR:N	2.54	0.40
1:S:143:LYS:HG3	1:S:147:ASN:ND2	2.37	0.40
1:W:97:MET:HG2	1:W:149:LEU:HG	2.02	0.40
1:B:180:LEU:HA	1:B:180:LEU:HD23	1.78	0.40
1:C:149:LEU:O	1:C:153:ARG:HG3	2.21	0.40
1:E:135:LEU:HD23	1:E:135:LEU:HA	1.93	0.40
1:I:26:ARG:O	1:I:30:THR:HG22	2.21	0.40
1:I:70:GLN:HG2	1:I:77:ALA:HB2	2.02	0.40
1:K:64:GLU:HG2	1:L:36:PHE:CZ	2.56	0.40
1:M:153:ARG:NH2	1:T:4:GLN:OE1	2.43	0.40
1:Q:4:GLN:H	1:Q:4:GLN:HG2	1.58	0.40
1:S:46:GLU:N	1:S:176:GLU:OE2	2.54	0.40
1:U:46:GLU:N	1:U:176:GLU:OE2	2.54	0.40
1:C:183:ASP:O	1:C:187:GLU:HB2	2.20	0.40
1:G:82:VAL:HG23	1:B:29:TYR:CE2	2.56	0.40
1:I:135:LEU:HD23	1:I:135:LEU:HA	1.94	0.40
1:K:60:ARG:HD2	1:L:60:ARG:CZ	2.50	0.40
1:L:183:ASP:HA	1:L:186:ILE:CG1	2.52	0.40
1:O:121:ARG:HH12	1:O:123:ASP:HB2	1.86	0.40
1:T:36:PHE:HZ	1:U:64:GLU:HG2	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:181:LYS:HD2	1:T:181:LYS:HA	1.73	0.40
1:Z:149:LEU:O	1:Z:153:ARG:HG3	2.21	0.40
1:Z:169:SER:HB2	1:Z:172:GLU:HB3	2.03	0.40
1:A:183:ASP:OD2	1:A:184:GLY:N	2.54	0.40
1:C:6:ARG:NH2	1:C:14:GLU:OE1	2.51	0.40
1:H:29:TYR:CE2	1:S:82:VAL:HG23	2.56	0.40
1:O:13:VAL:HG23	1:O:114:LEU:HD11	2.02	0.40
1:Q:57:GLU:OE2	1:R:60:ARG:NH2	2.54	0.40
1:U:135:LEU:HD23	1:U:135:LEU:HA	1.95	0.40
1:B:10:SER:O	1:B:13:VAL:HG13	2.20	0.40
1:B:55:LEU:HD11	1:B:141:LEU:HD21	2.03	0.40
1:F:23:LEU:HA	1:F:23:LEU:HD12	1.68	0.40
1:Z:34:LEU:HD13	1:Z:90:TRP:CG	2.56	0.40
1:C:4:GLN:H	1:C:4:GLN:HG2	1.57	0.40
1:E:142:ILE:HG22	1:O:5:ILE:HB	2.04	0.40
1:E:149:LEU:O	1:E:153:ARG:HG3	2.21	0.40
1:I:9:TYR:OH	1:I:70:GLN:NE2	2.51	0.40
1:J:46:GLU:N	1:J:176:GLU:OE2	2.53	0.40
1:K:136:ASP:OD1	1:K:140:LYS:NZ	2.47	0.40
1:L:46:GLU:N	1:L:176:GLU:OE2	2.54	0.40
1:M:150:THR:OG1	1:U:41:ASP:O	2.22	0.40
1:P:97:MET:HG2	1:P:149:LEU:HG	2.03	0.40
1:S:87:GLN:NE2	1:S:89:GLU:O	2.54	0.40
1:B:181:LYS:HA	1:B:181:LYS:HD2	1.82	0.40
1:D:4:GLN:H	1:D:4:GLN:HG2	1.69	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 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	A	170/216 (79%)	166 (98%)	4 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	171/216 (79%)	165 (96%)	6 (4%)	0	100	100
1	C	170/216 (79%)	163 (96%)	7 (4%)	0	100	100
1	D	170/216 (79%)	165 (97%)	5 (3%)	0	100	100
1	E	170/216 (79%)	165 (97%)	5 (3%)	0	100	100
1	F	170/216 (79%)	165 (97%)	5 (3%)	0	100	100
1	G	170/216 (79%)	165 (97%)	5 (3%)	0	100	100
1	H	171/216 (79%)	166 (97%)	5 (3%)	0	100	100
1	I	171/216 (79%)	165 (96%)	6 (4%)	0	100	100
1	J	170/216 (79%)	165 (97%)	5 (3%)	0	100	100
1	K	170/216 (79%)	165 (97%)	5 (3%)	0	100	100
1	L	171/216 (79%)	160 (94%)	11 (6%)	0	100	100
1	M	170/216 (79%)	163 (96%)	7 (4%)	0	100	100
1	N	171/216 (79%)	165 (96%)	6 (4%)	0	100	100
1	O	171/216 (79%)	164 (96%)	7 (4%)	0	100	100
1	P	170/216 (79%)	162 (95%)	8 (5%)	0	100	100
1	Q	171/216 (79%)	165 (96%)	6 (4%)	0	100	100
1	R	170/216 (79%)	164 (96%)	6 (4%)	0	100	100
1	S	170/216 (79%)	162 (95%)	8 (5%)	0	100	100
1	T	170/216 (79%)	167 (98%)	3 (2%)	0	100	100
1	U	171/216 (79%)	165 (96%)	6 (4%)	0	100	100
1	V	171/216 (79%)	163 (95%)	8 (5%)	0	100	100
1	W	170/216 (79%)	163 (96%)	7 (4%)	0	100	100
1	Z	170/216 (79%)	165 (97%)	5 (3%)	0	100	100
All	All	4089/5184 (79%)	3943 (96%)	146 (4%)	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	A	147/180 (82%)	136 (92%)	11 (8%)	13	39
1	B	148/180 (82%)	141 (95%)	7 (5%)	26	57
1	C	147/180 (82%)	138 (94%)	9 (6%)	18	48
1	D	147/180 (82%)	139 (95%)	8 (5%)	22	53
1	E	147/180 (82%)	136 (92%)	11 (8%)	13	39
1	F	147/180 (82%)	140 (95%)	7 (5%)	25	56
1	G	147/180 (82%)	139 (95%)	8 (5%)	22	53
1	H	148/180 (82%)	139 (94%)	9 (6%)	18	48
1	I	148/180 (82%)	139 (94%)	9 (6%)	18	48
1	J	147/180 (82%)	135 (92%)	12 (8%)	11	36
1	K	147/180 (82%)	139 (95%)	8 (5%)	22	53
1	L	148/180 (82%)	138 (93%)	10 (7%)	16	44
1	M	147/180 (82%)	140 (95%)	7 (5%)	25	56
1	N	148/180 (82%)	138 (93%)	10 (7%)	16	44
1	O	148/180 (82%)	136 (92%)	12 (8%)	11	36
1	P	147/180 (82%)	140 (95%)	7 (5%)	25	56
1	Q	148/180 (82%)	136 (92%)	12 (8%)	11	36
1	R	147/180 (82%)	138 (94%)	9 (6%)	18	48
1	S	147/180 (82%)	136 (92%)	11 (8%)	13	39
1	T	147/180 (82%)	138 (94%)	9 (6%)	18	48
1	U	148/180 (82%)	139 (94%)	9 (6%)	18	48
1	V	148/180 (82%)	137 (93%)	11 (7%)	13	40
1	W	147/180 (82%)	138 (94%)	9 (6%)	18	48
1	Z	147/180 (82%)	137 (93%)	10 (7%)	16	44
All	All	3537/4320 (82%)	3312 (94%)	225 (6%)	21	46

