



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 09:42 AM UTC

PDB ID : 4GQH / pdb_00004gqh
Title : The Conformations and Interactions of the Four-Layer Aggregate Revealed by X-ray Crystallography Diffraction Implied the Importance of Peptides at Opposite Ends in Their Assemblies
Authors : Li, X.Y.; Song, B.A.; Hu, D.Y.; Chen, X.; Wang, Z.C.; Zeng, M.J.; Yu, D.D.; Chen, Z.; Jin, L.H.; Yang, S.
Deposited on : 2012-08-23
Resolution : 3.06 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

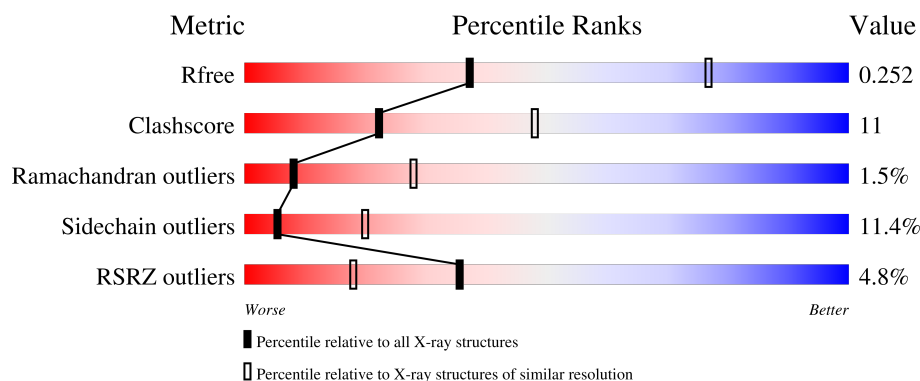
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.06 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



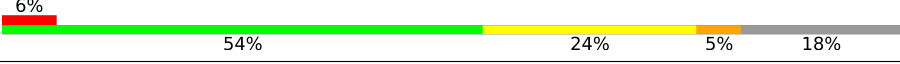
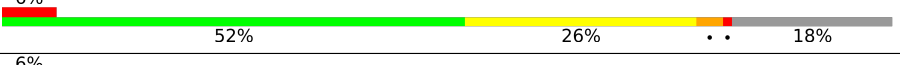
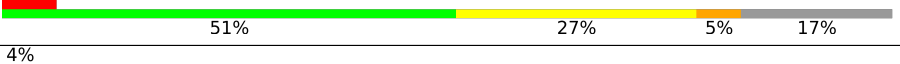
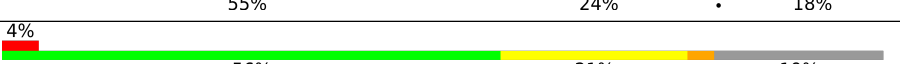
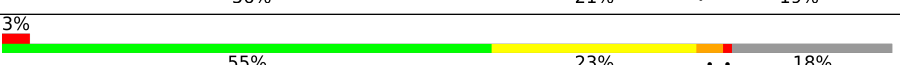
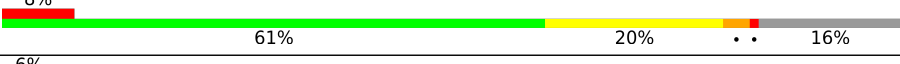
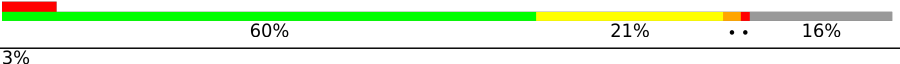
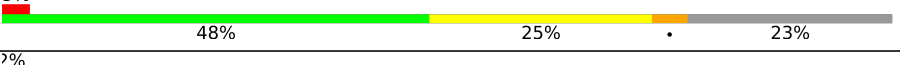
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	174	5% 61% 16% • • 18%
1	B	174	2% 61% 17% • 20%
1	C	174	5% 57% 21% • • 17%
1	D	174	6% 59% 22% • 18%
1	E	174	4% 58% 19% • 20%

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Mol	Chain	Length	Quality of chain
1	F	174	
1	G	174	
1	H	174	
1	I	174	
1	J	174	
1	K	174	
1	L	174	
1	M	174	
1	N	174	
1	O	174	
1	P	174	
1	Q	174	
1	R	174	
1	S	174	
1	T	174	
1	U	174	
1	V	174	
1	W	174	
1	X	174	
1	Y	174	
1	Z	174	
1	a	174	
1	b	174	
1	c	174	
1	d	174	

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Mol	Chain	Length	Quality of chain
1	e	174	
1	f	174	
1	h	174	
1	i	174	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 36918 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	142	Total	C	N	O	S	0	0	0
			1115	703	195	216	1			
1	B	139	Total	C	N	O	S	0	0	0
			1096	691	192	212	1			
1	C	144	Total	C	N	O	S	0	0	0
			1132	713	197	221	1			
1	D	143	Total	C	N	O	S	0	0	0
			1126	709	199	217	1			
1	E	140	Total	C	N	O	S	0	0	0
			1100	693	193	213	1			
1	F	143	Total	C	N	O	S	0	0	0
			1131	712	199	219	1			
1	G	143	Total	C	N	O	S	0	0	0
			1131	715	199	216	1			
1	H	144	Total	C	N	O	S	0	0	0
			1135	714	200	220	1			
1	I	141	Total	C	N	O	S	0	0	0
			1111	701	194	215	1			
1	J	145	Total	C	N	O	S	0	0	0
			1143	719	201	222	1			
1	K	143	Total	C	N	O	S	0	0	0
			1131	712	199	219	1			
1	L	141	Total	C	N	O	S	0	0	0
			1111	701	194	215	1			
1	M	142	Total	C	N	O	S	0	0	0
			1122	707	198	216	1			
1	N	142	Total	C	N	O	S	0	0	0
			1122	707	198	216	1			
1	O	140	Total	C	N	O	S	0	0	0
			1100	693	193	213	1			
1	P	147	Total	C	N	O	S	0	0	0
			1157	728	203	225	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	146	Total	C	N	O	S	0	0	0
			1150	723	202	224	1			
1	R	133	Total	C	N	O	S	0	0	0
			1046	664	179	202	1			
1	S	133	Total	C	N	O	S	0	0	0
			1046	664	179	202	1			
1	T	132	Total	C	N	O	S	0	0	0
			1039	659	178	201	1			
1	U	133	Total	C	N	O	S	0	0	0
			1046	664	179	202	1			
1	V	134	Total	C	N	O	S	0	0	0
			1054	668	181	204	1			
1	W	134	Total	C	N	O	S	0	0	0
			1054	668	181	204	1			
1	X	131	Total	C	N	O	S	0	0	0
			1028	653	174	200	1			
1	Y	132	Total	C	N	O	S	0	0	0
			1035	658	175	201	1			
1	Z	134	Total	C	N	O	S	0	0	0
			1054	668	181	204	1			
1	a	131	Total	C	N	O	S	0	0	0
			1029	655	174	199	1			
1	b	132	Total	C	N	O	S	0	0	0
			1035	658	175	201	1			
1	c	136	Total	C	N	O	S	0	0	0
			1069	676	186	206	1			
1	d	134	Total	C	N	O	S	0	0	0
			1054	668	181	204	1			
1	e	134	Total	C	N	O	S	0	0	0
			1054	668	181	204	1			
1	f	134	Total	C	N	O	S	0	0	0
			1054	668	181	204	1			
1	h	134	Total	C	N	O	S	0	0	0
			1054	668	181	204	1			
1	i	134	Total	C	N	O	S	0	0	0
			1054	668	181	204	1			