All (225) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Z	10	SER
1	Z	29	TYR
1	Z	42	ASP
1	Z	71	ASN
1	Z	78	LEU
1	Z	89	GLU

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Mol	Chain	Res	Type
1	Z	128	ASP
1	Z	132	SER
1	Z	176	GLU
1	Z	185	ASP
1	A	22	ASN
1	A	29	TYR
1	A	42	ASP
1	A	55	LEU
1	A	65	ARG
1	A	66	LEU
1	A	71	ASN
1	A	73	ARG
1	A	78	LEU
1	A	127	CYS
1	A	128	ASP
1	C	7	GLN
1	C	29	TYR
1	C	42	ASP
1	C	72	ASP
1	C	73	ARG
1	C	78	LEU
1	C	128	ASP
1	C	132	SER
1	C	176	GLU
1	E	10	SER
1	E	28	SER
1	E	29	TYR
1	E	32	LEU
1	E	39	ASP
1	E	42	ASP
1	E	78	LEU
1	E	84	LYS
1	E	128	ASP
1	E	132	SER
1	E	176	GLU
1	G	10	SER
1	G	29	TYR
1	G	32	LEU
1	G	39	ASP
1	G	72	ASP
1	G	78	LEU
1	G	132	SER

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Mol	Chain	Res	Type
1	G	176	GLU
1	H	10	SER
1	H	13	VAL
1	H	29	TYR
1	H	30	THR
1	H	66	LEU
1	H	71	ASN
1	H	73	ARG
1	H	78	LEU
1	H	128	ASP
1	I	10	SER
1	I	29	TYR
1	I	30	THR
1	I	42	ASP
1	I	66	LEU
1	I	71	ASN
1	I	73	ARG
1	I	78	LEU
1	I	128	ASP
1	J	4	GLN
1	J	10	SER
1	J	14	GLU
1	J	21	VAL
1	J	29	TYR
1	J	41	ASP
1	J	42	ASP
1	J	55	LEU
1	J	71	ASN
1	J	78	LEU
1	J	89	GLU
1	J	143	LYS
1	K	29	TYR
1	K	30	THR
1	K	42	ASP
1	K	55	LEU
1	K	61	GLU
1	K	66	LEU
1	K	78	LEU
1	K	132	SER
1	L	29	TYR
1	L	55	LEU
1	L	66	LEU

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Mol	Chain	Res	Type
1	L	71	ASN
1	L	73	ARG
1	L	78	LEU
1	L	83	GLN
1	L	107	LEU
1	L	115	HIS
1	L	127	CYS
1	M	29	TYR
1	M	30	THR
1	M	42	ASP
1	M	55	LEU
1	M	66	LEU
1	M	78	LEU
1	M	132	SER
1	N	14	GLU
1	N	29	TYR
1	N	30	THR
1	N	42	ASP
1	N	55	LEU
1	N	66	LEU
1	N	78	LEU
1	N	83	GLN
1	N	127	CYS
1	N	128	ASP
1	O	10	SER
1	O	29	TYR
1	O	30	THR
1	O	42	ASP
1	O	55	LEU
1	O	71	ASN
1	O	73	ARG
1	O	78	LEU
1	O	83	GLN
1	O	127	CYS
1	O	128	ASP
1	O	155	VAL
1	P	4	GLN
1	P	29	TYR
1	P	41	ASP
1	P	66	LEU
1	P	78	LEU
1	P	89	GLU

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Mol	Chain	Res	Type
1	P	132	SER
1	Q	10	SER
1	Q	13	VAL
1	Q	28	SER
1	Q	29	TYR
1	Q	42	ASP
1	Q	55	LEU
1	Q	66	LEU
1	Q	71	ASN
1	Q	73	ARG
1	Q	78	LEU
1	Q	128	ASP
1	Q	132	SER
1	R	14	GLU
1	R	29	TYR
1	R	30	THR
1	R	41	ASP
1	R	55	LEU
1	R	66	LEU
1	R	71	ASN
1	R	78	LEU
1	R	143	LYS
1	S	10	SER
1	S	29	TYR
1	S	41	ASP
1	S	55	LEU
1	S	66	LEU
1	S	71	ASN
1	S	78	LEU
1	S	128	ASP
1	S	138	GLU
1	S	143	LYS
1	S	178	LEU
1	T	10	SER
1	T	29	TYR
1	T	30	THR
1	T	42	ASP
1	T	55	LEU
1	T	66	LEU
1	T	71	ASN
1	T	78	LEU
1	T	106	ASN

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Mol	Chain	Res	Type
1	U	10	SER
1	U	29	TYR
1	U	30	THR
1	U	41	ASP
1	U	66	LEU
1	U	71	ASN
1	U	73	ARG
1	U	78	LEU
1	U	128	ASP
1	V	10	SER
1	V	14	GLU
1	V	29	TYR
1	V	30	THR
1	V	42	ASP
1	V	55	LEU
1	V	66	LEU
1	V	78	LEU
1	V	83	GLN
1	V	127	CYS
1	V	128	ASP
1	W	10	SER
1	W	29	TYR
1	W	30	THR
1	W	41	ASP
1	W	66	LEU
1	W	73	ARG
1	W	78	LEU
1	W	89	GLU
1	W	132	SER
1	B	13	VAL
1	B	30	THR
1	B	42	ASP
1	B	60	ARG
1	B	66	LEU
1	B	73	ARG
1	B	78	LEU
1	D	29	TYR
1	D	30	THR
1	D	42	ASP
1	D	55	LEU
1	D	66	LEU
1	D	78	LEU

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Mol	Chain	Res	Type
1	D	107	LEU
1	D	129	PHE
1	F	29	TYR
1	F	30	THR
1	F	42	ASP
1	F	55	LEU
1	F	73	ARG
1	F	78	LEU
1	F	132	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (117) such sidechains are listed below:

Mol	Chain	Res	Type
1	Z	70	GLN
1	Z	109	GLN
1	Z	147	ASN
1	A	8	ASN
1	A	83	GLN
1	A	147	ASN
1	A	148	HIS
1	C	7	GLN
1	C	8	ASN
1	C	115	HIS
1	C	147	ASN
1	E	8	ASN
1	E	22	ASN
1	E	109	GLN
1	E	115	HIS
1	E	147	ASN
1	E	148	HIS
1	G	8	ASN
1	G	70	GLN
1	G	115	HIS
1	G	147	ASN
1	G	148	HIS
1	H	8	ASN
1	H	83	GLN
1	H	87	GLN
1	H	133	HIS
1	H	147	ASN
1	H	148	HIS
1	I	8	ASN

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Mol	Chain	Res	Type
1	I	83	GLN
1	I	87	GLN
1	I	133	HIS
1	I	147	ASN
1	I	148	HIS
1	J	8	ASN
1	J	87	GLN
1	J	115	HIS
1	J	147	ASN
1	K	8	ASN
1	K	70	GLN
1	K	83	GLN
1	K	115	HIS
1	K	147	ASN
1	L	8	ASN
1	L	22	ASN
1	L	83	GLN
1	L	133	HIS
1	L	147	ASN
1	L	148	HIS
1	M	8	ASN
1	M	70	GLN
1	M	83	GLN
1	M	147	ASN
1	M	148	HIS
1	N	8	ASN
1	N	22	ASN
1	N	70	GLN
1	N	83	GLN
1	N	109	GLN
1	N	147	ASN
1	N	148	HIS
1	O	8	ASN
1	O	22	ASN
1	O	83	GLN
1	O	133	HIS
1	O	147	ASN
1	O	148	HIS
1	P	8	ASN
1	P	70	GLN
1	P	83	GLN
1	P	115	HIS

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Mol	Chain	Res	Type
1	P	147	ASN
1	Q	8	ASN
1	Q	83	GLN
1	Q	147	ASN
1	R	8	ASN
1	R	87	GLN
1	R	115	HIS
1	R	147	ASN
1	S	8	ASN
1	S	147	ASN
1	T	8	ASN
1	T	115	HIS
1	T	147	ASN
1	U	8	ASN
1	U	70	GLN
1	U	87	GLN
1	U	133	HIS
1	U	147	ASN
1	U	148	HIS
1	V	8	ASN
1	V	22	ASN
1	V	70	GLN
1	V	83	GLN
1	V	133	HIS
1	V	147	ASN
1	W	8	ASN
1	W	70	GLN
1	W	83	GLN
1	W	115	HIS
1	W	147	ASN
1	B	4	GLN
1	B	8	ASN
1	B	83	GLN
1	B	87	GLN
1	B	133	HIS
1	B	147	ASN
1	D	8	ASN
1	D	83	GLN
1	D	133	HIS
1	D	147	ASN
1	D	148	HIS
1	F	8	ASN

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Mol	Chain	Res	Type
1	F	83	GLN
1	F	108	ASN
1	F	115	HIS
1	F	147	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 16 ligands modelled in this entry, 16 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.