There are 680 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP P69687
A	-18	GLY	-	expression tag	UNP P69687
A	-17	SER	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	SER	-	expression tag	UNP P69687
A	-15	HIS	-	expression tag	UNP P69687
A	-14	HIS	-	expression tag	UNP P69687
A	-13	HIS	-	expression tag	UNP P69687
A	-12	HIS	-	expression tag	UNP P69687
A	-11	HIS	-	expression tag	UNP P69687
A	-10	HIS	-	expression tag	UNP P69687
A	-9	SER	-	expression tag	UNP P69687
A	-8	SER	-	expression tag	UNP P69687
A	-7	GLY	-	expression tag	UNP P69687
A	-6	LEU	-	expression tag	UNP P69687
A	-5	VAL	-	expression tag	UNP P69687
A	-4	PRO	-	expression tag	UNP P69687
A	-3	ARG	-	expression tag	UNP P69687
A	-2	GLY	-	expression tag	UNP P69687
A	-1	SER	-	expression tag	UNP P69687
A	0	HIS	-	expression tag	UNP P69687
B	-19	MET	-	expression tag	UNP P69687
B	-18	GLY	-	expression tag	UNP P69687
B	-17	SER	-	expression tag	UNP P69687
B	-16	SER	-	expression tag	UNP P69687
B	-15	HIS	-	expression tag	UNP P69687
B	-14	HIS	-	expression tag	UNP P69687
B	-13	HIS	-	expression tag	UNP P69687
B	-12	HIS	-	expression tag	UNP P69687
B	-11	HIS	-	expression tag	UNP P69687
B	-10	HIS	-	expression tag	UNP P69687
B	-9	SER	-	expression tag	UNP P69687
B	-8	SER	-	expression tag	UNP P69687
B	-7	GLY	-	expression tag	UNP P69687
B	-6	LEU	-	expression tag	UNP P69687
B	-5	VAL	-	expression tag	UNP P69687
B	-4	PRO	-	expression tag	UNP P69687
B	-3	ARG	-	expression tag	UNP P69687
B	-2	GLY	-	expression tag	UNP P69687
B	-1	SER	-	expression tag	UNP P69687
B	0	HIS	-	expression tag	UNP P69687
C	-19	MET	-	expression tag	UNP P69687
C	-18	GLY	-	expression tag	UNP P69687
C	-17	SER	-	expression tag	UNP P69687
C	-16	SER	-	expression tag	UNP P69687
C	-15	HIS	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-14	HIS	-	expression tag	UNP P69687
C	-13	HIS	-	expression tag	UNP P69687
C	-12	HIS	-	expression tag	UNP P69687
C	-11	HIS	-	expression tag	UNP P69687
C	-10	HIS	-	expression tag	UNP P69687
C	-9	SER	-	expression tag	UNP P69687
C	-8	SER	-	expression tag	UNP P69687
C	-7	GLY	-	expression tag	UNP P69687
C	-6	LEU	-	expression tag	UNP P69687
C	-5	VAL	-	expression tag	UNP P69687
C	-4	PRO	-	expression tag	UNP P69687
C	-3	ARG	-	expression tag	UNP P69687
C	-2	GLY	-	expression tag	UNP P69687
C	-1	SER	-	expression tag	UNP P69687
C	0	HIS	-	expression tag	UNP P69687
D	-19	MET	-	expression tag	UNP P69687
D	-18	GLY	-	expression tag	UNP P69687
D	-17	SER	-	expression tag	UNP P69687
D	-16	SER	-	expression tag	UNP P69687
D	-15	HIS	-	expression tag	UNP P69687
D	-14	HIS	-	expression tag	UNP P69687
D	-13	HIS	-	expression tag	UNP P69687
D	-12	HIS	-	expression tag	UNP P69687
D	-11	HIS	-	expression tag	UNP P69687
D	-10	HIS	-	expression tag	UNP P69687
D	-9	SER	-	expression tag	UNP P69687
D	-8	SER	-	expression tag	UNP P69687
D	-7	GLY	-	expression tag	UNP P69687
D	-6	LEU	-	expression tag	UNP P69687
D	-5	VAL	-	expression tag	UNP P69687
D	-4	PRO	-	expression tag	UNP P69687
D	-3	ARG	-	expression tag	UNP P69687
D	-2	GLY	-	expression tag	UNP P69687
D	-1	SER	-	expression tag	UNP P69687
D	0	HIS	-	expression tag	UNP P69687
E	-19	MET	-	expression tag	UNP P69687
E	-18	GLY	-	expression tag	UNP P69687
E	-17	SER	-	expression tag	UNP P69687
E	-16	SER	-	expression tag	UNP P69687
E	-15	HIS	-	expression tag	UNP P69687
E	-14	HIS	-	expression tag	UNP P69687
E	-13	HIS	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-12	HIS	-	expression tag	UNP P69687
E	-11	HIS	-	expression tag	UNP P69687
E	-10	HIS	-	expression tag	UNP P69687
E	-9	SER	-	expression tag	UNP P69687
E	-8	SER	-	expression tag	UNP P69687
E	-7	GLY	-	expression tag	UNP P69687
E	-6	LEU	-	expression tag	UNP P69687
E	-5	VAL	-	expression tag	UNP P69687
E	-4	PRO	-	expression tag	UNP P69687
E	-3	ARG	-	expression tag	UNP P69687
E	-2	GLY	-	expression tag	UNP P69687
E	-1	SER	-	expression tag	UNP P69687
E	0	HIS	-	expression tag	UNP P69687
F	-19	MET	-	expression tag	UNP P69687
F	-18	GLY	-	expression tag	UNP P69687
F	-17	SER	-	expression tag	UNP P69687
F	-16	SER	-	expression tag	UNP P69687
F	-15	HIS	-	expression tag	UNP P69687
F	-14	HIS	-	expression tag	UNP P69687
F	-13	HIS	-	expression tag	UNP P69687
F	-12	HIS	-	expression tag	UNP P69687
F	-11	HIS	-	expression tag	UNP P69687
F	-10	HIS	-	expression tag	UNP P69687
F	-9	SER	-	expression tag	UNP P69687
F	-8	SER	-	expression tag	UNP P69687
F	-7	GLY	-	expression tag	UNP P69687
F	-6	LEU	-	expression tag	UNP P69687
F	-5	VAL	-	expression tag	UNP P69687
F	-4	PRO	-	expression tag	UNP P69687
F	-3	ARG	-	expression tag	UNP P69687
F	-2	GLY	-	expression tag	UNP P69687
F	-1	SER	-	expression tag	UNP P69687
F	0	HIS	-	expression tag	UNP P69687
G	-19	MET	-	expression tag	UNP P69687
G	-18	GLY	-	expression tag	UNP P69687
G	-17	SER	-	expression tag	UNP P69687
G	-16	SER	-	expression tag	UNP P69687
G	-15	HIS	-	expression tag	UNP P69687
G	-14	HIS	-	expression tag	UNP P69687
G	-13	HIS	-	expression tag	UNP P69687
G	-12	HIS	-	expression tag	UNP P69687
G	-11	HIS	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-10	HIS	-	expression tag	UNP P69687
G	-9	SER	-	expression tag	UNP P69687
G	-8	SER	-	expression tag	UNP P69687
G	-7	GLY	-	expression tag	UNP P69687
G	-6	LEU	-	expression tag	UNP P69687
G	-5	VAL	-	expression tag	UNP P69687
G	-4	PRO	-	expression tag	UNP P69687
G	-3	ARG	-	expression tag	UNP P69687
G	-2	GLY	-	expression tag	UNP P69687
G	-1	SER	-	expression tag	UNP P69687
G	0	HIS	-	expression tag	UNP P69687
H	-19	MET	-	expression tag	UNP P69687
H	-18	GLY	-	expression tag	UNP P69687
H	-17	SER	-	expression tag	UNP P69687
H	-16	SER	-	expression tag	UNP P69687
H	-15	HIS	-	expression tag	UNP P69687
H	-14	HIS	-	expression tag	UNP P69687
H	-13	HIS	-	expression tag	UNP P69687
H	-12	HIS	-	expression tag	UNP P69687
H	-11	HIS	-	expression tag	UNP P69687
H	-10	HIS	-	expression tag	UNP P69687
H	-9	SER	-	expression tag	UNP P69687
H	-8	SER	-	expression tag	UNP P69687
H	-7	GLY	-	expression tag	UNP P69687
H	-6	LEU	-	expression tag	UNP P69687
H	-5	VAL	-	expression tag	UNP P69687
H	-4	PRO	-	expression tag	UNP P69687
H	-3	ARG	-	expression tag	UNP P69687
H	-2	GLY	-	expression tag	UNP P69687
H	-1	SER	-	expression tag	UNP P69687
H	0	HIS	-	expression tag	UNP P69687
I	-19	MET	-	expression tag	UNP P69687
I	-18	GLY	-	expression tag	UNP P69687
I	-17	SER	-	expression tag	UNP P69687
I	-16	SER	-	expression tag	UNP P69687
I	-15	HIS	-	expression tag	UNP P69687
I	-14	HIS	-	expression tag	UNP P69687
I	-13	HIS	-	expression tag	UNP P69687
I	-12	HIS	-	expression tag	UNP P69687
I	-11	HIS	-	expression tag	UNP P69687
I	-10	HIS	-	expression tag	UNP P69687
I	-9	SER	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-8	SER	-	expression tag	UNP P69687
I	-7	GLY	-	expression tag	UNP P69687
I	-6	LEU	-	expression tag	UNP P69687
I	-5	VAL	-	expression tag	UNP P69687
I	-4	PRO	-	expression tag	UNP P69687
I	-3	ARG	-	expression tag	UNP P69687
I	-2	GLY	-	expression tag	UNP P69687
I	-1	SER	-	expression tag	UNP P69687
I	0	HIS	-	expression tag	UNP P69687
J	-19	MET	-	expression tag	UNP P69687
J	-18	GLY	-	expression tag	UNP P69687
J	-17	SER	-	expression tag	UNP P69687
J	-16	SER	-	expression tag	UNP P69687
J	-15	HIS	-	expression tag	UNP P69687
J	-14	HIS	-	expression tag	UNP P69687
J	-13	HIS	-	expression tag	UNP P69687
J	-12	HIS	-	expression tag	UNP P69687
J	-11	HIS	-	expression tag	UNP P69687
J	-10	HIS	-	expression tag	UNP P69687
J	-9	SER	-	expression tag	UNP P69687
J	-8	SER	-	expression tag	UNP P69687
J	-7	GLY	-	expression tag	UNP P69687
J	-6	LEU	-	expression tag	UNP P69687
J	-5	VAL	-	expression tag	UNP P69687
J	-4	PRO	-	expression tag	UNP P69687
J	-3	ARG	-	expression tag	UNP P69687
J	-2	GLY	-	expression tag	UNP P69687
J	-1	SER	-	expression tag	UNP P69687
J	0	HIS	-	expression tag	UNP P69687
K	-19	MET	-	expression tag	UNP P69687
K	-18	GLY	-	expression tag	UNP P69687
K	-17	SER	-	expression tag	UNP P69687
K	-16	SER	-	expression tag	UNP P69687
K	-15	HIS	-	expression tag	UNP P69687
K	-14	HIS	-	expression tag	UNP P69687
K	-13	HIS	-	expression tag	UNP P69687
K	-12	HIS	-	expression tag	UNP P69687
K	-11	HIS	-	expression tag	UNP P69687
K	-10	HIS	-	expression tag	UNP P69687
K	-9	SER	-	expression tag	UNP P69687
K	-8	SER	-	expression tag	UNP P69687
K	-7	GLY	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
K	-6	LEU	-	expression tag	UNP P69687
K	-5	VAL	-	expression tag	UNP P69687
K	-4	PRO	-	expression tag	UNP P69687
K	-3	ARG	-	expression tag	UNP P69687
K	-2	GLY	-	expression tag	UNP P69687
K	-1	SER	-	expression tag	UNP P69687
K	0	HIS	-	expression tag	UNP P69687
L	-19	MET	-	expression tag	UNP P69687
L	-18	GLY	-	expression tag	UNP P69687
L	-17	SER	-	expression tag	UNP P69687
L	-16	SER	-	expression tag	UNP P69687
L	-15	HIS	-	expression tag	UNP P69687
L	-14	HIS	-	expression tag	UNP P69687
L	-13	HIS	-	expression tag	UNP P69687
L	-12	HIS	-	expression tag	UNP P69687
L	-11	HIS	-	expression tag	UNP P69687
L	-10	HIS	-	expression tag	UNP P69687
L	-9	SER	-	expression tag	UNP P69687
L	-8	SER	-	expression tag	UNP P69687
L	-7	GLY	-	expression tag	UNP P69687
L	-6	LEU	-	expression tag	UNP P69687
L	-5	VAL	-	expression tag	UNP P69687
L	-4	PRO	-	expression tag	UNP P69687
L	-3	ARG	-	expression tag	UNP P69687
L	-2	GLY	-	expression tag	UNP P69687
L	-1	SER	-	expression tag	UNP P69687
L	0	HIS	-	expression tag	UNP P69687
M	-19	MET	-	expression tag	UNP P69687
M	-18	GLY	-	expression tag	UNP P69687
M	-17	SER	-	expression tag	UNP P69687
M	-16	SER	-	expression tag	UNP P69687
M	-15	HIS	-	expression tag	UNP P69687
M	-14	HIS	-	expression tag	UNP P69687
M	-13	HIS	-	expression tag	UNP P69687
M	-12	HIS	-	expression tag	UNP P69687
M	-11	HIS	-	expression tag	UNP P69687
M	-10	HIS	-	expression tag	UNP P69687
M	-9	SER	-	expression tag	UNP P69687
M	-8	SER	-	expression tag	UNP P69687
M	-7	GLY	-	expression tag	UNP P69687
M	-6	LEU	-	expression tag	UNP P69687
M	-5	VAL	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
M	-4	PRO	-	expression tag	UNP P69687
M	-3	ARG	-	expression tag	UNP P69687
M	-2	GLY	-	expression tag	UNP P69687
M	-1	SER	-	expression tag	UNP P69687
M	0	HIS	-	expression tag	UNP P69687
N	-19	MET	-	expression tag	UNP P69687
N	-18	GLY	-	expression tag	UNP P69687
N	-17	SER	-	expression tag	UNP P69687
N	-16	SER	-	expression tag	UNP P69687
N	-15	HIS	-	expression tag	UNP P69687
N	-14	HIS	-	expression tag	UNP P69687
N	-13	HIS	-	expression tag	UNP P69687
N	-12	HIS	-	expression tag	UNP P69687
N	-11	HIS	-	expression tag	UNP P69687
N	-10	HIS	-	expression tag	UNP P69687
N	-9	SER	-	expression tag	UNP P69687
N	-8	SER	-	expression tag	UNP P69687
N	-7	GLY	-	expression tag	UNP P69687
N	-6	LEU	-	expression tag	UNP P69687
N	-5	VAL	-	expression tag	UNP P69687
N	-4	PRO	-	expression tag	UNP P69687
N	-3	ARG	-	expression tag	UNP P69687
N	-2	GLY	-	expression tag	UNP P69687
N	-1	SER	-	expression tag	UNP P69687
N	0	HIS	-	expression tag	UNP P69687
O	-19	MET	-	expression tag	UNP P69687
O	-18	GLY	-	expression tag	UNP P69687
O	-17	SER	-	expression tag	UNP P69687
O	-16	SER	-	expression tag	UNP P69687
O	-15	HIS	-	expression tag	UNP P69687
O	-14	HIS	-	expression tag	UNP P69687
O	-13	HIS	-	expression tag	UNP P69687
O	-12	HIS	-	expression tag	UNP P69687
O	-11	HIS	-	expression tag	UNP P69687
O	-10	HIS	-	expression tag	UNP P69687
O	-9	SER	-	expression tag	UNP P69687
O	-8	SER	-	expression tag	UNP P69687
O	-7	GLY	-	expression tag	UNP P69687
O	-6	LEU	-	expression tag	UNP P69687
O	-5	VAL	-	expression tag	UNP P69687
O	-4	PRO	-	expression tag	UNP P69687
O	-3	ARG	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
O	-2	GLY	-	expression tag	UNP P69687
O	-1	SER	-	expression tag	UNP P69687
O	0	HIS	-	expression tag	UNP P69687
P	-19	MET	-	expression tag	UNP P69687
P	-18	GLY	-	expression tag	UNP P69687
P	-17	SER	-	expression tag	UNP P69687
P	-16	SER	-	expression tag	UNP P69687
P	-15	HIS	-	expression tag	UNP P69687
P	-14	HIS	-	expression tag	UNP P69687
P	-13	HIS	-	expression tag	UNP P69687
P	-12	HIS	-	expression tag	UNP P69687
P	-11	HIS	-	expression tag	UNP P69687
P	-10	HIS	-	expression tag	UNP P69687
P	-9	SER	-	expression tag	UNP P69687
P	-8	SER	-	expression tag	UNP P69687
P	-7	GLY	-	expression tag	UNP P69687
P	-6	LEU	-	expression tag	UNP P69687
P	-5	VAL	-	expression tag	UNP P69687
P	-4	PRO	-	expression tag	UNP P69687
P	-3	ARG	-	expression tag	UNP P69687
P	-2	GLY	-	expression tag	UNP P69687
P	-1	SER	-	expression tag	UNP P69687
P	0	HIS	-	expression tag	UNP P69687
Q	-19	MET	-	expression tag	UNP P69687
Q	-18	GLY	-	expression tag	UNP P69687
Q	-17	SER	-	expression tag	UNP P69687
Q	-16	SER	-	expression tag	UNP P69687
Q	-15	HIS	-	expression tag	UNP P69687
Q	-14	HIS	-	expression tag	UNP P69687
Q	-13	HIS	-	expression tag	UNP P69687
Q	-12	HIS	-	expression tag	UNP P69687
Q	-11	HIS	-	expression tag	UNP P69687
Q	-10	HIS	-	expression tag	UNP P69687
Q	-9	SER	-	expression tag	UNP P69687
Q	-8	SER	-	expression tag	UNP P69687
Q	-7	GLY	-	expression tag	UNP P69687
Q	-6	LEU	-	expression tag	UNP P69687
Q	-5	VAL	-	expression tag	UNP P69687
Q	-4	PRO	-	expression tag	UNP P69687
Q	-3	ARG	-	expression tag	UNP P69687
Q	-2	GLY	-	expression tag	UNP P69687
Q	-1	SER	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
Q	0	HIS	-	expression tag	UNP P69687
R	-19	MET	-	expression tag	UNP P69687
R	-18	GLY	-	expression tag	UNP P69687
R	-17	SER	-	expression tag	UNP P69687
R	-16	SER	-	expression tag	UNP P69687
R	-15	HIS	-	expression tag	UNP P69687
R	-14	HIS	-	expression tag	UNP P69687
R	-13	HIS	-	expression tag	UNP P69687
R	-12	HIS	-	expression tag	UNP P69687
R	-11	HIS	-	expression tag	UNP P69687
R	-10	HIS	-	expression tag	UNP P69687
R	-9	SER	-	expression tag	UNP P69687
R	-8	SER	-	expression tag	UNP P69687
R	-7	GLY	-	expression tag	UNP P69687
R	-6	LEU	-	expression tag	UNP P69687
R	-5	VAL	-	expression tag	UNP P69687
R	-4	PRO	-	expression tag	UNP P69687
R	-3	ARG	-	expression tag	UNP P69687
R	-2	GLY	-	expression tag	UNP P69687
R	-1	SER	-	expression tag	UNP P69687
R	0	HIS	-	expression tag	UNP P69687
S	-19	MET	-	expression tag	UNP P69687
S	-18	GLY	-	expression tag	UNP P69687
S	-17	SER	-	expression tag	UNP P69687
S	-16	SER	-	expression tag	UNP P69687
S	-15	HIS	-	expression tag	UNP P69687
S	-14	HIS	-	expression tag	UNP P69687
S	-13	HIS	-	expression tag	UNP P69687
S	-12	HIS	-	expression tag	UNP P69687
S	-11	HIS	-	expression tag	UNP P69687
S	-10	HIS	-	expression tag	UNP P69687
S	-9	SER	-	expression tag	UNP P69687
S	-8	SER	-	expression tag	UNP P69687
S	-7	GLY	-	expression tag	UNP P69687
S	-6	LEU	-	expression tag	UNP P69687
S	-5	VAL	-	expression tag	UNP P69687
S	-4	PRO	-	expression tag	UNP P69687
S	-3	ARG	-	expression tag	UNP P69687
S	-2	GLY	-	expression tag	UNP P69687
S	-1	SER	-	expression tag	UNP P69687
S	0	HIS	-	expression tag	UNP P69687
T	-19	MET	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
T	-18	GLY	-	expression tag	UNP P69687
T	-17	SER	-	expression tag	UNP P69687
T	-16	SER	-	expression tag	UNP P69687
T	-15	HIS	-	expression tag	UNP P69687
T	-14	HIS	-	expression tag	UNP P69687
T	-13	HIS	-	expression tag	UNP P69687
T	-12	HIS	-	expression tag	UNP P69687
T	-11	HIS	-	expression tag	UNP P69687
T	-10	HIS	-	expression tag	UNP P69687
T	-9	SER	-	expression tag	UNP P69687
T	-8	SER	-	expression tag	UNP P69687
T	-7	GLY	-	expression tag	UNP P69687
T	-6	LEU	-	expression tag	UNP P69687
T	-5	VAL	-	expression tag	UNP P69687
T	-4	PRO	-	expression tag	UNP P69687
T	-3	ARG	-	expression tag	UNP P69687
T	-2	GLY	-	expression tag	UNP P69687
T	-1	SER	-	expression tag	UNP P69687
T	0	HIS	-	expression tag	UNP P69687
U	-19	MET	-	expression tag	UNP P69687
U	-18	GLY	-	expression tag	UNP P69687
U	-17	SER	-	expression tag	UNP P69687
U	-16	SER	-	expression tag	UNP P69687
U	-15	HIS	-	expression tag	UNP P69687
U	-14	HIS	-	expression tag	UNP P69687
U	-13	HIS	-	expression tag	UNP P69687
U	-12	HIS	-	expression tag	UNP P69687
U	-11	HIS	-	expression tag	UNP P69687
U	-10	HIS	-	expression tag	UNP P69687
U	-9	SER	-	expression tag	UNP P69687
U	-8	SER	-	expression tag	UNP P69687
U	-7	GLY	-	expression tag	UNP P69687
U	-6	LEU	-	expression tag	UNP P69687
U	-5	VAL	-	expression tag	UNP P69687
U	-4	PRO	-	expression tag	UNP P69687
U	-3	ARG	-	expression tag	UNP P69687
U	-2	GLY	-	expression tag	UNP P69687
U	-1	SER	-	expression tag	UNP P69687
U	0	HIS	-	expression tag	UNP P69687
V	-19	MET	-	expression tag	UNP P69687
V	-18	GLY	-	expression tag	UNP P69687
V	-17	SER	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
V	-16	SER	-	expression tag	UNP P69687
V	-15	HIS	-	expression tag	UNP P69687
V	-14	HIS	-	expression tag	UNP P69687
V	-13	HIS	-	expression tag	UNP P69687
V	-12	HIS	-	expression tag	UNP P69687
V	-11	HIS	-	expression tag	UNP P69687
V	-10	HIS	-	expression tag	UNP P69687
V	-9	SER	-	expression tag	UNP P69687
V	-8	SER	-	expression tag	UNP P69687
V	-7	GLY	-	expression tag	UNP P69687
V	-6	LEU	-	expression tag	UNP P69687
V	-5	VAL	-	expression tag	UNP P69687
V	-4	PRO	-	expression tag	UNP P69687
V	-3	ARG	-	expression tag	UNP P69687
V	-2	GLY	-	expression tag	UNP P69687
V	-1	SER	-	expression tag	UNP P69687
V	0	HIS	-	expression tag	UNP P69687
W	-19	MET	-	expression tag	UNP P69687
W	-18	GLY	-	expression tag	UNP P69687
W	-17	SER	-	expression tag	UNP P69687
W	-16	SER	-	expression tag	UNP P69687
W	-15	HIS	-	expression tag	UNP P69687
W	-14	HIS	-	expression tag	UNP P69687
W	-13	HIS	-	expression tag	UNP P69687
W	-12	HIS	-	expression tag	UNP P69687
W	-11	HIS	-	expression tag	UNP P69687
W	-10	HIS	-	expression tag	UNP P69687
W	-9	SER	-	expression tag	UNP P69687
W	-8	SER	-	expression tag	UNP P69687
W	-7	GLY	-	expression tag	UNP P69687
W	-6	LEU	-	expression tag	UNP P69687
W	-5	VAL	-	expression tag	UNP P69687
W	-4	PRO	-	expression tag	UNP P69687
W	-3	ARG	-	expression tag	UNP P69687
W	-2	GLY	-	expression tag	UNP P69687
W	-1	SER	-	expression tag	UNP P69687
W	0	HIS	-	expression tag	UNP P69687
X	-19	MET	-	expression tag	UNP P69687
X	-18	GLY	-	expression tag	UNP P69687
X	-17	SER	-	expression tag	UNP P69687
X	-16	SER	-	expression tag	UNP P69687
X	-15	HIS	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
X	-14	HIS	-	expression tag	UNP P69687
X	-13	HIS	-	expression tag	UNP P69687
X	-12	HIS	-	expression tag	UNP P69687
X	-11	HIS	-	expression tag	UNP P69687
X	-10	HIS	-	expression tag	UNP P69687
X	-9	SER	-	expression tag	UNP P69687
X	-8	SER	-	expression tag	UNP P69687
X	-7	GLY	-	expression tag	UNP P69687
X	-6	LEU	-	expression tag	UNP P69687
X	-5	VAL	-	expression tag	UNP P69687
X	-4	PRO	-	expression tag	UNP P69687
X	-3	ARG	-	expression tag	UNP P69687
X	-2	GLY	-	expression tag	UNP P69687
X	-1	SER	-	expression tag	UNP P69687
X	0	HIS	-	expression tag	UNP P69687
Y	-19	MET	-	expression tag	UNP P69687
Y	-18	GLY	-	expression tag	UNP P69687
Y	-17	SER	-	expression tag	UNP P69687
Y	-16	SER	-	expression tag	UNP P69687
Y	-15	HIS	-	expression tag	UNP P69687
Y	-14	HIS	-	expression tag	UNP P69687
Y	-13	HIS	-	expression tag	UNP P69687
Y	-12	HIS	-	expression tag	UNP P69687
Y	-11	HIS	-	expression tag	UNP P69687
Y	-10	HIS	-	expression tag	UNP P69687
Y	-9	SER	-	expression tag	UNP P69687
Y	-8	SER	-	expression tag	UNP P69687
Y	-7	GLY	-	expression tag	UNP P69687
Y	-6	LEU	-	expression tag	UNP P69687
Y	-5	VAL	-	expression tag	UNP P69687
Y	-4	PRO	-	expression tag	UNP P69687
Y	-3	ARG	-	expression tag	UNP P69687
Y	-2	GLY	-	expression tag	UNP P69687
Y	-1	SER	-	expression tag	UNP P69687
Y	0	HIS	-	expression tag	UNP P69687
Z	-19	MET	-	expression tag	UNP P69687
Z	-18	GLY	-	expression tag	UNP P69687
Z	-17	SER	-	expression tag	UNP P69687
Z	-16	SER	-	expression tag	UNP P69687
Z	-15	HIS	-	expression tag	UNP P69687
Z	-14	HIS	-	expression tag	UNP P69687
Z	-13	HIS	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
Z	-12	HIS	-	expression tag	UNP P69687
Z	-11	HIS	-	expression tag	UNP P69687
Z	-10	HIS	-	expression tag	UNP P69687
Z	-9	SER	-	expression tag	UNP P69687
Z	-8	SER	-	expression tag	UNP P69687
Z	-7	GLY	-	expression tag	UNP P69687
Z	-6	LEU	-	expression tag	UNP P69687
Z	-5	VAL	-	expression tag	UNP P69687
Z	-4	PRO	-	expression tag	UNP P69687
Z	-3	ARG	-	expression tag	UNP P69687
Z	-2	GLY	-	expression tag	UNP P69687
Z	-1	SER	-	expression tag	UNP P69687
Z	0	HIS	-	expression tag	UNP P69687
a	-19	MET	-	expression tag	UNP P69687
a	-18	GLY	-	expression tag	UNP P69687
a	-17	SER	-	expression tag	UNP P69687
a	-16	SER	-	expression tag	UNP P69687
a	-15	HIS	-	expression tag	UNP P69687
a	-14	HIS	-	expression tag	UNP P69687
a	-13	HIS	-	expression tag	UNP P69687
a	-12	HIS	-	expression tag	UNP P69687
a	-11	HIS	-	expression tag	UNP P69687
a	-10	HIS	-	expression tag	UNP P69687
a	-9	SER	-	expression tag	UNP P69687
a	-8	SER	-	expression tag	UNP P69687
a	-7	GLY	-	expression tag	UNP P69687
a	-6	LEU	-	expression tag	UNP P69687
a	-5	VAL	-	expression tag	UNP P69687
a	-4	PRO	-	expression tag	UNP P69687
a	-3	ARG	-	expression tag	UNP P69687
a	-2	GLY	-	expression tag	UNP P69687
a	-1	SER	-	expression tag	UNP P69687
a	0	HIS	-	expression tag	UNP P69687
b	-19	MET	-	expression tag	UNP P69687
b	-18	GLY	-	expression tag	UNP P69687
b	-17	SER	-	expression tag	UNP P69687
b	-16	SER	-	expression tag	UNP P69687
b	-15	HIS	-	expression tag	UNP P69687
b	-14	HIS	-	expression tag	UNP P69687
b	-13	HIS	-	expression tag	UNP P69687
b	-12	HIS	-	expression tag	UNP P69687
b	-11	HIS	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
b	-10	HIS	-	expression tag	UNP P69687
b	-9	SER	-	expression tag	UNP P69687
b	-8	SER	-	expression tag	UNP P69687
b	-7	GLY	-	expression tag	UNP P69687
b	-6	LEU	-	expression tag	UNP P69687
b	-5	VAL	-	expression tag	UNP P69687
b	-4	PRO	-	expression tag	UNP P69687
b	-3	ARG	-	expression tag	UNP P69687
b	-2	GLY	-	expression tag	UNP P69687
b	-1	SER	-	expression tag	UNP P69687
b	0	HIS	-	expression tag	UNP P69687
c	-19	MET	-	expression tag	UNP P69687
c	-18	GLY	-	expression tag	UNP P69687
c	-17	SER	-	expression tag	UNP P69687
c	-16	SER	-	expression tag	UNP P69687
c	-15	HIS	-	expression tag	UNP P69687
c	-14	HIS	-	expression tag	UNP P69687
c	-13	HIS	-	expression tag	UNP P69687
c	-12	HIS	-	expression tag	UNP P69687
c	-11	HIS	-	expression tag	UNP P69687
c	-10	HIS	-	expression tag	UNP P69687
c	-9	SER	-	expression tag	UNP P69687
c	-8	SER	-	expression tag	UNP P69687
c	-7	GLY	-	expression tag	UNP P69687
c	-6	LEU	-	expression tag	UNP P69687
c	-5	VAL	-	expression tag	UNP P69687
c	-4	PRO	-	expression tag	UNP P69687
c	-3	ARG	-	expression tag	UNP P69687
c	-2	GLY	-	expression tag	UNP P69687
c	-1	SER	-	expression tag	UNP P69687
c	0	HIS	-	expression tag	UNP P69687
d	-19	MET	-	expression tag	UNP P69687
d	-18	GLY	-	expression tag	UNP P69687
d	-17	SER	-	expression tag	UNP P69687
d	-16	SER	-	expression tag	UNP P69687
d	-15	HIS	-	expression tag	UNP P69687
d	-14	HIS	-	expression tag	UNP P69687
d	-13	HIS	-	expression tag	UNP P69687
d	-12	HIS	-	expression tag	UNP P69687
d	-11	HIS	-	expression tag	UNP P69687
d	-10	HIS	-	expression tag	UNP P69687
d	-9	SER	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
d	-8	SER	-	expression tag	UNP P69687
d	-7	GLY	-	expression tag	UNP P69687
d	-6	LEU	-	expression tag	UNP P69687
d	-5	VAL	-	expression tag	UNP P69687
d	-4	PRO	-	expression tag	UNP P69687
d	-3	ARG	-	expression tag	UNP P69687
d	-2	GLY	-	expression tag	UNP P69687
d	-1	SER	-	expression tag	UNP P69687
d	0	HIS	-	expression tag	UNP P69687
e	-19	MET	-	expression tag	UNP P69687
e	-18	GLY	-	expression tag	UNP P69687
e	-17	SER	-	expression tag	UNP P69687
e	-16	SER	-	expression tag	UNP P69687
e	-15	HIS	-	expression tag	UNP P69687
e	-14	HIS	-	expression tag	UNP P69687
e	-13	HIS	-	expression tag	UNP P69687
e	-12	HIS	-	expression tag	UNP P69687
e	-11	HIS	-	expression tag	UNP P69687
e	-10	HIS	-	expression tag	UNP P69687
e	-9	SER	-	expression tag	UNP P69687
e	-8	SER	-	expression tag	UNP P69687
e	-7	GLY	-	expression tag	UNP P69687
e	-6	LEU	-	expression tag	UNP P69687
e	-5	VAL	-	expression tag	UNP P69687
e	-4	PRO	-	expression tag	UNP P69687
e	-3	ARG	-	expression tag	UNP P69687
e	-2	GLY	-	expression tag	UNP P69687
e	-1	SER	-	expression tag	UNP P69687
e	0	HIS	-	expression tag	UNP P69687
f	-19	MET	-	expression tag	UNP P69687
f	-18	GLY	-	expression tag	UNP P69687
f	-17	SER	-	expression tag	UNP P69687
f	-16	SER	-	expression tag	UNP P69687
f	-15	HIS	-	expression tag	UNP P69687
f	-14	HIS	-	expression tag	UNP P69687
f	-13	HIS	-	expression tag	UNP P69687
f	-12	HIS	-	expression tag	UNP P69687
f	-11	HIS	-	expression tag	UNP P69687
f	-10	HIS	-	expression tag	UNP P69687
f	-9	SER	-	expression tag	UNP P69687
f	-8	SER	-	expression tag	UNP P69687
f	-7	GLY	-	expression tag	UNP P69687

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Chain	Residue	Modelled	Actual	Comment	Reference
f	-6	LEU	-	expression tag	UNP P69687
f	-5	VAL	-	expression tag	UNP P69687
f	-4	PRO	-	expression tag	UNP P69687
f	-3	ARG	-	expression tag	UNP P69687
f	-2	GLY	-	expression tag	UNP P69687
f	-1	SER	-	expression tag	UNP P69687
f	0	HIS	-	expression tag	UNP P69687
h	-19	MET	-	expression tag	UNP P69687
h	-18	GLY	-	expression tag	UNP P69687
h	-17	SER	-	expression tag	UNP P69687
h	-16	SER	-	expression tag	UNP P69687
h	-15	HIS	-	expression tag	UNP P69687
h	-14	HIS	-	expression tag	UNP P69687
h	-13	HIS	-	expression tag	UNP P69687
h	-12	HIS	-	expression tag	UNP P69687
h	-11	HIS	-	expression tag	UNP P69687
h	-10	HIS	-	expression tag	UNP P69687
h	-9	SER	-	expression tag	UNP P69687
h	-8	SER	-	expression tag	UNP P69687
h	-7	GLY	-	expression tag	UNP P69687
h	-6	LEU	-	expression tag	UNP P69687
h	-5	VAL	-	expression tag	UNP P69687
h	-4	PRO	-	expression tag	UNP P69687
h	-3	ARG	-	expression tag	UNP P69687
h	-2	GLY	-	expression tag	UNP P69687
h	-1	SER	-	expression tag	UNP P69687
h	0	HIS	-	expression tag	UNP P69687
i	-19	MET	-	expression tag	UNP P69687
i	-18	GLY	-	expression tag	UNP P69687
i	-17	SER	-	expression tag	UNP P69687
i	-16	SER	-	expression tag	UNP P69687
i	-15	HIS	-	expression tag	UNP P69687
i	-14	HIS	-	expression tag	UNP P69687
i	-13	HIS	-	expression tag	UNP P69687
i	-12	HIS	-	expression tag	UNP P69687
i	-11	HIS	-	expression tag	UNP P69687
i	-10	HIS	-	expression tag	UNP P69687
i	-9	SER	-	expression tag	UNP P69687
i	-8	SER	-	expression tag	UNP P69687
i	-7	GLY	-	expression tag	UNP P69687
i	-6	LEU	-	expression tag	UNP P69687
i	-5	VAL	-	expression tag	UNP P69687

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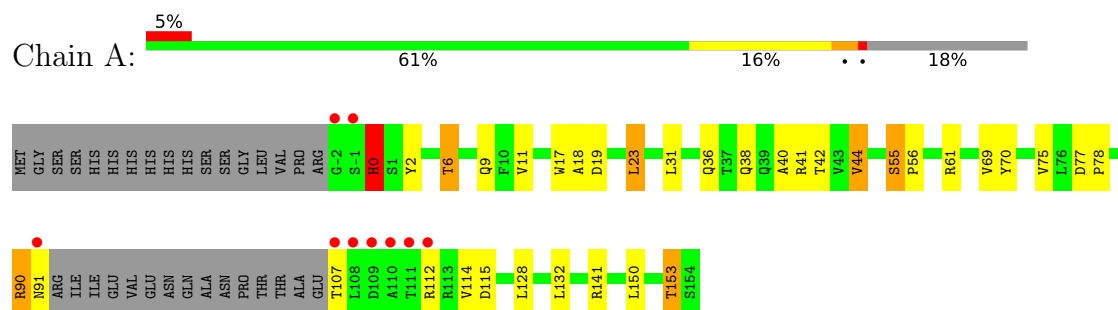
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Chain	Residue	Modelled	Actual	Comment	Reference
i	-4	PRO	-	expression tag	UNP P69687
i	-3	ARG	-	expression tag	UNP P69687
i	-2	GLY	-	expression tag	UNP P69687
i	-1	SER	-	expression tag	UNP P69687
i	0	HIS	-	expression tag	UNP P69687

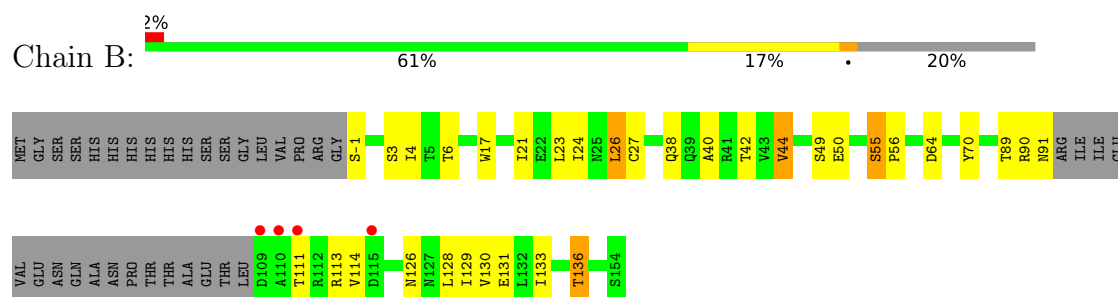
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