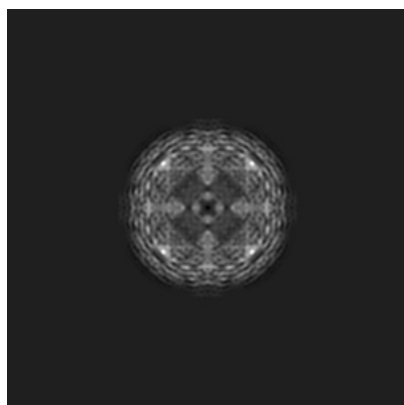
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11272. These allow visual inspection of the internal detail of the map and identification of artifacts.

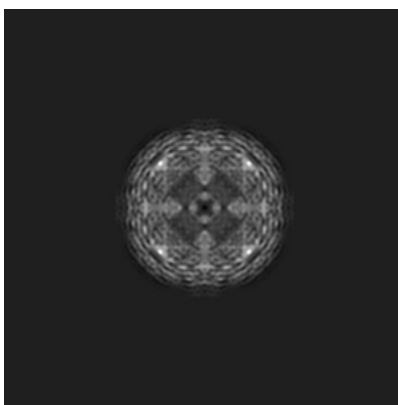
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

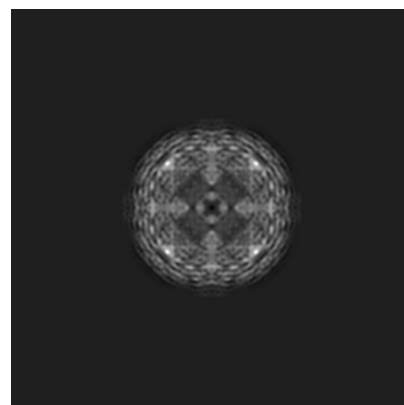
6.1.1 Primary map



X



Y

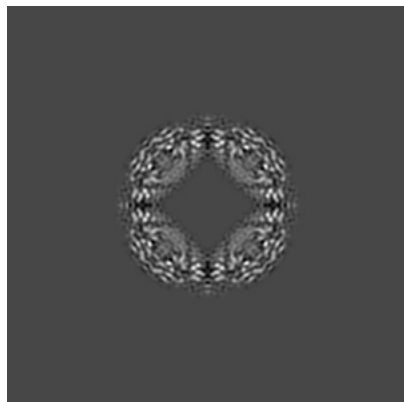


Z

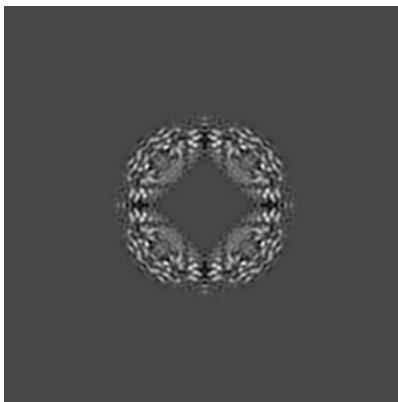
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

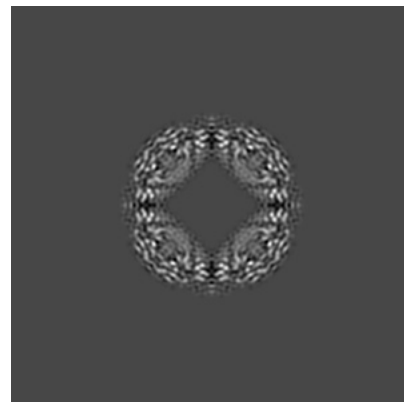
6.2.1 Primary map



X Index: 128



Y Index: 128

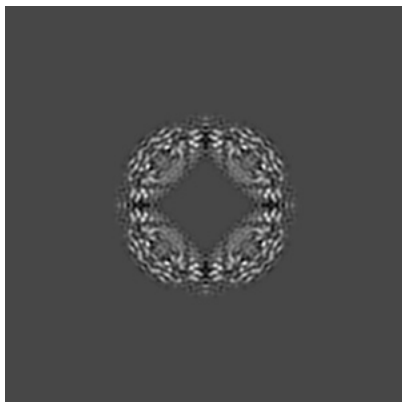


Z Index: 128

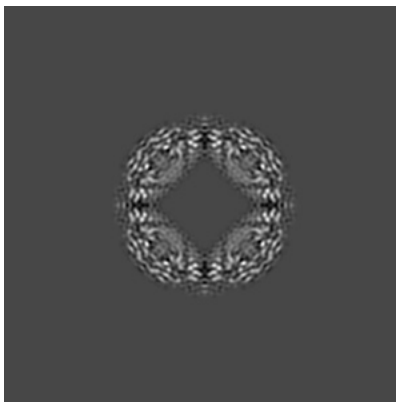
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

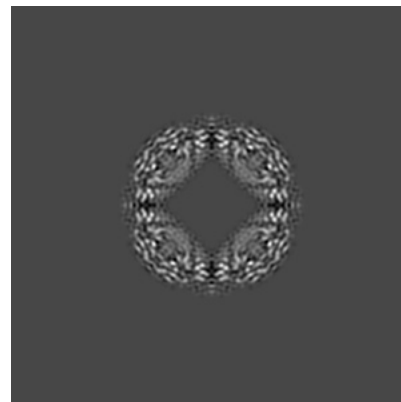
6.3.1 Primary map



X Index: 128



Y Index: 128

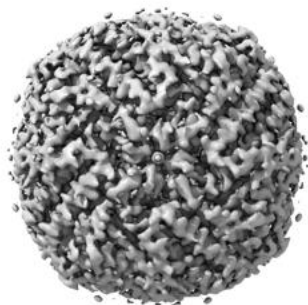


Z Index: 128

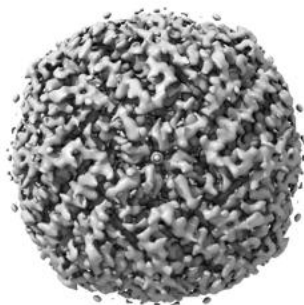
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