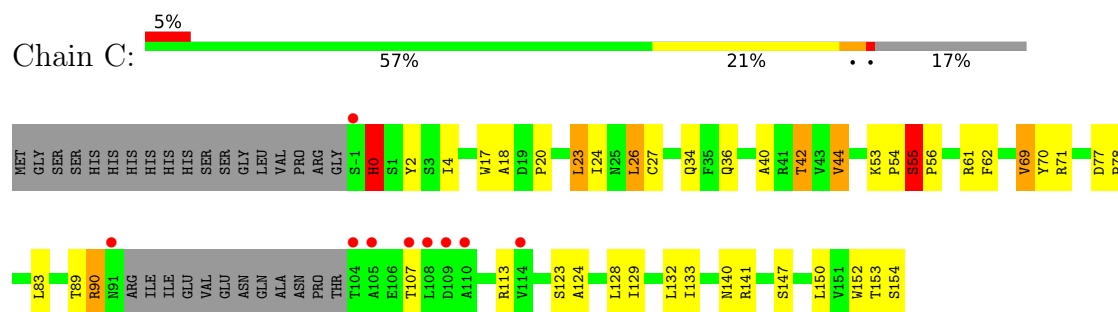
• Molecule 1: Capsid protein



• Molecule 1: Capsid protein

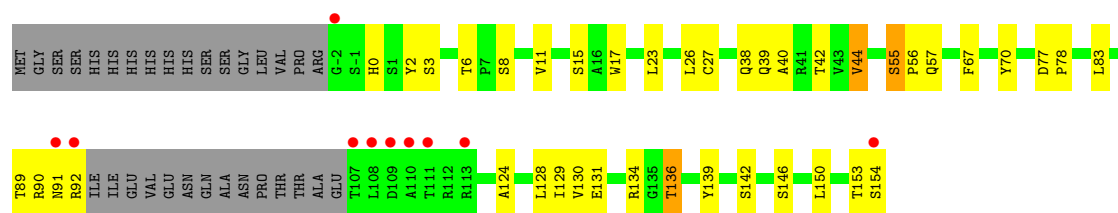


• Molecule 1: Capsid protein

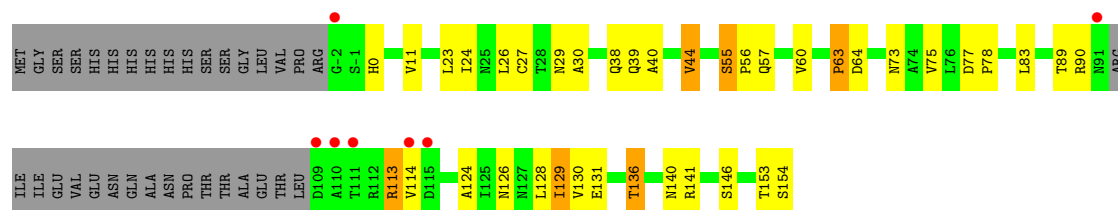


• Molecule 1: Capsid protein

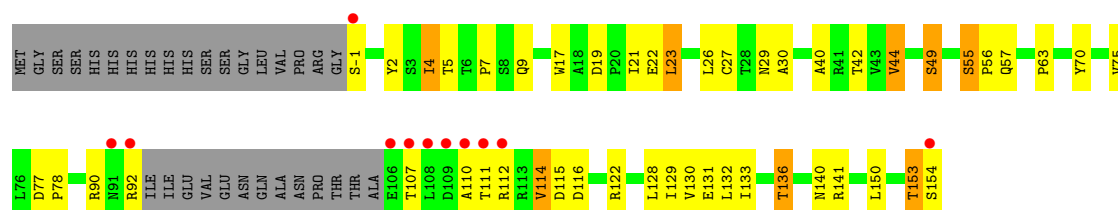




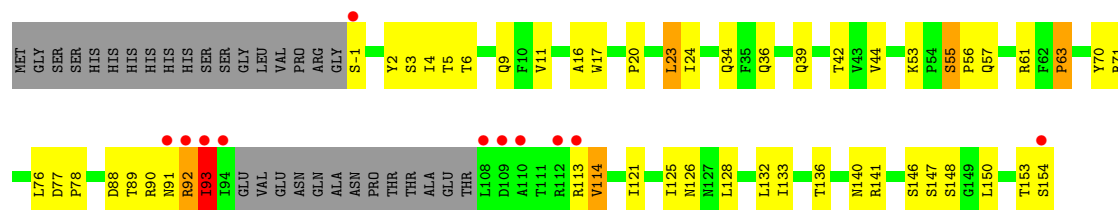
• Molecule 1: Capsid protein



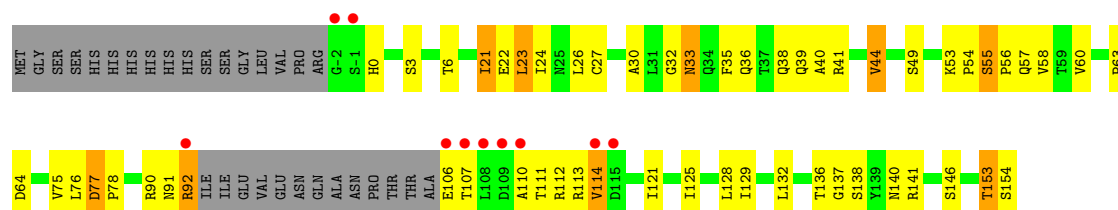
• Molecule 1: Capsid protein



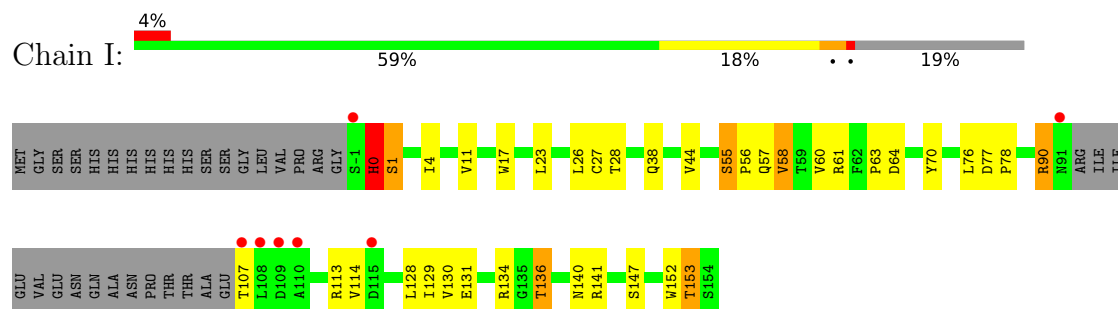
• Molecule 1: Capsid protein



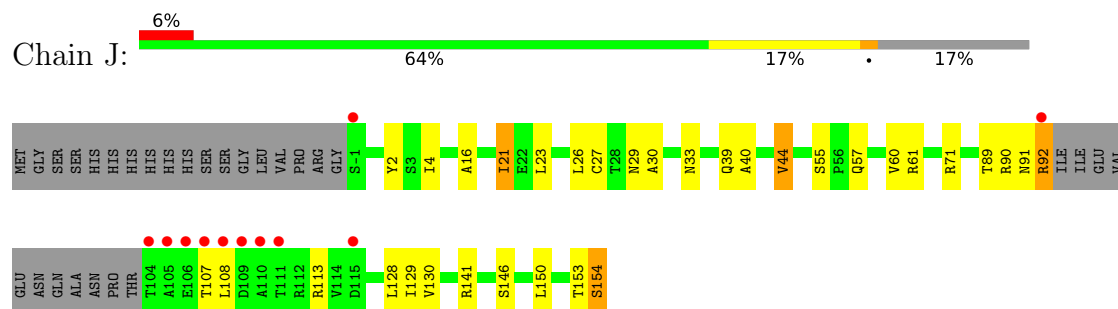
• Molecule 1: Capsid protein



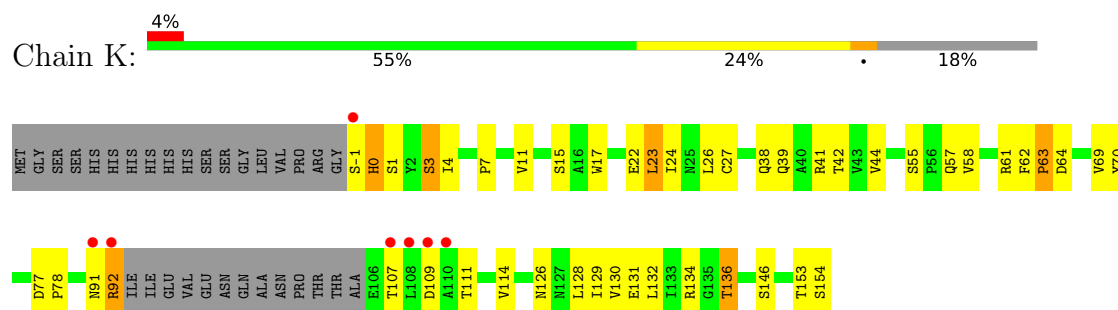
- Molecule 1: Capsid protein



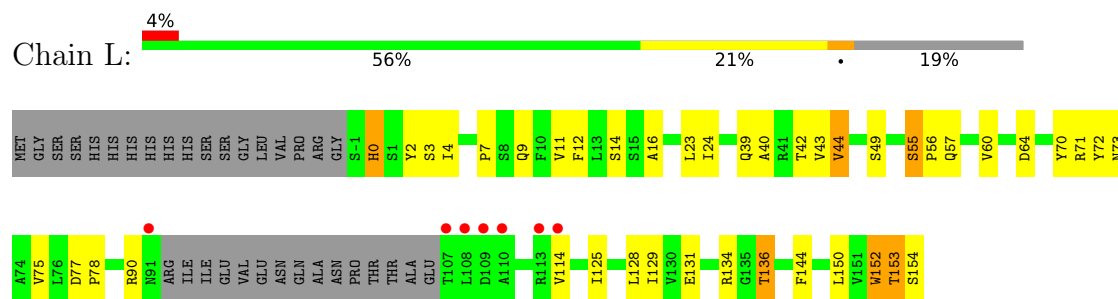
- Molecule 1: Capsid protein



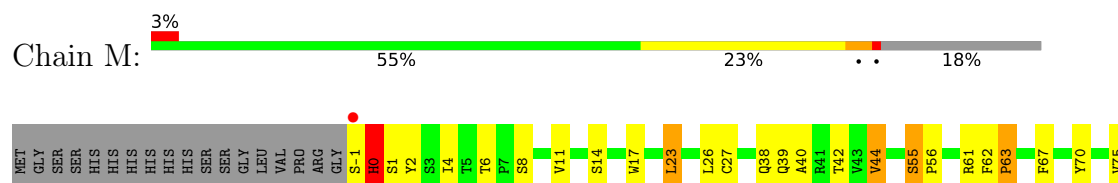
- Molecule 1: Capsid protein



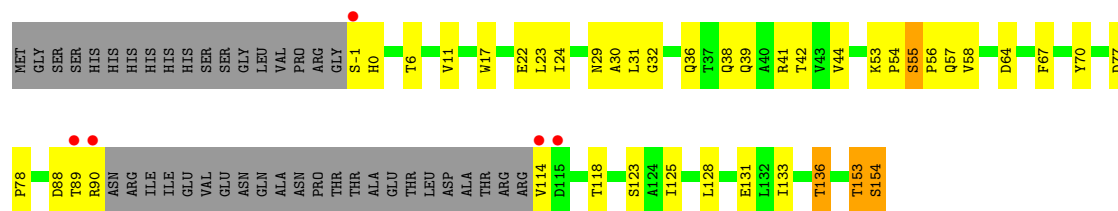
- Molecule 1: Capsid protein



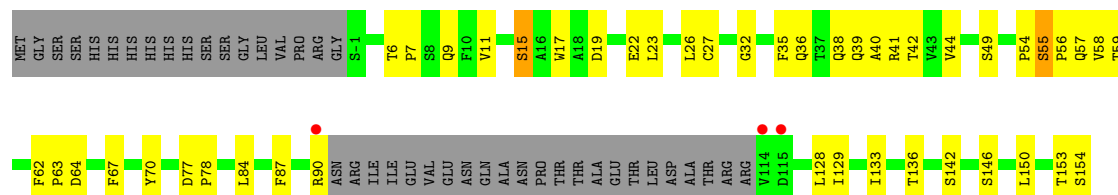
- Molecule 1: Capsid protein



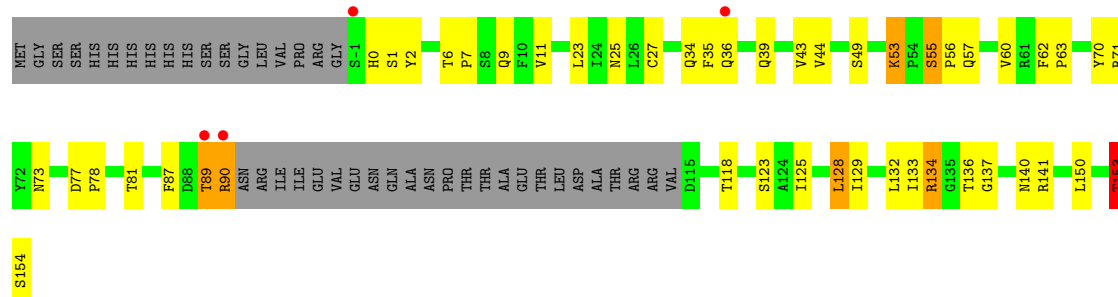




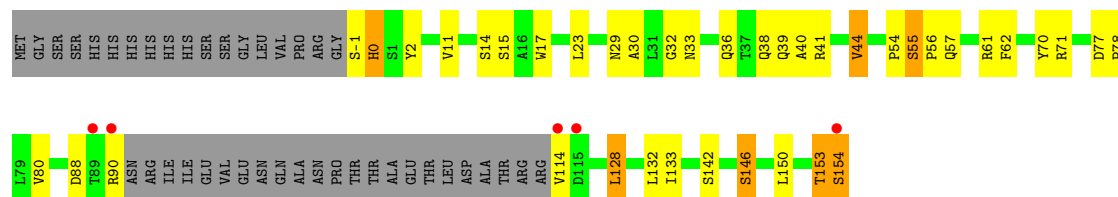
• Molecule 1: Capsid protein



• Molecule 1: Capsid protein

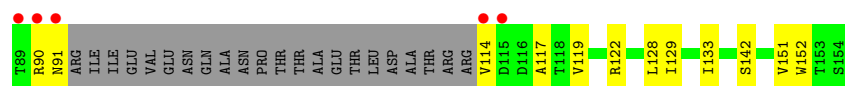


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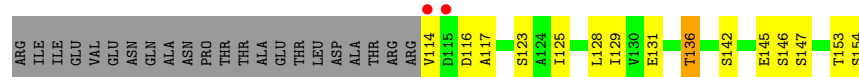


• Molecule 1: Capsid protein

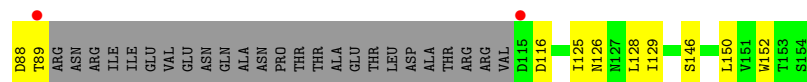
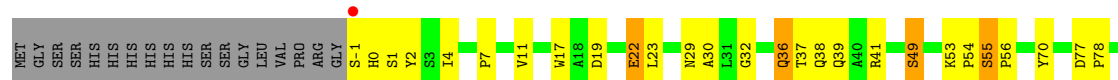




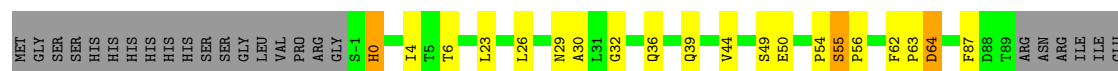
- Molecule 1: Capsid protein



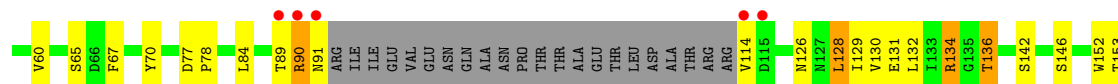
- Molecule 1: Capsid protein



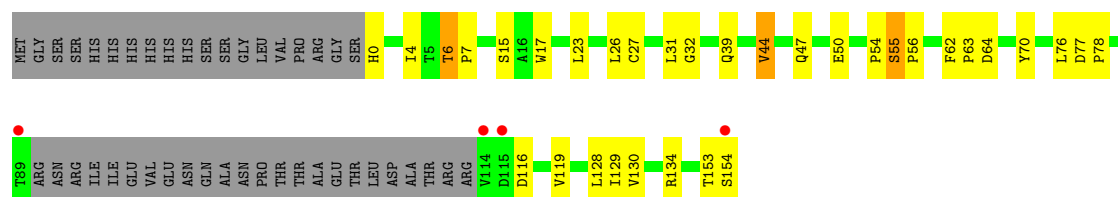
- Molecule 1: Capsid protein



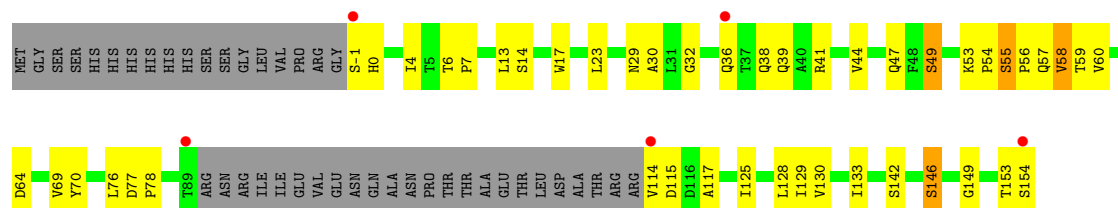
- Molecule 1: Capsid protein



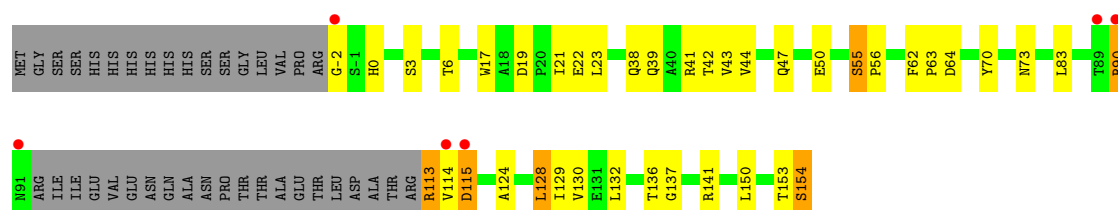
- Molecule 1: Capsid protein



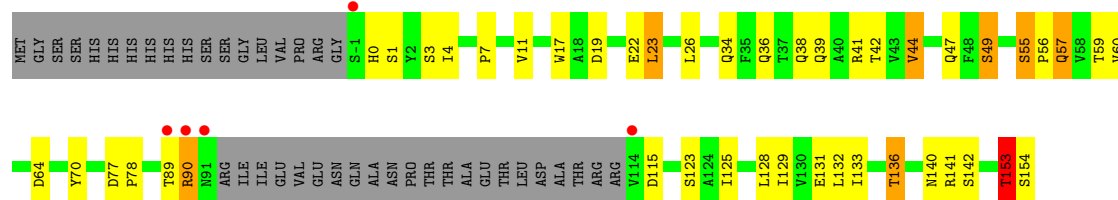
• Molecule 1: Capsid protein



• Molecule 1: Capsid protein

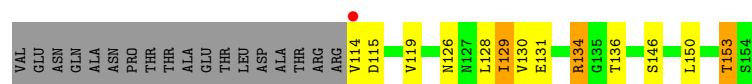


• Molecule 1: Capsid protein

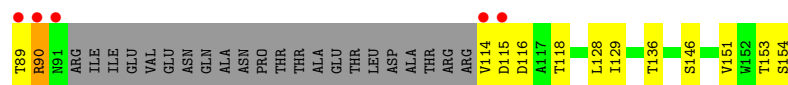


• Molecule 1: Capsid protein

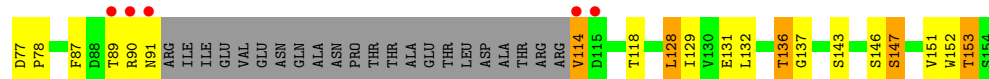




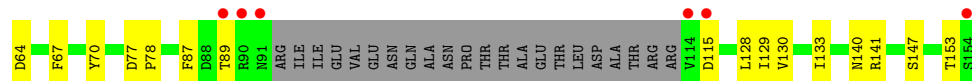
• Molecule 1: Capsid protein



• Molecule 1: Capsid protein



• Molecule 1: Capsid protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	173.07Å 221.68Å 225.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.06 50.00 – 3.06	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.00-3.06) 99.7 (50.00-3.06)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.90 (at 3.07Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.204 , 0.255 0.202 , 0.252	Depositor DCC
R_{free} test set	8201 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	51.4	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 16.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.007 for -h,l,k	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	36918	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.80	0/1138	1.02	1/1552 (0.1%)
1	B	0.76	0/1119	0.98	0/1526
1	C	0.81	0/1155	1.11	8/1576 (0.5%)
1	D	0.82	0/1149	1.06	2/1566 (0.1%)
1	E	0.79	0/1123	1.06	0/1531
1	F	0.78	0/1154	1.01	1/1573 (0.1%)
1	G	0.82	1/1154 (0.1%)	1.03	3/1573 (0.2%)
1	H	0.78	0/1158	1.00	2/1578 (0.1%)
1	I	0.74	0/1134	0.98	2/1547 (0.1%)
1	J	0.79	0/1166	1.02	2/1590 (0.1%)
1	K	0.81	0/1154	1.00	2/1573 (0.1%)
1	L	0.79	0/1134	1.09	4/1547 (0.3%)
1	M	0.79	0/1145	0.97	1/1561 (0.1%)
1	N	0.76	0/1145	1.01	2/1561 (0.1%)
1	O	0.75	0/1123	0.98	1/1531 (0.1%)
1	P	0.81	0/1181	0.96	3/1611 (0.2%)
1	Q	0.81	1/1173 (0.1%)	0.99	1/1600 (0.1%)
1	R	0.83	0/1069	1.04	0/1459
1	S	0.81	0/1069	1.00	0/1459
1	T	0.79	0/1062	1.01	2/1449 (0.1%)
1	U	0.76	0/1069	0.96	0/1459
1	V	0.83	0/1077	1.04	1/1470 (0.1%)
1	W	0.79	0/1077	1.00	1/1470 (0.1%)
1	X	0.73	0/1051	1.00	1/1435 (0.1%)
1	Y	0.82	0/1058	1.01	1/1445 (0.1%)
1	Z	0.80	0/1077	1.05	4/1470 (0.3%)
1	a	0.77	0/1052	0.97	0/1437
1	b	0.74	0/1058	1.02	1/1445 (0.1%)
1	c	0.83	0/1092	1.07	4/1489 (0.3%)
1	d	0.86	0/1077	1.06	1/1470 (0.1%)
1	e	0.81	0/1077	1.04	3/1470 (0.2%)
1	f	0.82	0/1077	1.03	1/1470 (0.1%)
1	h	0.79	0/1077	1.01	1/1470 (0.1%)
1	i	0.83	0/1077	1.03	1/1470 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.80	2/37701 (0.0%)	1.02	57/51433 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	L	0	1
1	d	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Q	103	THR	CB-OG1	6.75	1.54	1.43
1	G	93	ILE	CA-CB	5.27	1.59	1.53

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	c	90	ARG	N-CA-C	10.10	123.52	109.18
1	C	0	HIS	N-CA-C	9.40	124.22	110.59
1	Z	90	ARG	N-CA-C	9.31	123.55	109.41
1	K	0	HIS	N-CA-C	8.58	121.92	109.14
1	F	153	THR	N-CA-C	8.22	118.74	107.73
1	f	90	ARG	N-CA-C	7.65	120.70	109.69
1	L	152	TRP	CA-C-N	7.56	135.32	121.70
1	L	152	TRP	C-N-CA	7.56	135.32	121.70
1	G	93	ILE	N-CA-C	7.51	117.12	106.53
1	C	55	SER	CA-C-N	-7.40	112.29	120.14
1	C	55	SER	C-N-CA	-7.40	112.29	120.14
1	C	62	PHE	CA-C-N	7.14	128.76	119.84
1	C	62	PHE	C-N-CA	7.14	128.76	119.84
1	V	1	SER	N-CA-C	6.80	118.48	108.14
1	M	1	SER	N-CA-C	6.78	116.81	107.73
1	i	1	SER	N-CA-C	6.63	118.61	108.07
1	A	90	ARG	N-CA-C	6.28	119.42	109.50
1	L	0	HIS	N-CA-C	6.25	118.59	108.34
1	P	131	GLU	N-CA-C	6.16	118.07	111.36
1	N	1	SER	N-CA-C	6.11	116.63	108.38
1	c	19	ASP	CA-C-N	6.04	125.52	119.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	c	19	ASP	C-N-CA	6.04	125.52	119.24
1	D	55	SER	CA-C-N	-5.99	113.80	119.85
1	D	55	SER	C-N-CA	-5.99	113.80	119.85
1	G	53	LYS	CA-C-N	-5.88	113.91	120.14
1	G	53	LYS	C-N-CA	-5.88	113.91	120.14
1	I	0	HIS	N-CA-C	5.83	121.88	110.56
1	P	55	SER	CA-C-N	-5.77	114.02	120.14
1	P	55	SER	C-N-CA	-5.77	114.02	120.14
1	C	42	THR	N-CA-C	5.74	118.41	111.40
1	d	1	SER	N-CA-C	5.66	116.74	108.14
1	H	153	THR	N-CA-C	5.65	115.48	108.19
1	C	26	LEU	N-CA-C	-5.56	105.30	111.36
1	X	116	ASP	N-CA-C	-5.55	106.55	113.55
1	Y	153	THR	CB-CA-C	-5.54	109.09	117.07
1	I	90	ARG	N-CA-C	5.53	118.27	109.81
1	e	129	ILE	CB-CA-C	-5.52	104.82	111.88
1	N	153	THR	N-CA-C	5.50	117.62	108.99
1	e	53	LYS	CA-C-N	-5.49	114.32	120.14
1	e	53	LYS	C-N-CA	-5.49	114.32	120.14
1	h	90	ARG	N-CA-C	5.41	116.86	109.18
1	T	1	SER	N-CA-C	5.41	115.68	108.38
1	c	50	GLU	N-CA-C	5.39	119.12	112.54
1	Z	142	SER	N-CA-C	5.35	116.81	110.97
1	T	153	THR	N-CA-C	5.28	117.01	109.14
1	Q	33	ASN	N-CA-C	5.23	118.52	110.42
1	Z	53	LYS	CA-C-N	-5.21	115.21	120.31
1	Z	53	LYS	C-N-CA	-5.21	115.21	120.31
1	C	90	ARG	N-CA-C	5.18	117.54	109.52
1	H	114	VAL	N-CA-C	-5.16	107.69	112.43
1	J	21	ILE	CB-CA-C	-5.15	105.28	112.02
1	L	43	VAL	N-CA-C	5.12	115.55	110.23
1	b	149	GLY	N-CA-C	-5.10	108.29	114.92
1	K	69	VAL	N-CA-C	-5.07	102.31	109.21
1	W	145	GLU	N-CA-C	-5.05	105.85	111.36
1	J	29	ASN	N-CA-C	5.02	116.83	111.36
1	O	1	SER	N-CA-C	5.00	115.75	108.14

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	L	152	TRP	Peptide

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Mol	Chain	Res	Type	Group
1	d	153	THR	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1115	0	1092	21	0
1	B	1096	0	1071	16	0
1	C	1132	0	1107	27	0
1	D	1126	0	1105	17	0
1	E	1100	0	1074	26	0
1	F	1131	0	1108	27	0
1	G	1131	0	1117	31	0
1	H	1135	0	1111	31	0
1	I	1111	0	1089	20	0
1	J	1143	0	1120	20	0
1	K	1131	0	1108	30	0
1	L	1111	0	1089	25	0
1	M	1122	0	1102	29	0
1	N	1122	0	1102	33	0
1	O	1100	0	1074	23	0
1	P	1157	0	1135	29	0
1	Q	1150	0	1127	20	0
1	R	1046	0	1023	27	0
1	S	1046	0	1023	33	0
1	T	1039	0	1014	37	0
1	U	1046	0	1023	34	0
1	V	1054	0	1029	28	0
1	W	1054	0	1029	25	0
1	X	1028	0	1001	24	0
1	Y	1035	0	1010	17	0
1	Z	1054	0	1029	40	0
1	a	1029	0	1005	16	0
1	b	1035	0	1010	34	0
1	c	1069	0	1045	23	0
1	d	1054	0	1029	28	0
1	e	1054	0	1029	26	0
1	f	1054	0	1029	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	h	1054	0	1029	32	0
1	i	1054	0	1029	29	0
All	All	36918	0	36117	772	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 11.