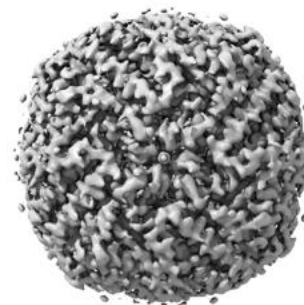
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0134. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

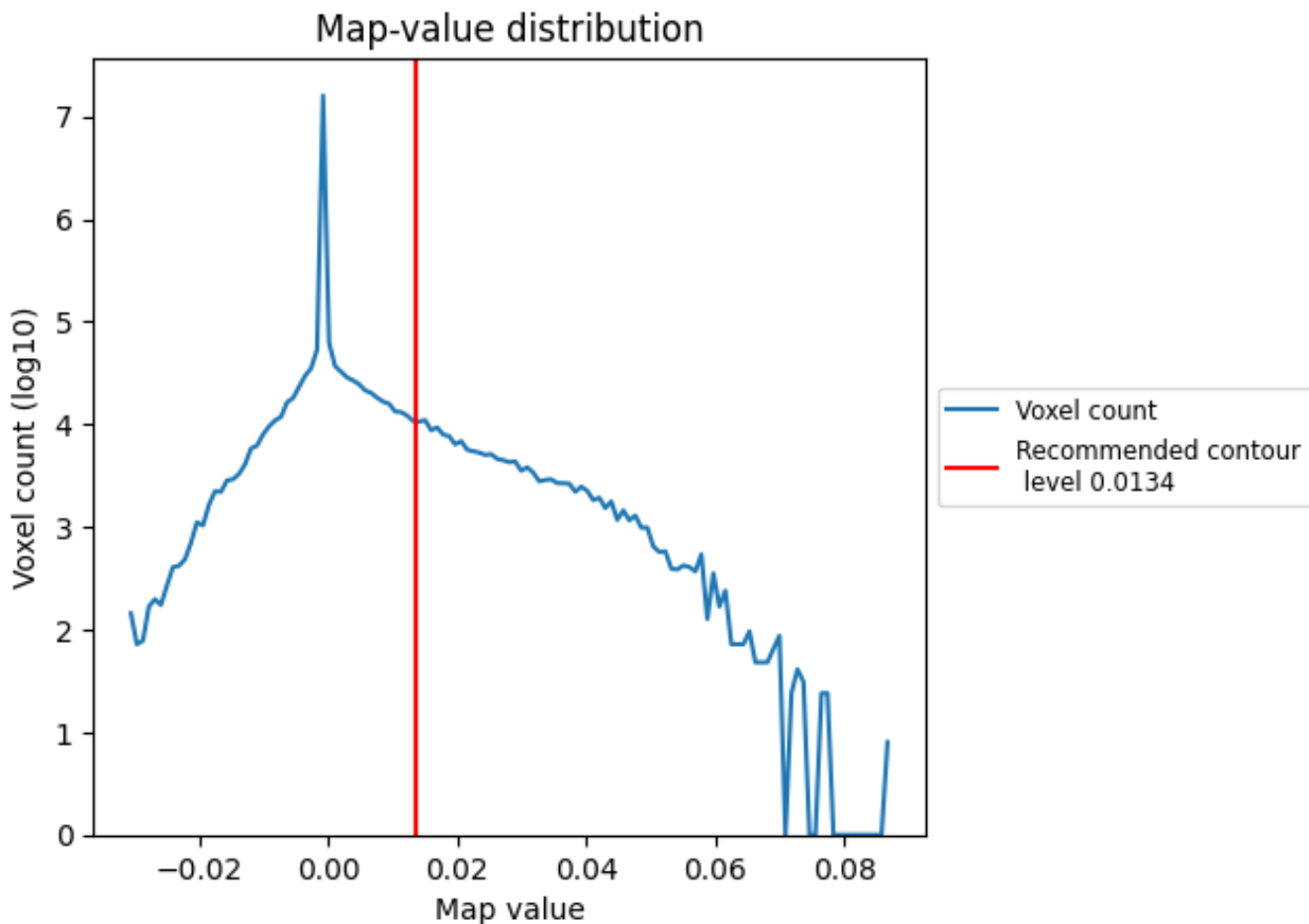
6.5 Mask visualisation

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

7 Map analysis [i](#)

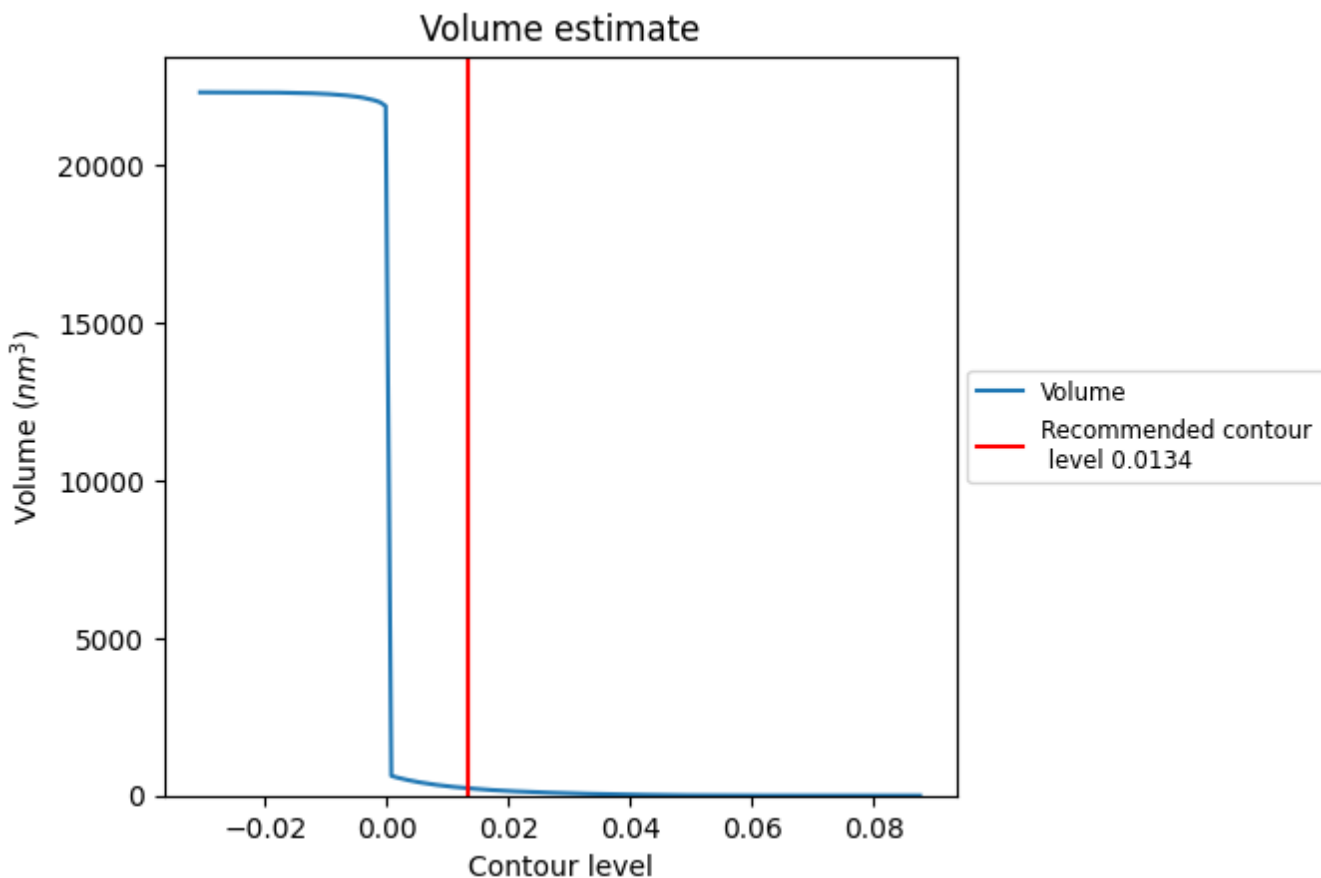
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

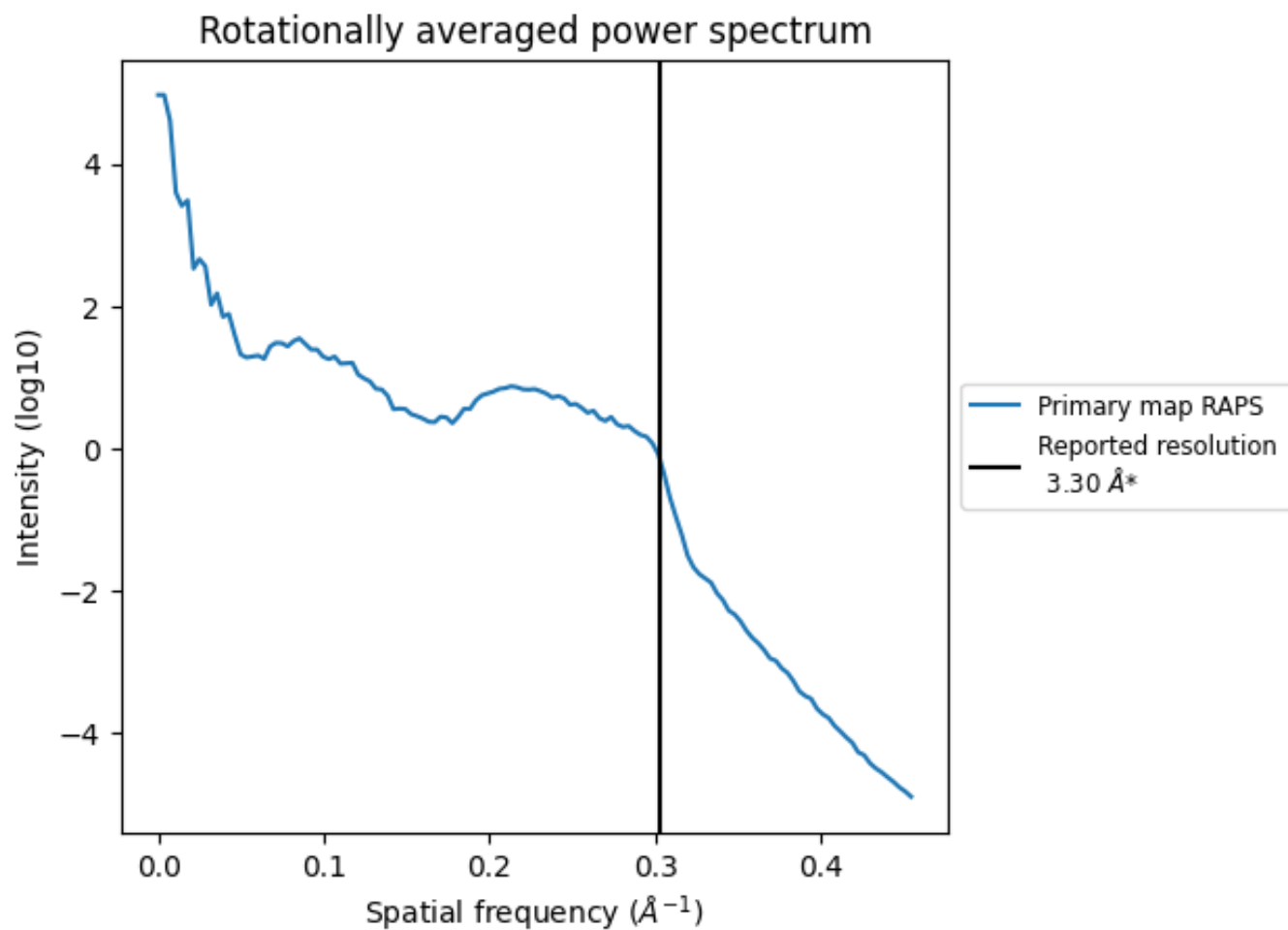
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 233 nm³; this corresponds to an approximate mass of 210 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.303\AA^{-1}