All (772) 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:Q:27:CYS:HB3	1:Q:129:ILE:HD11	1.27	1.15
1:E:27:CYS:HB3	1:E:129:ILE:HD11	1.19	1.14
1:H:27:CYS:HB3	1:H:129:ILE:HD11	1.31	1.12
1:e:0:HIS:HB3	1:e:153:THR:O	1.48	1.11
1:T:36:GLN:HB2	1:U:90:ARG:HD2	1.32	1.09
1:T:134:ARG:HG2	1:T:134:ARG:HH11	1.18	1.08
1:K:0:HIS:HB3	1:K:154:SER:HA	1.28	1.08
1:K:0:HIS:CB	1:K:154:SER:HA	1.89	1.03
1:h:55:SER:HB3	1:h:56:PRO:HD3	1.43	0.99
1:I:27:CYS:HB3	1:I:129:ILE:HD11	1.43	0.97
1:N:27:CYS:HB3	1:N:129:ILE:HD11	1.47	0.96
1:L:131:GLU:OE1	1:L:136:THR:HG21	1.65	0.96
1:Q:77:ASP:HB3	1:Q:78:PRO:HD3	1.49	0.95
1:R:36:GLN:HE21	1:T:89:THR:HA	1.29	0.94
1:N:57:GLN:HE22	1:P:57:GLN:HE22	1.12	0.93
1:Y:0:HIS:HB3	1:Y:153:THR:O	1.69	0.93
1:E:27:CYS:HB3	1:E:129:ILE:CD1	1.99	0.93
1:S:90:ARG:HD3	1:Z:36:GLN:HB2	1.49	0.92
1:E:27:CYS:CB	1:E:129:ILE:HD11	2.00	0.92
1:S:38:GLN:HE22	1:S:90:ARG:HG2	1.32	0.92
1:H:57:GLN:HE22	1:O:57:GLN:HE22	1.17	0.91
1:V:49:SER:OG	1:Y:32:GLY:HA3	1.70	0.91
1:e:55:SER:HB3	1:e:56:PRO:HD3	1.51	0.90
1:c:55:SER:HB3	1:c:56:PRO:HD3	1.52	0.89
1:i:55:SER:HB3	1:i:56:PRO:HD3	1.56	0.88
1:U:-1:SER:O	1:U:0:HIS:HB2	1.71	0.88
1:G:57:GLN:HE22	1:L:57:GLN:HE22	1.22	0.88
1:b:55:SER:HB3	1:b:56:PRO:CD	2.03	0.87
1:D:27:CYS:HB3	1:D:129:ILE:HD11	1.56	0.87
1:a:55:SER:HB3	1:a:56:PRO:HD3	1.57	0.87
1:X:32:GLY:HA3	1:Y:49:SER:OG	1.74	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:36:GLN:OE1	1:X:36:GLN:HA	1.72	0.87
1:Z:55:SER:HB3	1:Z:56:PRO:CD	2.05	0.86
1:d:90:ARG:HH11	1:i:36:GLN:CB	1.87	0.86
1:V:36:GLN:HA	1:V:36:GLN:NE2	1.89	0.85
1:F:27:CYS:HB3	1:F:129:ILE:HD11	1.58	0.84
1:h:55:SER:HB3	1:h:56:PRO:CD	2.05	0.84
1:V:36:GLN:HA	1:V:36:GLN:HE21	1.42	0.84
1:T:55:SER:HB3	1:T:56:PRO:HD3	1.59	0.84
1:a:55:SER:HB3	1:a:56:PRO:CD	2.08	0.84
1:D:57:GLN:HE22	1:E:57:GLN:HE22	1.22	0.84
1:Q:55:SER:HB3	1:Q:56:PRO:CD	2.07	0.83
1:B:55:SER:HB3	1:B:56:PRO:CD	2.09	0.83
1:N:91:ASN:O	1:N:92:ARG:NH1	2.12	0.83
1:f:55:SER:HB3	1:f:56:PRO:HD3	1.60	0.82
1:E:38:GLN:HE22	1:E:90:ARG:HA	1.43	0.82
1:U:36:GLN:HE21	1:e:89:THR:HA	1.44	0.81
1:Y:55:SER:HB3	1:Y:56:PRO:CD	2.10	0.81
1:c:90:ARG:HD2	1:h:36:GLN:HB2	1.62	0.81
1:C:27:CYS:HB3	1:C:129:ILE:HD11	1.63	0.81
1:J:153:THR:HG22	1:J:154:SER:H	1.46	0.81
1:W:55:SER:HB3	1:W:56:PRO:HD3	1.62	0.81
1:F:57:GLN:HE22	1:J:57:GLN:HE22	1.26	0.81
1:J:90:ARG:H	1:J:113:ARG:HH22	1.29	0.80
1:e:55:SER:HB3	1:e:56:PRO:CD	2.09	0.80
1:V:55:SER:HB3	1:V:56:PRO:CD	2.11	0.80
1:I:77:ASP:HB3	1:I:78:PRO:HD3	1.63	0.79
1:O:55:SER:HB3	1:O:56:PRO:CD	2.12	0.79
1:F:77:ASP:HB3	1:F:78:PRO:HD3	1.63	0.79
1:X:77:ASP:HB3	1:X:78:PRO:HD3	1.65	0.78
1:U:55:SER:HB3	1:U:56:PRO:HD3	1.64	0.78
1:S:142:SER:O	1:S:146:SER:HB2	1.84	0.78
1:D:77:ASP:HB3	1:D:78:PRO:HD3	1.66	0.77
1:b:55:SER:HB3	1:b:56:PRO:HD3	1.66	0.76
1:c:90:ARG:CD	1:h:36:GLN:HB2	2.14	0.76
1:F:75:VAL:HG22	1:Z:54:PRO:HD2	1.68	0.76
1:C:36:GLN:HB2	1:E:90:ARG:HG3	1.67	0.76
1:I:57:GLN:HE22	1:K:57:GLN:HE22	1.34	0.75
1:U:36:GLN:HA	1:U:36:GLN:OE1	1.84	0.75
1:E:77:ASP:HB3	1:E:78:PRO:HD3	1.67	0.75
1:H:77:ASP:HB3	1:H:78:PRO:HD3	1.69	0.75
1:R:32:GLY:HA3	1:T:49:SER:OG	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:134:ARG:HH11	1:Z:134:ARG:HG2	1.50	0.75
1:Z:55:SER:HB3	1:Z:56:PRO:HD3	1.68	0.74
1:d:90:ARG:HH11	1:i:36:GLN:HB3	1.51	0.74
1:A:40:ALA:O	1:A:44:VAL:HG13	1.87	0.74
1:U:36:GLN:HG3	1:e:90:ARG:HG3	1.70	0.73
1:T:77:ASP:HB3	1:T:78:PRO:HD3	1.70	0.73
1:R:38:GLN:NE2	1:R:41:ARG:HH21	1.86	0.73
1:c:55:SER:HB3	1:c:56:PRO:CD	2.18	0.73
1:Z:77:ASP:HB3	1:Z:78:PRO:HD3	1.70	0.73
1:G:77:ASP:HB3	1:G:78:PRO:HD3	1.69	0.73
1:S:38:GLN:NE2	1:S:90:ARG:HG2	2.04	0.72
1:Q:153:THR:HG22	1:Q:154:SER:H	1.53	0.72
1:R:36:GLN:NE2	1:T:89:THR:HA	2.03	0.72
1:K:131:GLU:OE1	1:K:136:THR:HG21	1.90	0.72
1:V:55:SER:HB3	1:V:56:PRO:HD3	1.72	0.72
1:A:55:SER:HB3	1:A:56:PRO:CD	2.18	0.72
1:S:55:SER:HB3	1:S:56:PRO:CD	2.19	0.72
1:L:90:ARG:HG3	1:P:36:GLN:CB	2.20	0.72
1:V:36:GLN:HG3	1:f:90:ARG:HG3	1.72	0.72
1:T:36:GLN:HB2	1:U:90:ARG:CD	2.17	0.71
1:T:55:SER:HB3	1:T:56:PRO:CD	2.20	0.71
1:T:134:ARG:HG2	1:T:134:ARG:NH1	1.97	0.71
1:Z:153:THR:HG23	1:Z:154:SER:H	1.56	0.71
1:Q:55:SER:HB3	1:Q:56:PRO:HD3	1.72	0.71
1:Z:134:ARG:HG2	1:Z:134:ARG:NH1	2.04	0.71
1:R:67:PHE:CE2	1:T:7:PRO:HG3	2.26	0.71
1:S:90:ARG:HG3	1:Z:36:GLN:HG3	1.73	0.71
1:d:90:ARG:HH11	1:i:36:GLN:HB2	1.54	0.71
1:G:23:LEU:HD13	1:G:132:LEU:HD11	1.71	0.71
1:P:126:ASN:O	1:P:130:VAL:HG23	1.90	0.70
1:c:38:GLN:NE2	1:c:41:ARG:HH21	1.88	0.70
1:f:55:SER:HB3	1:f:56:PRO:CD	2.20	0.70
1:T:134:ARG:HH11	1:T:134:ARG:CG	2.02	0.70
1:Y:55:SER:HB3	1:Y:56:PRO:HD3	1.73	0.70
1:P:113:ARG:HH11	1:P:113:ARG:HB3	1.56	0.70
1:C:23:LEU:HD13	1:C:132:LEU:HD11	1.75	0.69
1:V:114:VAL:HA	1:V:117:ALA:HB3	1.73	0.69
1:d:38:GLN:NE2	1:d:41:ARG:HH21	1.91	0.69
1:J:153:THR:HG22	1:J:154:SER:N	2.06	0.69
1:d:55:SER:HB3	1:d:56:PRO:HD3	1.74	0.69
1:V:133:ILE:HA	1:f:11:VAL:HG21	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:h:38:GLN:NE2	1:h:41:ARG:HH21	1.90	0.69
1:C:36:GLN:CB	1:E:90:ARG:HG3	2.23	0.69
1:X:55:SER:HB3	1:X:56:PRO:CD	2.23	0.69
1:H:55:SER:HB3	1:H:56:PRO:CD	2.22	0.68
1:M:38:GLN:HE22	1:M:90:ARG:HA	1.58	0.68
1:d:17:TRP:CZ3	1:d:70:TYR:HB2	2.28	0.68
1:M:38:GLN:NE2	1:M:90:ARG:HA	2.09	0.68
1:S:35:PHE:CE1	1:S:44:VAL:HG21	2.29	0.68
1:M:27:CYS:HB3	1:M:129:ILE:HD11	1.76	0.68
1:C:83:LEU:HA	1:C:124:ALA:HB1	1.75	0.68
1:H:27:CYS:CB	1:H:129:ILE:HD11	2.18	0.67
1:R:55:SER:HB3	1:R:56:PRO:HD3	1.76	0.67
1:L:57:GLN:HB2	1:L:60:VAL:HB	1.75	0.67
1:V:17:TRP:CZ3	1:V:70:TYR:HB2	2.29	0.67
1:O:17:TRP:CZ3	1:O:70:TYR:HB2	2.30	0.67
1:R:55:SER:HB3	1:R:56:PRO:CD	2.25	0.67
1:A:23:LEU:HD13	1:A:132:LEU:HD11	1.74	0.67
1:A:0:HIS:HD2	1:A:153:THR:O	1.77	0.67
1:S:27:CYS:HB3	1:S:129:ILE:HD11	1.77	0.67
1:d:131:GLU:OE1	1:d:136:THR:HG21	1.94	0.67
1:D:40:ALA:O	1:D:44:VAL:HG13	1.94	0.66
1:P:55:SER:HB3	1:P:56:PRO:HD3	1.76	0.66
1:A:36:GLN:CB	1:C:90:ARG:HG3	2.26	0.66
1:A:55:SER:HB3	1:A:56:PRO:HD3	1.76	0.66
1:R:36:GLN:HB3	1:T:90:ARG:HG3	1.77	0.66
1:K:0:HIS:HB2	1:K:153:THR:O	1.96	0.66
1:O:27:CYS:HB3	1:O:129:ILE:HD11	1.77	0.66
1:a:77:ASP:HB3	1:a:78:PRO:HD3	1.78	0.66
1:d:90:ARG:NH1	1:i:36:GLN:HB2	2.10	0.66
1:P:57:GLN:HB2	1:P:60:VAL:HB	1.76	0.66
1:J:153:THR:CG2	1:J:154:SER:H	2.10	0.65
1:b:13:LEU:HD22	1:b:57:GLN:O	1.96	0.65
1:M:90:ARG:HG3	1:N:36:GLN:HB2	1.78	0.65
1:K:134:ARG:HB2	1:K:136:THR:HG22	1.77	0.65
1:S:35:PHE:HE1	1:S:44:VAL:HG21	1.61	0.65
1:Z:26:LEU:HD21	1:Z:47:GLN:HB3	1.77	0.65
1:X:55:SER:HB3	1:X:56:PRO:HD3	1.79	0.65
1:a:44:VAL:HA	1:a:47:GLN:HG3	1.79	0.65
1:B:55:SER:HB3	1:B:56:PRO:HD3	1.77	0.65
1:P:75:VAL:HG22	1:e:54:PRO:HD2	1.77	0.65
1:J:91:ASN:O	1:J:92:ARG:HD2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:e:0:HIS:HB3	1:e:153:THR:C	2.22	0.64
1:F:55:SER:HB3	1:F:56:PRO:HD3	1.79	0.64
1:O:55:SER:HB3	1:O:56:PRO:HD2	1.79	0.64
1:W:153:THR:HG22	1:W:154:SER:N	2.12	0.64
1:Q:77:ASP:HB3	1:Q:78:PRO:CD	2.27	0.64
1:J:40:ALA:O	1:J:44:VAL:HG13	1.97	0.64
1:K:91:ASN:HD22	1:K:114:VAL:HG21	1.63	0.63
1:P:113:ARG:HB3	1:P:113:ARG:NH1	2.14	0.63
1:T:27:CYS:HB3	1:T:129:ILE:HD11	1.81	0.63
1:W:77:ASP:HB3	1:W:78:PRO:CD	2.28	0.63
1:d:44:VAL:HA	1:d:47:GLN:HG3	1.79	0.63
1:P:55:SER:HB3	1:P:56:PRO:CD	2.28	0.63
1:F:55:SER:HB3	1:F:56:PRO:CD	2.29	0.63
1:G:55:SER:HB3	1:G:56:PRO:CD	2.28	0.63
1:O:21:ILE:HG22	1:O:25:ASN:ND2	2.14	0.63
1:S:67:PHE:CE2	1:X:7:PRO:HG3	2.34	0.63
1:N:55:SER:HB3	1:N:56:PRO:CD	2.28	0.63
1:Z:55:SER:CB	1:Z:56:PRO:CD	2.77	0.63
1:Z:0:HIS:ND1	1:Z:153:THR:O	2.33	0.62
1:P:109:ASP:O	1:P:113:ARG:HB2	1.99	0.62
1:Z:49:SER:OG	1:b:32:GLY:HA3	1.99	0.62
1:b:57:GLN:HB2	1:b:60:VAL:HB	1.79	0.62
1:e:91:ASN:ND2	1:e:114:VAL:HG21	2.15	0.62
1:f:0:HIS:CD2	1:f:154:SER:HA	2.35	0.62
1:f:27:CYS:HB3	1:f:129:ILE:HD11	1.82	0.61
1:i:55:SER:CB	1:i:56:PRO:HD3	2.29	0.61
1:U:32:GLY:HA3	1:e:49:SER:HB2	1.80	0.61
1:e:32:GLY:HA3	1:h:49:SER:OG	2.00	0.61
1:X:126:ASN:HD22	1:X:129:ILE:HD12	1.66	0.61
1:b:77:ASP:HB3	1:b:78:PRO:HD3	1.82	0.61
1:e:77:ASP:HB3	1:e:78:PRO:HD3	1.83	0.61
1:Y:64:ASP:HA	1:Y:141:ARG:NH2	2.16	0.61
1:d:49:SER:OG	1:i:32:GLY:HA3	2.00	0.61
1:C:77:ASP:HB3	1:C:78:PRO:HD3	1.82	0.61
1:K:7:PRO:HG3	1:M:67:PHE:CE2	2.36	0.61
1:K:131:GLU:O	1:K:136:THR:HG23	2.01	0.61
1:C:34:GLN:HE21	1:E:90:ARG:NH1	1.99	0.61
1:Z:153:THR:HG23	1:Z:154:SER:N	2.15	0.61
1:C:153:THR:HG22	1:C:154:SER:N	2.16	0.60
1:V:27:CYS:HB3	1:V:129:ILE:HD11	1.83	0.60
1:b:55:SER:CB	1:b:56:PRO:CD	2.78	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Z:131:GLU:OE1	1:Z:136:THR:HG21	2.01	0.60
1:H:57:GLN:HB2	1:H:60:VAL:HB	1.83	0.60
1:G:133:ILE:HA	1:N:11:VAL:HG21	1.83	0.60
1:L:90:ARG:HG3	1:P:36:GLN:HB3	1.83	0.60
1:M:-1:SER:O	1:M:0:HIS:HB2	2.00	0.60
1:O:40:ALA:O	1:O:44:VAL:HG13	2.01	0.60
1:f:77:ASP:HB3	1:f:78:PRO:HD3	1.83	0.60
1:F:40:ALA:O	1:F:44:VAL:HG13	2.02	0.60
1:S:55:SER:HB3	1:S:56:PRO:HD3	1.82	0.60
1:W:36:GLN:HA	1:W:36:GLN:OE1	2.02	0.60
1:R:90:ARG:HG3	1:d:36:GLN:HB3	1.84	0.60
1:A:36:GLN:HB3	1:C:90:ARG:HG3	1.84	0.59
1:U:36:GLN:HB3	1:e:90:ARG:HD2	1.82	0.59
1:O:55:SER:CB	1:O:56:PRO:CD	2.79	0.59
1:S:90:ARG:CD	1:Z:36:GLN:HB2	2.29	0.59
1:J:16:ALA:HB1	1:J:71:ARG:HB3	1.84	0.59
1:W:77:ASP:HB3	1:W:78:PRO:HD3	1.84	0.59
1:A:0:HIS:HD2	1:A:153:THR:C	2.11	0.59
1:Z:17:TRP:CZ3	1:Z:70:TYR:HB2	2.37	0.59
1:d:77:ASP:HB3	1:d:78:PRO:HD3	1.85	0.59
1:M:151:VAL:HG12	1:M:153:THR:HG23	1.85	0.59
1:V:90:ARG:HG3	1:Y:36:GLN:HB3	1.85	0.59
1:C:40:ALA:O	1:C:44:VAL:HG13	2.03	0.59
1:F:4:ILE:HD12	1:F:4:ILE:H	1.67	0.59
1:K:27:CYS:HB3	1:K:129:ILE:HD11	1.84	0.58
1:c:0:HIS:HA	1:c:153:THR:O	2.02	0.58
1:G:6:THR:O	1:G:9:GLN:HG3	2.04	0.58
1:M:17:TRP:CZ3	1:M:70:TYR:HB2	2.39	0.58
1:C:24:ILE:HG12	1:E:11:VAL:HG13	1.85	0.58
1:G:17:TRP:CZ3	1:G:70:TYR:HB2	2.39	0.58
1:K:91:ASN:ND2	1:K:114:VAL:HG21	2.18	0.58
1:W:142:SER:O	1:W:146:SER:HB2	2.03	0.58
1:K:17:TRP:CZ3	1:K:70:TYR:HB2	2.39	0.58
1:M:55:SER:HB3	1:M:56:PRO:CD	2.33	0.58
1:V:36:GLN:HE21	1:V:36:GLN:CA	2.16	0.58
1:c:113:ARG:C	1:c:115:ASP:H	2.12	0.58
1:b:29:ASN:O	1:b:30:ALA:C	2.46	0.58
1:b:153:THR:HG23	1:b:154:SER:N	2.18	0.58
1:H:75:VAL:HG22	1:b:54:PRO:HD2	1.85	0.58
1:I:0:HIS:HD2	1:K:-1:SER:HB3	1.68	0.58
1:T:133:ILE:HA	1:U:11:VAL:HG21	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:17:TRP:CZ3	1:I:70:TYR:HB2	2.39	0.57
1:d:131:GLU:O	1:d:136:THR:HG23	2.04	0.57
1:h:131:GLU:OE1	1:h:136:THR:HG21	2.04	0.57
1:Z:134:ARG:HH11	1:Z:134:ARG:CG	2.16	0.57
1:Y:29:ASN:O	1:Y:30:ALA:C	2.48	0.57
1:b:55:SER:HB3	1:b:56:PRO:HD2	1.86	0.57
1:e:131:GLU:HA	1:e:134:ARG:HG3	1.87	0.57
1:F:27:CYS:CB	1:F:129:ILE:HD11	2.33	0.57
1:L:77:ASP:HB3	1:L:78:PRO:HD3	1.85	0.57
1:M:90:ARG:HG3	1:N:36:GLN:CB	2.34	0.57
1:O:55:SER:HB3	1:O:56:PRO:HD3	1.86	0.57
1:X:17:TRP:CZ3	1:X:70:TYR:HB2	2.39	0.57
1:P:38:GLN:NE2	1:P:41:ARG:HH21	2.03	0.57
1:T:153:THR:HG22	1:T:154:SER:H	1.70	0.56
1:B:131:GLU:OE1	1:B:136:THR:HG21	2.05	0.56
1:M:23:LEU:HD13	1:M:132:LEU:HD11	1.87	0.56
1:T:57:GLN:HB2	1:T:60:VAL:HB	1.87	0.56
1:G:55:SER:HB3	1:G:56:PRO:HD3	1.87	0.56
1:H:23:LEU:HD13	1:H:132:LEU:HD11	1.87	0.56
1:Q:153:THR:HG22	1:Q:154:SER:N	2.20	0.56
1:R:53:LYS:HB3	1:R:54:PRO:HD2	1.87	0.56
1:C:20:PRO:O	1:C:24:ILE:HG22	2.04	0.56
1:E:55:SER:HB3	1:E:56:PRO:CD	2.35	0.56
1:O:16:ALA:HB1	1:O:71:ARG:HB3	1.87	0.56
1:c:90:ARG:CD	1:h:36:GLN:CB	2.84	0.56