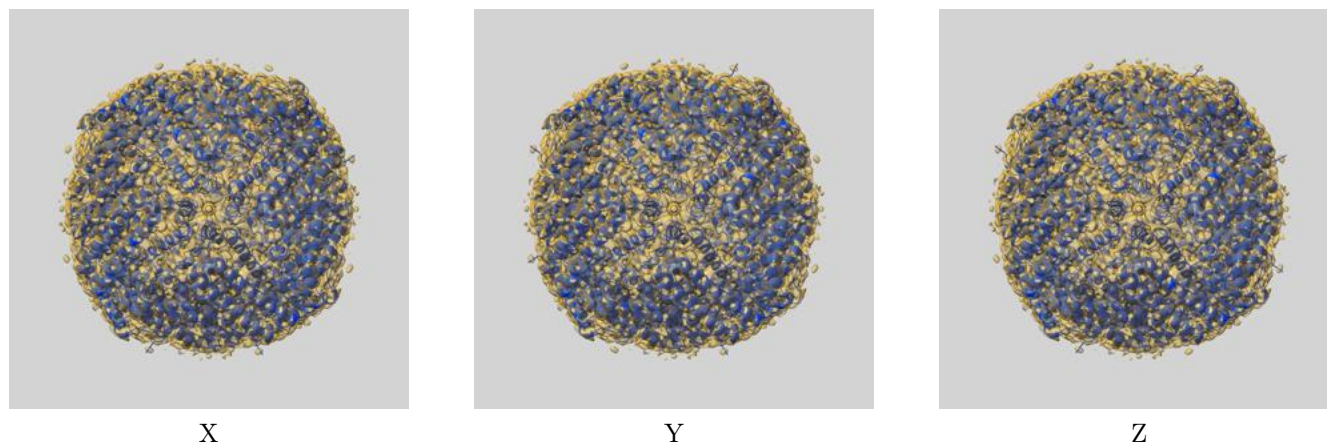
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

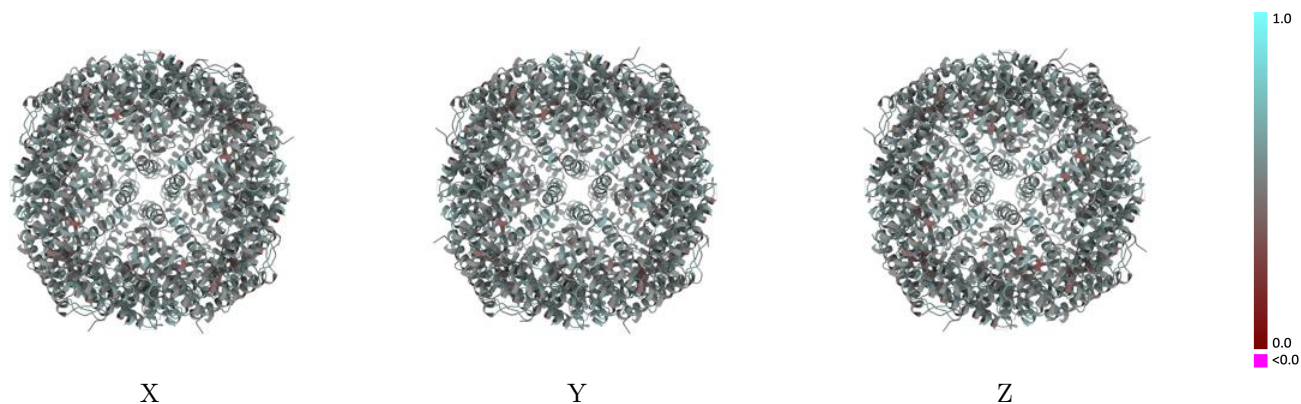
This section contains information regarding the fit between EMDB map EMD-11272 and PDB model 6ZLQ. Per-residue inclusion information can be found in section 3 on page 26.

9.1 Map-model overlay [i](#)



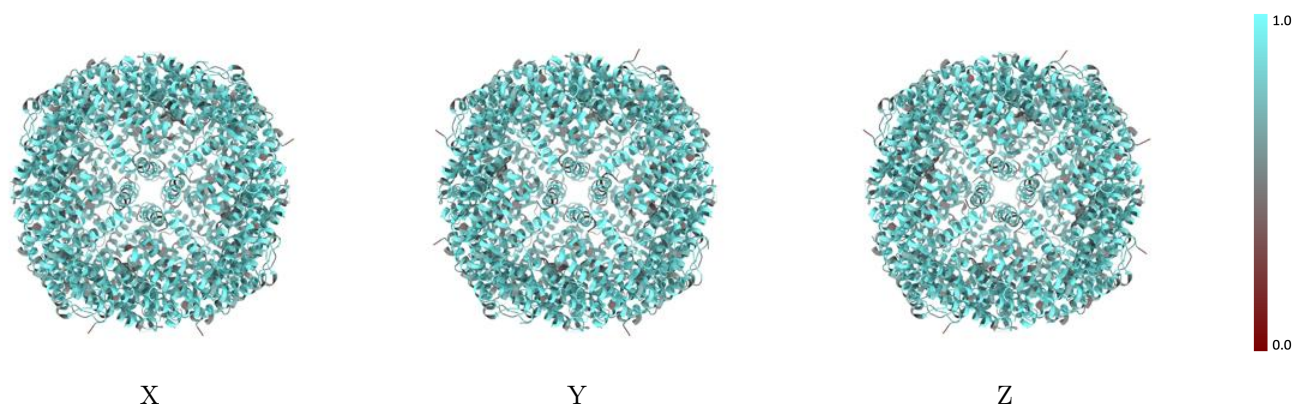
The images above show the 3D surface view of the map at the recommended contour level 0.0134 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



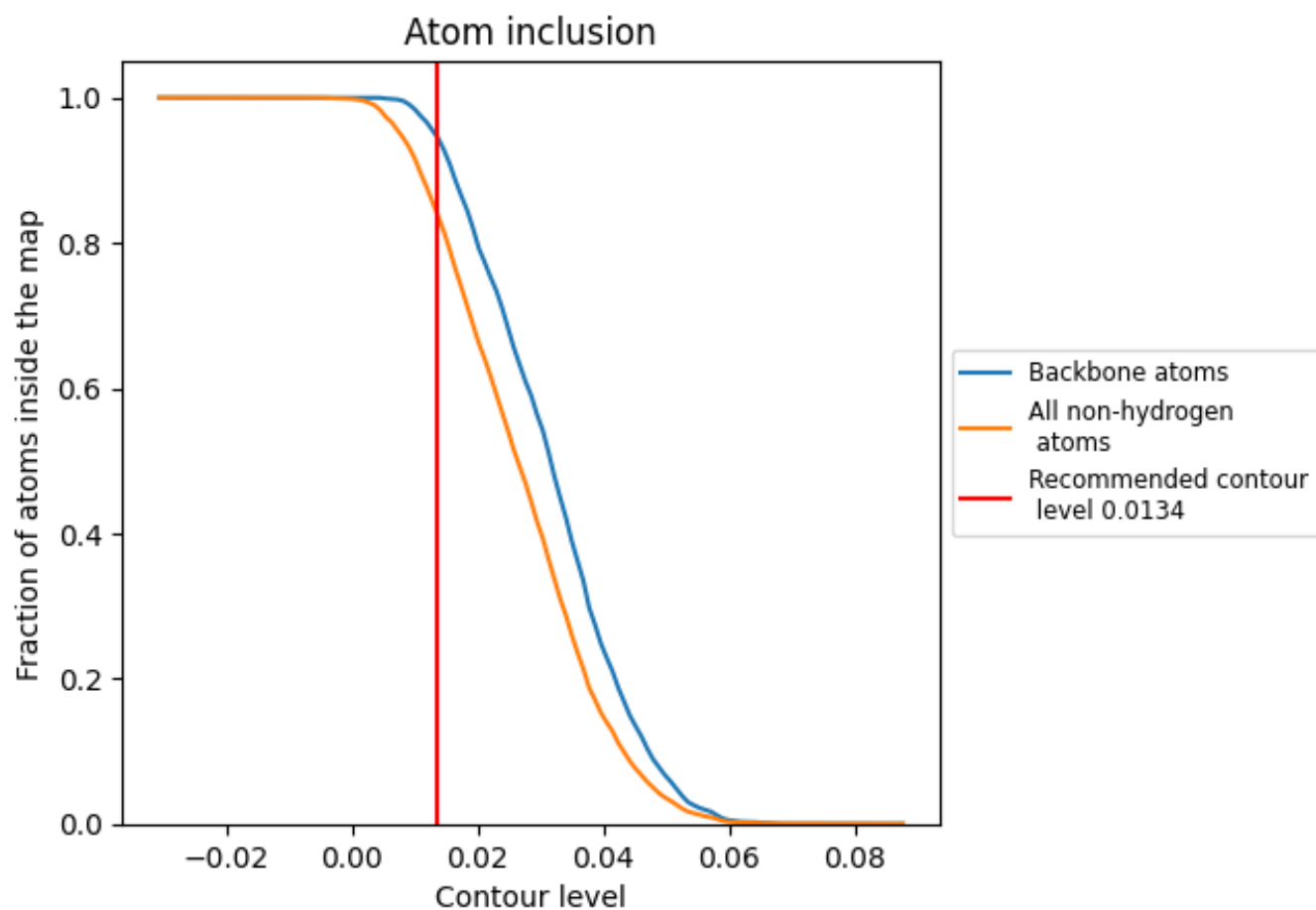
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0134).



















































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0134) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8432	 0.5280
A	 0.8422	 0.5250
B	 0.8430	 0.5310
C	 0.8458	 0.5270
D	 0.8503	 0.5260
E	 0.8493	 0.5300
F	 0.8407	 0.5270
G	 0.8413	 0.5290
H	 0.8379	 0.5280
I	 0.8395	 0.5310
J	 0.8451	 0.5310
K	 0.8421	 0.5290
L	 0.8421	 0.5240
M	 0.8428	 0.5290
N	 0.8414	 0.5250
O	 0.8466	 0.5250
P	 0.8464	 0.5280
Q	 0.8408	 0.5270
R	 0.8429	 0.5290
S	 0.8415	 0.5300
T	 0.8428	 0.5310
U	 0.8386	 0.5290
V	 0.8459	 0.5250
W	 0.8428	 0.5290
Z	 0.8457	 0.5240