1:i:55:SER:HB3	1:i:56:PRO:CD	2.31	0.56
1:T:34:GLN:HA	1:U:88:ASP:OD1	2.06	0.56
1:G:90:ARG:HD3	1:G:93:ILE:CG2	2.36	0.56
1:P:153:THR:HG22	1:P:154:SER:N	2.20	0.56
1:P:91:ASN:ND2	1:P:114:VAL:HG21	2.21	0.56
1:Z:55:SER:HB3	1:Z:56:PRO:HD2	1.87	0.56
1:f:38:GLN:NE2	1:f:41:ARG:HH21	2.04	0.56
1:D:134:ARG:HB2	1:D:136:THR:CG2	2.36	0.55
1:V:90:ARG:HG3	1:Y:36:GLN:CB	2.35	0.55
1:D:153:THR:HG22	1:D:154:SER:N	2.20	0.55
1:E:57:GLN:HB2	1:E:60:VAL:HB	1.89	0.55
1:H:57:GLN:NE2	1:O:57:GLN:HE22	1.97	0.55
1:Q:53:LYS:HB3	1:Q:54:PRO:HD2	1.89	0.55
1:Y:55:SER:CB	1:Y:56:PRO:CD	2.83	0.55
1:K:126:ASN:O	1:K:130:VAL:HG23	2.07	0.55
1:L:40:ALA:O	1:L:44:VAL:HG13	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:77:ASP:HB3	1:M:78:PRO:HD3	1.88	0.55
1:O:2:TYR:HB3	1:O:150:LEU:HD22	1.89	0.55
1:a:153:THR:HG22	1:a:154:SER:N	2.21	0.55
1:b:38:GLN:HA	1:b:41:ARG:NH2	2.21	0.55
1:K:0:HIS:HB2	1:K:154:SER:HA	1.82	0.55
1:L:131:GLU:O	1:L:136:THR:HG23	2.06	0.55
1:F:49:SER:OG	1:H:32:GLY:HA3	2.07	0.55
1:V:20:PRO:O	1:V:24:ILE:HG22	2.06	0.55
1:B:17:TRP:CZ3	1:B:70:TYR:HB2	2.42	0.55
1:U:40:ALA:O	1:U:44:VAL:HG13	2.07	0.55
1:W:114:VAL:HG12	1:W:114:VAL:O	2.07	0.55
1:K:1:SER:HB2	1:K:58:VAL:O	2.06	0.54
1:R:90:ARG:HG3	1:d:36:GLN:CB	2.37	0.54
1:T:128:LEU:HD13	1:T:132:LEU:HD11	1.88	0.54
1:G:36:GLN:OE1	1:N:89:THR:HA	2.07	0.54
1:F:17:TRP:CZ3	1:F:70:TYR:HB2	2.42	0.54
1:S:77:ASP:HB3	1:S:78:PRO:HD3	1.89	0.54
1:B:40:ALA:O	1:B:44:VAL:HG13	2.07	0.54
1:f:29:ASN:O	1:f:30:ALA:C	2.50	0.54
1:D:11:VAL:HG22	1:K:24:ILE:HG12	1.90	0.54
1:E:38:GLN:NE2	1:E:90:ARG:HA	2.17	0.54
1:b:153:THR:HG23	1:b:154:SER:H	1.73	0.54
1:A:6:THR:O	1:A:9:GLN:HG3	2.08	0.54
1:S:7:PRO:HG3	1:Z:67:PHE:CE2	2.43	0.54
1:E:153:THR:HG22	1:E:154:SER:N	2.23	0.53
1:G:34:GLN:HE21	1:N:90:ARG:NH1	2.06	0.53
1:H:121:ILE:O	1:H:125:ILE:HG13	2.07	0.53
1:h:41:ARG:HH12	1:h:114:VAL:HG22	1.73	0.53
1:W:29:ASN:O	1:W:30:ALA:C	2.51	0.53
1:Q:55:SER:HB3	1:Q:56:PRO:HD2	1.88	0.53
1:B:38:GLN:NE2	1:B:90:ARG:HG2	2.24	0.53
1:G:23:LEU:HD13	1:G:132:LEU:CD1	2.39	0.53
1:b:17:TRP:CZ3	1:b:70:TYR:HB2	2.44	0.53
1:L:90:ARG:HG3	1:P:36:GLN:HB2	1.89	0.53
1:F:133:ILE:HA	1:G:11:VAL:HG21	1.91	0.53
1:M:134:ARG:HB2	1:M:136:THR:HG23	1.91	0.53
1:H:55:SER:HB3	1:H:56:PRO:HD3	1.91	0.53
1:J:153:THR:CG2	1:J:154:SER:N	2.71	0.53
1:P:-1:SER:O	1:P:0:HIS:HB2	2.09	0.53
1:B:27:CYS:HB3	1:B:129:ILE:HD11	1.90	0.53
1:V:55:SER:CB	1:V:56:PRO:CD	2.85	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:153:THR:CG2	1:W:154:SER:N	2.72	0.52
1:U:153:THR:HG22	1:U:154:SER:H	1.75	0.52
1:I:27:CYS:O	1:I:28:THR:C	2.52	0.52
1:E:75:VAL:HG22	1:R:54:PRO:HG2	1.92	0.52
1:H:40:ALA:O	1:H:44:VAL:HG13	2.09	0.52
1:S:133:ILE:HA	1:X:11:VAL:HG21	1.90	0.52
1:U:38:GLN:HE21	1:U:41:ARG:HH21	1.56	0.52
1:K:92:ARG:HA	1:K:92:ARG:HH11	1.73	0.52
1:N:40:ALA:O	1:N:44:VAL:HG13	2.09	0.52
1:C:55:SER:HB3	1:C:56:PRO:CD	2.39	0.52
1:a:17:TRP:CZ3	1:a:70:TYR:HB2	2.43	0.52
1:Z:90:ARG:HD2	1:b:36:GLN:HB3	1.91	0.52
1:a:4:ILE:N	1:a:4:ILE:HD12	2.25	0.52
1:c:83:LEU:HA	1:c:124:ALA:HB1	1.91	0.52
1:e:126:ASN:O	1:e:130:VAL:HG23	2.08	0.52
1:H:53:LYS:HB3	1:H:54:PRO:HD2	1.91	0.52
1:U:77:ASP:HB3	1:U:78:PRO:HD3	1.91	0.52
1:b:6:THR:HB	1:b:7:PRO:HD2	1.91	0.52
1:A:38:GLN:NE2	1:A:41:ARG:HH21	2.08	0.52
1:L:125:ILE:O	1:L:129:ILE:HG13	2.09	0.52
1:N:55:SER:HB3	1:N:56:PRO:HD3	1.91	0.52
1:b:30:ALA:HB1	1:b:125:ILE:HD13	1.91	0.51
1:d:7:PRO:HG3	1:i:67:PHE:CE2	2.44	0.51
1:F:23:LEU:HD13	1:F:132:LEU:HD11	1.92	0.51
1:L:55:SER:HB3	1:L:56:PRO:CD	2.40	0.51
1:P:0:HIS:HA	1:P:153:THR:O	2.11	0.51
1:C:23:LEU:HD13	1:C:132:LEU:CD1	2.40	0.51
1:D:77:ASP:HB3	1:D:78:PRO:CD	2.40	0.51
1:h:55:SER:CB	1:h:56:PRO:CD	2.84	0.51
1:a:62:PHE:O	1:a:63:PRO:C	2.53	0.51
1:C:0:HIS:H	1:C:0:HIS:CD2	2.27	0.51
1:M:91:ASN:HD22	1:M:114:VAL:HG21	1.75	0.51
1:R:11:VAL:HG21	1:d:133:ILE:HA	1.92	0.51
1:W:125:ILE:O	1:W:129:ILE:HG13	2.11	0.51
1:A:2:TYR:HB3	1:A:150:LEU:HD22	1.93	0.51
1:G:36:GLN:CB	1:N:90:ARG:HG3	2.40	0.51
1:U:17:TRP:CZ3	1:U:70:TYR:HB2	2.46	0.51
1:D:83:LEU:HA	1:D:124:ALA:HB1	1.93	0.51
1:X:36:GLN:OE1	1:X:36:GLN:CA	2.52	0.51
1:a:15:SER:OG	1:a:54:PRO:HD3	2.10	0.51
1:d:55:SER:HB3	1:d:56:PRO:CD	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:i:29:ASN:O	1:i:30:ALA:C	2.53	0.51
1:F:19:ASP:HB3	1:F:22:GLU:HB3	1.92	0.51
1:i:45:GLN:HB2	1:i:87:PHE:CG	2.46	0.50
1:D:2:TYR:HB3	1:D:150:LEU:HD22	1.93	0.50
1:L:134:ARG:HB2	1:L:136:THR:HG22	1.94	0.50
1:O:126:ASN:O	1:O:130:VAL:HG23	2.11	0.50
1:X:2:TYR:CD1	1:X:150:LEU:HB3	2.46	0.50
1:a:153:THR:HG22	1:a:154:SER:H	1.77	0.50
1:G:20:PRO:O	1:G:24:ILE:HG22	2.11	0.50
1:S:142:SER:O	1:S:146:SER:CB	2.59	0.50
1:Y:44:VAL:HG23	1:Y:87:PHE:CE1	2.46	0.50
1:H:57:GLN:O	1:H:58:VAL:C	2.55	0.50
1:W:131:GLU:OE1	1:W:136:THR:HG21	2.11	0.50
1:c:17:TRP:CZ3	1:c:70:TYR:HB2	2.46	0.50
1:I:57:GLN:HB2	1:I:60:VAL:HB	1.93	0.50
1:F:7:PRO:CB	1:H:138:SER:HB2	2.42	0.50
1:M:40:ALA:O	1:M:44:VAL:HG13	2.11	0.50
1:S:15:SER:OG	1:S:54:PRO:HD3	2.12	0.50
1:V:122:ARG:HG2	1:V:122:ARG:HH11	1.77	0.50
1:L:75:VAL:HG22	1:h:54:PRO:HG2	1.93	0.50
1:e:55:SER:CB	1:e:56:PRO:CD	2.87	0.50
1:h:57:GLN:O	1:h:58:VAL:C	2.54	0.50
1:e:130:VAL:O	1:e:134:ARG:HG2	2.11	0.50
1:C:53:LYS:HB3	1:C:54:PRO:HD2	1.94	0.50
1:I:129:ILE:O	1:I:130:VAL:C	2.54	0.50
1:L:7:PRO:HD3	1:P:67:PHE:CE2	2.47	0.50
1:U:30:ALA:O	1:U:33:ASN:HB2	2.12	0.50
1:A:77:ASP:HB3	1:A:78:PRO:CD	2.42	0.49
1:Q:33:ASN:O	1:Q:122:ARG:NH2	2.46	0.49
1:T:134:ARG:NH1	1:T:134:ARG:CG	2.68	0.49
1:X:125:ILE:O	1:X:129:ILE:HG13	2.12	0.49
1:f:0:HIS:HD2	1:f:154:SER:HA	1.75	0.49
1:h:44:VAL:HG22	1:h:87:PHE:CE1	2.47	0.49
1:M:91:ASN:ND2	1:M:114:VAL:HG21	2.27	0.49
1:U:2:TYR:CD1	1:U:150:LEU:HB3	2.48	0.49
1:F:90:ARG:HG3	1:H:36:GLN:HB2	1.93	0.49
1:J:90:ARG:O	1:J:113:ARG:NH1	2.45	0.49
1:f:6:THR:HB	1:f:7:PRO:HD2	1.94	0.49
1:E:40:ALA:O	1:E:44:VAL:HG13	2.11	0.49
1:J:129:ILE:O	1:J:130:VAL:C	2.55	0.49
1:L:11:VAL:HG21	1:P:133:ILE:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Y:0:HIS:H	1:Y:0:HIS:CD2	2.30	0.49
1:M:2:TYR:HB3	1:M:150:LEU:HD22	1.94	0.49
1:R:153:THR:HG23	1:R:154:SER:N	2.28	0.49
1:T:36:GLN:CB	1:U:90:ARG:HD2	2.21	0.49
1:d:125:ILE:O	1:d:129:ILE:HG13	2.13	0.49
1:J:27:CYS:HB3	1:J:129:ILE:HD11	1.95	0.49
1:P:153:THR:CG2	1:P:154:SER:N	2.76	0.49
1:Q:134:ARG:HB2	1:Q:136:THR:HG23	1.95	0.49
1:i:13:LEU:HD22	1:i:57:GLN:HA	1.94	0.49
1:A:18:ALA:HB3	1:A:69:VAL:HB	1.94	0.49
1:D:17:TRP:CD1	1:D:56:PRO:HD2	2.48	0.49
1:b:38:GLN:HA	1:b:41:ARG:HH21	1.77	0.49
1:i:17:TRP:CZ3	1:i:70:TYR:HB2	2.48	0.49
1:A:11:VAL:HG21	1:B:133:ILE:HA	1.95	0.48
1:U:133:ILE:HA	1:e:11:VAL:HG21	1.94	0.48
1:a:130:VAL:O	1:a:134:ARG:HG3	2.12	0.48
1:H:38:GLN:HE22	1:H:90:ARG:HA	1.78	0.48
1:H:55:SER:CB	1:H:56:PRO:CD	2.91	0.48
1:f:39:GLN:O	1:f:43:VAL:HG23	2.13	0.48
1:L:11:VAL:O	1:L:14:SER:OG	2.26	0.48
1:L:16:ALA:HB1	1:L:71:ARG:HB3	1.95	0.48
1:X:2:TYR:HB3	1:X:150:LEU:HD22	1.95	0.48
1:D:38:GLN:HE22	1:D:90:ARG:HA	1.79	0.48
1:G:61:ARG:HD3	1:G:141:ARG:NH1	2.29	0.48
1:Q:55:SER:CB	1:Q:56:PRO:CD	2.83	0.48
1:V:11:VAL:HG21	1:Y:133:ILE:HA	1.95	0.48
1:d:19:ASP:HB3	1:d:22:GLU:HB3	1.95	0.48
1:e:2:TYR:CD1	1:e:150:LEU:HB3	2.48	0.48
1:G:90:ARG:HD3	1:G:93:ILE:HG21	1.96	0.48
1:R:29:ASN:O	1:R:30:ALA:C	2.56	0.48
1:W:11:VAL:HG12	1:W:70:TYR:OH	2.13	0.48
1:O:117:ALA:O	1:O:121:ILE:HG13	2.14	0.48
1:U:29:ASN:O	1:U:30:ALA:C	2.57	0.48
1:B:55:SER:HB3	1:B:56:PRO:HD2	1.93	0.48
1:C:71:ARG:HG3	1:C:71:ARG:HH11	1.77	0.48
1:J:57:GLN:HB2	1:J:60:VAL:HB	1.96	0.48
1:R:57:GLN:O	1:R:58:VAL:C	2.55	0.48
1:X:55:SER:CB	1:X:56:PRO:CD	2.91	0.48
1:b:38:GLN:NE2	1:b:41:ARG:HH21	2.12	0.48
1:H:38:GLN:NE2	1:H:90:ARG:HA	2.29	0.48
1:I:131:GLU:OE2	1:T:53:LYS:HE2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:17:TRP:CZ3	1:W:70:TYR:HB2	2.48	0.48
1:b:36:GLN:OE1	1:b:114:VAL:HG12	2.14	0.48
1:f:16:ALA:HB1	1:f:71:ARG:HB3	1.95	0.48
1:D:67:PHE:HA	1:D:139:TYR:O	2.14	0.47
1:F:131:GLU:OE1	1:F:136:THR:HG21	2.14	0.47
1:Q:75:VAL:HG22	1:U:54:PRO:HG2	1.96	0.47
1:d:64:ASP:HA	1:d:141:ARG:NH2	2.29	0.47
1:h:27:CYS:HB3	1:h:129:ILE:HD11	1.95	0.47
1:Y:55:SER:HB3	1:Y:56:PRO:HD2	1.94	0.47
1:a:27:CYS:HB3	1:a:129:ILE:HD11	1.96	0.47
1:h:57:GLN:HB2	1:h:60:VAL:HB	1.96	0.47
1:A:38:GLN:HE22	1:A:90:ARG:HA	1.80	0.47
1:A:91:ASN:ND2	1:A:114:VAL:HG21	2.29	0.47
1:H:27:CYS:HB3	1:H:129:ILE:CD1	2.22	0.47
1:Q:17:TRP:CZ3	1:Q:70:TYR:HB2	2.48	0.47
1:W:41:ARG:HH22	1:W:91:ASN:ND2	2.12	0.47
1:W:62:PHE:CD1	1:W:63:PRO:HD2	2.48	0.47
1:I:0:HIS:O	1:I:153:THR:O	2.33	0.47
1:N:38:GLN:HE22	1:N:90:ARG:HA	1.79	0.47
1:h:131:GLU:O	1:h:136:THR:HG23	2.15	0.47
1:X:126:ASN:HA	1:X:129:ILE:HD12	1.95	0.47
1:F:140:ASN:O	1:F:141:ARG:C	2.56	0.47
1:T:35:PHE:CE1	1:T:44:VAL:HG21	2.49	0.47
1:U:128:LEU:HD13	1:U:132:LEU:HD11	1.96	0.47
1:b:13:LEU:HD13	1:b:57:GLN:O	2.15	0.47
1:b:129:ILE:O	1:b:130:VAL:C	2.56	0.47
1:G:2:TYR:HB3	1:G:150:LEU:HD22	1.97	0.47
1:M:61:ARG:HD3	1:M:141:ARG:CZ	2.45	0.47
1:P:90:ARG:H	1:P:113:ARG:HH22	1.62	0.47
1:R:67:PHE:HE2	1:T:7:PRO:HG3	1.75	0.47
1:C:2:TYR:HB3	1:C:150:LEU:HD22	1.97	0.47
1:L:9:GLN:HG2	1:L:150:LEU:HG	1.97	0.47
1:W:39:GLN:O	1:W:43:VAL:HG23	2.14	0.47
1:Z:11:VAL:HG21	1:b:133:ILE:HA	1.97	0.47
1:L:131:GLU:OE1	1:L:136:THR:CG2	2.52	0.47
1:N:90:ARG:H	1:N:113:ARG:HH22	1.63	0.47
1:R:77:ASP:HB3	1:R:78:PRO:HD3	1.95	0.47
1:R:88:ASP:OD1	1:d:34:GLN:HA	2.14	0.47
1:e:29:ASN:O	1:e:30:ALA:C	2.57	0.47
1:i:55:SER:CB	1:i:56:PRO:CD	2.92	0.47
1:J:146:SER:HA	1:c:-2:GLY:HA3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:38:GLN:HA	1:K:41:ARG:NH2	2.31	0.46
1:A:61:ARG:HD3	1:A:141:ARG:NH1	2.30	0.46
1:I:55:SER:HB3	1:I:56:PRO:CD	2.44	0.46
1:N:16:ALA:HB1	1:N:71:ARG:HB3	1.97	0.46
1:Z:6:THR:O	1:Z:9:GLN:HG3	2.15	0.46
1:h:143:SER:O	1:h:147:SER:OG	2.33	0.46
1:H:92:ARG:CZ	1:H:110:ALA:HB2	2.45	0.46
1:N:-1:SER:O	1:N:154:SER:O	2.34	0.46
1:P:2:TYR:HB3	1:P:150:LEU:HD22	1.98	0.46
1:Q:91:ASN:O	1:Q:92:ARG:HD2	2.15	0.46
1:R:38:GLN:NE2	1:R:41:ARG:NH2	2.60	0.46
1:T:11:VAL:HG12	1:T:70:TYR:OH	2.16	0.46
1:Z:27:CYS:HB3	1:Z:129:ILE:HD11	1.97	0.46
1:c:73:ASN:ND2	1:c:137:GLY:HA2	2.31	0.46
1:h:73:ASN:ND2	1:h:137:GLY:HA2	2.31	0.46
1:i:77:ASP:HB3	1:i:78:PRO:HD3	1.96	0.46
1:C:17:TRP:CZ3	1:C:70:TYR:HB2	2.50	0.46
1:C:90:ARG:H	1:C:113:ARG:HH22	1.64	0.46
1:Z:90:ARG:HG3	1:b:36:GLN:HG3	1.97	0.46
1:d:153:THR:HB	1:d:154:SER:H	1.41	0.46
1:B:55:SER:CB	1:B:56:PRO:CD	2.88	0.46
1:O:-1:SER:O	1:O:154:SER:HB2	2.16	0.46
1:W:38:GLN:NE2	1:W:41:ARG:HH21	2.13	0.46
1:F:5:THR:N	1:F:9:GLN:OE1	2.42	0.46
1:H:57:GLN:HE22	1:O:57:GLN:NE2	1.99	0.46
1:K:38:GLN:NE2	1:K:41:ARG:HH21	2.14	0.46
1:V:55:SER:HB3	1:V:56:PRO:HD2	1.97	0.46
1:D:134:ARG:HB2	1:D:136:THR:HG23	1.98	0.46
1:W:0:HIS:ND1	1:W:153:THR:O	2.36	0.46
1:X:38:GLN:HA	1:X:41:ARG:NH2	2.30	0.46
1:b:142:SER:O	1:b:146:SER:HB3	2.15	0.46
1:i:77:ASP:HB3	1:i:78:PRO:CD	2.46	0.46
1:B:21:ILE:HA	1:B:24:ILE:HG22	1.98	0.46
1:h:77:ASP:HB3	1:h:78:PRO:HD3	1.98	0.46
1:G:9:GLN:NE2	1:G:148:SER:O	2.47	0.46
1:G:36:GLN:HB2	1:N:90:ARG:HG3	1.98	0.46
1:I:61:ARG:HD2	1:I:152:TRP:CD2	2.51	0.46
1:P:19:ASP:HB3	1:P:22:GLU:HB2	1.97	0.46
1:S:44:VAL:HG23	1:S:87:PHE:CE1	2.51	0.46
1:U:142:SER:O	1:U:146:SER:HB3	2.16	0.46
1:X:77:ASP:HB3	1:X:78:PRO:CD	2.43	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:c:153:THR:CG2	1:c:154:SER:N	2.79	0.46
1:h:57:GLN:O	1:h:59:THR:N	2.49	0.46
1:F:29:ASN:O	1:F:30:ALA:C	2.60	0.45
1:N:107:THR:HA	1:N:110:ALA:HB3	1.97	0.45
1:e:91:ASN:HD22	1:e:114:VAL:HG21	1.81	0.45
1:G:76:LEU:O	1:G:77:ASP:C	2.59	0.45
1:W:90:ARG:HH11	1:f:36:GLN:HB2	1.81	0.45
1:D:129:ILE:O	1:D:130:VAL:C	2.59	0.45
1:E:90:ARG:O	1:E:113:ARG:NH1	2.47	0.45
1:L:73:ASN:O	1:L:77:ASP:HB2	2.16	0.45
1:W:90:ARG:O	1:W:114:VAL:HG21	2.16	0.45
1:G:91:ASN:O	1:G:92:ARG:HD2	2.15	0.45
1:H:21:ILE:O	1:H:24:ILE:HG22	2.15	0.45
1:N:112:ARG:HA	1:N:115:ASP:HB2	1.98	0.45
1:O:62:PHE:O	1:O:63:PRO:C	2.59	0.45
1:V:36:GLN:HB3	1:f:90:ARG:HD2	1.99	0.45
1:b:125:ILE:O	1:b:129:ILE:HG13	2.16	0.45
1:C:133:ILE:HA	1:E:11:VAL:HG21	1.98	0.45
1:K:77:ASP:HB3	1:K:78:PRO:HD3	1.97	0.45
1:M:8:SER:HB2	1:N:133:ILE:O	2.16	0.45
1:M:11:VAL:HG21	1:N:133:ILE:HA	1.98	0.45
1:N:72:TYR:O	1:N:73:ASN:C	2.60	0.45
1:S:38:GLN:NE2	1:S:41:ARG:HH21	2.15	0.45
1:V:57:GLN:HB2	1:V:60:VAL:HB	1.98	0.45
1:P:129:ILE:O	1:P:130:VAL:C	2.60	0.45
1:Z:0:HIS:HB3	1:Z:152:TRP:CZ2	2.51	0.45
1:Z:57:GLN:HB2	1:Z:60:VAL:HB	1.99	0.45
1:Z:84:LEU:HD23	1:Z:84:LEU:HA	1.84	0.45
1:d:90:ARG:CG	1:i:36:GLN:HB3	2.46	0.45
1:e:38:GLN:NE2	1:e:41:ARG:HH21	2.14	0.45
1:E:24:ILE:HG12	1:I:11:VAL:HG22	1.97	0.45
1:F:90:ARG:HG3	1:H:36:GLN:CB	2.47	0.45
1:I:57:GLN:O	1:I:58:VAL:C	2.59	0.45
1:N:2:TYR:HB3	1:N:150:LEU:HD22	1.99	0.45
1:T:2:TYR:CD1	1:T:150:LEU:HB3	2.52	0.45
1:Z:29:ASN:O	1:Z:30:ALA:C	2.60	0.45
1:b:129:ILE:HG22	1:b:133:ILE:CD1	2.47	0.45
1:f:114:VAL:C	1:f:116:ASP:H	2.25	0.45
1:S:11:VAL:HG12	1:S:70:TYR:OH	2.16	0.45
1:S:57:GLN:O	1:S:58:VAL:C	2.59	0.45
1:h:53:LYS:HB3	1:h:54:PRO:HD2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:131:GLU:OE1	1:N:136:THR:HG21	2.16	0.45
1:G:133:ILE:O	1:N:8:SER:HB2	2.17	0.44
1:H:35:PHE:O	1:H:41:ARG:NH1	2.48	0.44
1:H:114:VAL:HG12	1:H:114:VAL:O	2.17	0.44
1:L:55:SER:HB3	1:L:56:PRO:HD3	1.99	0.44
1:P:11:VAL:HG21	1:Q:133:ILE:HA	1.99	0.44
1:S:38:GLN:HA	1:S:41:ARG:NH2	2.33	0.44
1:W:90:ARG:O	1:W:114:VAL:CG2	2.66	0.44
1:X:53:LYS:HB3	1:X:54:PRO:HD2	1.98	0.44
1:Z:129:ILE:O	1:Z:130:VAL:C	2.60	0.44
1:i:26:LEU:HD11	1:i:47:GLN:HE21	1.82	0.44
1:K:134:ARG:HB2	1:K:136:THR:CG2	2.43	0.44
1:R:131:GLU:OE1	1:R:136:THR:HG21	2.18	0.44
1:S:90:ARG:HD3	1:Z:36:GLN:CB	2.35	0.44
1:V:7:PRO:HB3	1:Y:138:SER:HB2	1.99	0.44
1:a:55:SER:CB	1:a:56:PRO:CD	2.85	0.44
1:h:128:LEU:HD22	1:h:132:LEU:HG	1.99	0.44
1:C:61:ARG:HD2	1:C:152:TRP:CD2	2.52	0.44
1:P:77:ASP:HB3	1:P:78:PRO:HD3	1.99	0.44
1:P:103:THR:H	1:P:106:GLU:HB3	1.82	0.44
1:M:17:TRP:CD1	1:M:56:PRO:HD2	2.52	0.44
1:N:20:PRO:O	1:N:24:ILE:HG22	2.17	0.44
1:X:-1:SER:OG	1:X:0:HIS:N	2.45	0.44
1:b:53:LYS:HB3	1:b:54:PRO:CD	2.47	0.44
1:C:18:ALA:O	1:C:69:VAL:HG23	2.17	0.44
1:G:121:ILE:O	1:G:125:ILE:HG13	2.17	0.44
1:N:17:TRP:CZ3	1:N:70:TYR:HB2	2.52	0.44
1:N:55:SER:CB	1:N:56:PRO:CD	2.95	0.44
1:O:140:ASN:O	1:O:141:ARG:C	2.59	0.44
1:X:29:ASN:O	1:X:30:ALA:C	2.60	0.44
1:K:0:HIS:HB3	1:K:154:SER:CA	2.21	0.44
1:d:11:VAL:HG21	1:i:133:ILE:HA	1.99	0.44
1:C:140:ASN:O	1:C:141:ARG:C	2.59	0.44
1:K:3:SER:HB3	1:K:153:THR:CG2	2.48	0.44
1:M:14:SER:HB2	1:N:25:ASN:OD1	2.18	0.44
1:U:38:GLN:NE2	1:U:41:ARG:HH21	2.15	0.44
1:V:53:LYS:HB3	1:V:54:PRO:HD2	2.00	0.44
1:b:69:VAL:CG1	1:b:76:LEU:CD1	2.96	0.44
1:E:83:LEU:HA	1:E:124:ALA:HB1	1.99	0.44
1:E:140:ASN:O	1:E:141:ARG:C	2.60	0.44
1:M:75:VAL:HG22	1:Y:54:PRO:HD2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:128:LEU:HD23	1:U:128:LEU:HA	1.81	0.44
1:Z:77:ASP:HB3	1:Z:78:PRO:CD	2.44	0.44
1:h:38:GLN:HE21	1:h:41:ARG:HH21	1.63	0.44
1:A:31:LEU:HD23	1:A:31:LEU:HA	1.77	0.44
1:R:36:GLN:CB	1:T:90:ARG:HG3	2.44	0.44
1:S:32:GLY:HA3	1:X:49:SER:OG	2.18	0.43
1:B:131:GLU:O	1:B:136:THR:HG23	2.17	0.43
1:J:90:ARG:H	1:J:113:ARG:NH2	2.07	0.43
1:M:55:SER:HB3	1:M:56:PRO:HD3	2.00	0.43
1:U:36:GLN:HB3	1:e:90:ARG:CD	2.48	0.43
1:i:140:ASN:O	1:i:141:ARG:C	2.60	0.43
1:I:140:ASN:O	1:I:141:ARG:C	2.61	0.43
1:O:57:GLN:HB2	1:O:60:VAL:HB	2.00	0.43
1:e:40:ALA:O	1:e:44:VAL:HG13	2.18	0.43
1:B:26:LEU:HD12	1:B:26:LEU:HA	1.87	0.43
1:E:131:GLU:OE1	1:E:136:THR:HG21	2.19	0.43
1:H:30:ALA:O	1:H:33:ASN:HB2	2.18	0.43
1:U:15:SER:OG	1:U:54:PRO:HD3	2.19	0.43
1:i:129:ILE:O	1:i:130:VAL:C	2.60	0.43
1:A:17:TRP:CZ3	1:A:70:TYR:HB2	2.54	0.43
1:I:134:ARG:HB2	1:I:136:THR:CG2	2.48	0.43
1:K:107:THR:C	1:K:109:ASP:H	2.26	0.43
1:P:77:ASP:HB3	1:P:78:PRO:CD	2.49	0.43
1:R:30:ALA:HB1	1:R:125:ILE:HD13	1.99	0.43
1:S:17:TRP:CZ3	1:S:70:TYR:HB2	2.53	0.43
1:Z:90:ARG:HG3	1:b:36:GLN:CB	2.48	0.43
1:Q:140:ASN:O	1:Q:141:ARG:C	2.61	0.43
1:Z:0:HIS:HB3	1:Z:152:TRP:CE2	2.54	0.43
1:Z:39:GLN:O	1:Z:43:VAL:HG23	2.18	0.43
1:c:62:PHE:O	1:c:63:PRO:C	2.62	0.43
1:c:129:ILE:O	1:c:130:VAL:C	2.61	0.43
1:F:122:ARG:NH2	1:G:88:ASP:OD2	2.41	0.43
1:L:134:ARG:HB2	1:L:136:THR:CG2	2.49	0.43
1:N:62:PHE:CD1	1:N:141:ARG:HA	2.54	0.43
1:R:17:TRP:CD1	1:R:56:PRO:HD2	2.53	0.43
1:R:17:TRP:CZ3	1:R:70:TYR:HB2	2.54	0.43
1:T:73:ASN:ND2	1:T:137:GLY:HA2	2.33	0.43
1:T:140:ASN:O	1:T:141:ARG:C	2.60	0.43
1:X:0:HIS:HB2	1:X:152:TRP:CE2	2.54	0.43
1:X:19:ASP:HB3	1:X:22:GLU:HB2	2.00	0.43
1:c:62:PHE:CD1	1:c:141:ARG:HA	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:d:23:LEU:HD13	1:d:132:LEU:HD13	2.01	0.43
1:d:57:GLN:HB2	1:d:60:VAL:HB	2.01	0.43
1:h:0:HIS:HB3	1:h:152:TRP:CE2	2.54	0.43
1:i:45:GLN:HB2	1:i:87:PHE:CB	2.49	0.43
1:L:2:TYR:CD1	1:L:150:LEU:HB3	2.54	0.43
1:C:71:ARG:HG3	1:C:71:ARG:NH1	2.34	0.43
1:D:17:TRP:CZ3	1:D:70:TYR:HB2	2.54	0.43
1:F:2:TYR:HB3	1:F:150:LEU:HD22	2.01	0.43
1:O:111:THR:HG22	1:O:112:ARG:N	2.33	0.43
1:h:17:TRP:CZ3	1:h:70:TYR:HB2	2.54	0.43
1:E:29:ASN:O	1:E:30:ALA:C	2.62	0.42
1:E:126:ASN:O	1:E:130:VAL:HG23	2.19	0.42
1:I:38:GLN:NE2	1:I:90:ARG:HG2	2.33	0.42
1:J:113:ARG:NH1	1:J:113:ARG:HB3	2.34	0.42
1:c:90:ARG:HD3	1:h:36:GLN:CB	2.48	0.42
1:h:16:ALA:HB1	1:h:71:ARG:HB3	2.01	0.42
1:E:73:ASN:O	1:E:77:ASP:HB2	2.19	0.42
1:S:40:ALA:O	1:S:44:VAL:HG22	2.19	0.42
1:a:6:THR:HG22	1:a:7:PRO:HD2	2.00	0.42
1:e:126:ASN:HD22	1:e:129:ILE:HD12	1.85	0.42
1:A:75:VAL:HG22	1:i:54:PRO:HG2	2.00	0.42
1:V:0:HIS:HB3	1:V:152:TRP:CE2	2.54	0.42
1:F:77:ASP:HB3	1:F:78:PRO:CD	2.44	0.42
1:I:55:SER:CB	1:I:56:PRO:CD	2.98	0.42
1:N:9:GLN:O	1:N:12:PHE:HB2	2.20	0.42
1:F:129:ILE:O	1:F:130:VAL:C	2.63	0.42
1:M:76:LEU:O	1:M:77:ASP:C	2.62	0.42
1:M:92:ARG:NH1	1:M:110:ALA:HA	2.35	0.42
1:W:89:THR:HG22	1:W:90:ARG:N	2.35	0.42
1:h:75:VAL:O	1:h:78:PRO:HD2	2.18	0.42
1:A:0:HIS:CD2	1:A:153:THR:C	2.96	0.42
1:O:77:ASP:HB3	1:O:78:PRO:CD	2.49	0.42
1:Z:126:ASN:HD22	1:Z:126:ASN:HA	1.71	0.42
1:b:114:VAL:HA	1:b:117:ALA:HB3	2.00	0.42
1:M:130:VAL:O	1:M:134:ARG:HG3	2.20	0.42
1:T:25:ASN:OD1	1:U:14:SER:HB2	2.19	0.42
1:V:122:ARG:HG2	1:V:122:ARG:NH1	2.35	0.42
1:W:90:ARG:HH11	1:f:36:GLN:CB	2.32	0.42
1:B:91:ASN:HD22	1:B:114:VAL:HG21	1.85	0.42
1:G:147:SER:HA	1:S:59:THR:HB	2.02	0.42
1:R:31:LEU:HD12	1:T:71:ARG:HH22	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:36:GLN:CG	1:f:90:ARG:HG3	2.45	0.42
1:Z:90:ARG:HG3	1:b:36:GLN:HB3	2.01	0.42
1:c:150:LEU:HD23	1:c:150:LEU:HA	1.84	0.42
1:d:140:ASN:O	1:d:141:ARG:C	2.61	0.42
1:G:77:ASP:HB3	1:G:78:PRO:CD	2.45	0.42
1:K:11:VAL:HG21	1:M:133:ILE:HA	2.00	0.42
1:O:84:LEU:HD23	1:O:84:LEU:HA	1.94	0.42
1:T:62:PHE:O	1:T:63:PRO:C	2.63	0.42
1:T:125:ILE:O	1:T:129:ILE:HG13	2.20	0.42
1:h:0:HIS:CD2	1:h:153:THR:C	2.98	0.42
1:S:9:GLN:HG2	1:S:150:LEU:HG	2.02	0.42
1:S:36:GLN:HG2	1:X:88:ASP:OD1	2.19	0.42
1:J:61:ARG:HD3	1:J:141:ARG:NH1	2.35	0.41
1:h:91:ASN:HD22	1:h:114:VAL:HG21	1.84	0.41
1:N:62:PHE:CG	1:N:63:PRO:HD2	2.55	0.41
1:U:61:ARG:O	1:U:62:PHE:C	2.63	0.41
1:U:71:ARG:NH1	1:U:80:VAL:HB	2.35	0.41
1:Z:128:LEU:HD22	1:Z:132:LEU:HG	2.02	0.41
1:E:24:ILE:O	1:E:27:CYS:HB2	2.19	0.41
1:H:41:ARG:HG3	1:H:41:ARG:HH11	1.85	0.41
1:J:90:ARG:N	1:J:113:ARG:HH22	2.07	0.41
1:K:61:ARG:O	1:K:62:PHE:C	2.63	0.41
1:K:62:PHE:O	1:K:63:PRO:C	2.63	0.41
1:Q:6:THR:HB	1:Q:7:PRO:HD2	2.02	0.41
1:h:57:GLN:C	1:h:59:THR:N	2.78	0.41
1:i:38:GLN:HA	1:i:41:ARG:NH2	2.35	0.41
1:O:29:ASN:O	1:O:30:ALA:C	2.64	0.41
1:S:19:ASP:HB3	1:S:22:GLU:HB3	2.02	0.41
1:S:84:LEU:HD23	1:S:84:LEU:HA	1.89	0.41
1:T:44:VAL:HG23	1:T:87:PHE:CZ	2.55	0.41
1:V:91:ASN:HA	1:V:114:VAL:HG21	2.01	0.41
1:i:62:PHE:O	1:i:63:PRO:C	2.60	0.41
1:U:32:GLY:HA3	1:e:49:SER:CB	2.49	0.41
1:Z:6:THR:HB	1:Z:7:PRO:HD2	2.02	0.41
1:F:153:THR:OG1	1:F:154:SER:N	2.53	0.41
1:N:17:TRP:CD1	1:N:56:PRO:HD2	2.56	0.41
1:Q:38:GLN:O	1:Q:39:GLN:C	2.63	0.41
1:S:62:PHE:O	1:S:63:PRO:C	2.60	0.41
1:W:114:VAL:HA	1:W:117:ALA:CB	2.50	0.41
1:G:91:ASN:HD22	1:G:114:VAL:HG21	1.86	0.41
1:H:76:LEU:HD11	1:H:137:GLY:HA3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:3:SER:HB3	1:K:153:THR:HG21	2.01	0.41
1:V:114:VAL:HA	1:V:117:ALA:CB	2.45	0.41
1:a:31:LEU:HD23	1:a:31:LEU:HA	1.83	0.41
1:a:32:GLY:HA3	1:b:49:SER:OG	2.20	0.41
1:i:56:PRO:HG3	1:i:62:PHE:HD2	1.85	0.41
1:c:21:ILE:O	1:c:22:GLU:C	2.63	0.41
1:B:126:ASN:O	1:B:130:VAL:HG23	2.21	0.41
1:F:110:ALA:O	1:F:114:VAL:HB	2.21	0.41
1:G:140:ASN:O	1:G:141:ARG:C	2.64	0.41
1:I:76:LEU:O	1:I:77:ASP:C	2.64	0.41
1:S:49:SER:HB2	1:Z:32:GLY:HA3	2.01	0.41
1:T:9:GLN:HB3	1:T:150:LEU:HD21	2.03	0.41
1:T:77:ASP:HB3	1:T:78:PRO:CD	2.47	0.41
1:D:131:GLU:OE1	1:D:136:THR:HG21	2.21	0.41
1:J:2:TYR:HB3	1:J:150:LEU:HD22	2.03	0.41
1:L:70:TYR:CZ	1:L:72:TYR:HB2	2.56	0.41
1:P:16:ALA:HB1	1:P:71:ARG:HB3	2.03	0.41
1:U:36:GLN:CB	1:e:90:ARG:HD2	2.50	0.41
1:c:62:PHE:CD1	1:c:63:PRO:HD2	2.56	0.41
1:d:90:ARG:HH12	1:i:34:GLN:HE21	1.69	0.41
1:i:26:LEU:HD11	1:i:47:GLN:NE2	2.35	0.41
1:i:56:PRO:HG3	1:i:62:PHE:CD2	2.56	0.41
1:B:91:ASN:ND2	1:B:114:VAL:HG21	2.36	0.40
1:G:126:ASN:HD22	1:G:126:ASN:HA	1.71	0.40
1:L:12:PHE:HB3	1:L:144:PHE:HE1	1.86	0.40
1:R:24:ILE:HG12	1:T:11:VAL:HG22	2.03	0.40
1:V:-1:SER:HB3	1:V:0:HIS:H	1.50	0.40
1:c:43:VAL:O	1:c:47:GLN:HG3	2.21	0.40
1:C:153:THR:O	1:C:154:SER:HB2	2.21	0.40
1:W:27:CYS:O	1:W:28:THR:C	2.64	0.40
1:b:13:LEU:HD13	1:b:58:VAL:HG22	2.03	0.40
1:G:16:ALA:HB1	1:G:71:ARG:HB3	2.04	0.40
1:I:77:ASP:HB3	1:I:78:PRO:CD	2.40	0.40
1:K:23:LEU:HD13	1:K:132:LEU:HD11	2.03	0.40
1:f:57:GLN:O	1:f:58:VAL:C	2.64	0.40
1:c:128:LEU:HD22	1:c:132:LEU:HG	2.02	0.40
1:h:91:ASN:HD22	1:h:91:ASN:HA	1.71	0.40
1:H:140:ASN:O	1:H:141:ARG:C	2.64	0.40
1:J:30:ALA:O	1:J:33:ASN:HB2	2.22	0.40
1:M:62:PHE:O	1:M:63:PRO:C	2.65	0.40
1:Q:62:PHE:O	1:Q:63:PRO:C	2.65	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:36:GLN:OE1	1:U:36:GLN:CA	2.61	0.40
1:Y:62:PHE:O	1:Y:63:PRO:C	2.65	0.40
1:c:38:GLN:NE2	1:c:41:ARG:NH2	2.62	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 X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	138/174 (79%)	129 (94%)	7 (5%)	2 (1%)	9	29
1	B	135/174 (78%)	129 (96%)	5 (4%)	1 (1%)	18	45
1	C	140/174 (80%)	130 (93%)	9 (6%)	1 (1%)	18	45
1	D	139/174 (80%)	128 (92%)	10 (7%)	1 (1%)	18	45
1	E	136/174 (78%)	126 (93%)	7 (5%)	3 (2%)	5	20
1	F	139/174 (80%)	127 (91%)	10 (7%)	2 (1%)	9	29
1	G	139/174 (80%)	129 (93%)	8 (6%)	2 (1%)	9	29
1	H	140/174 (80%)	126 (90%)	10 (7%)	4 (3%)	3	16
1	I	137/174 (79%)	121 (88%)	11 (8%)	5 (4%)	2	12
1	J	141/174 (81%)	129 (92%)	11 (8%)	1 (1%)	18	45
1	K	139/174 (80%)	128 (92%)	9 (6%)	2 (1%)	9	29
1	L	137/174 (79%)	128 (93%)	7 (5%)	2 (2%)	8	28
1	M	138/174 (79%)	131 (95%)	4 (3%)	3 (2%)	5	20
1	N	138/174 (79%)	129 (94%)	8 (6%)	1 (1%)	18	45
1	O	136/174 (78%)	127 (93%)	7 (5%)	2 (2%)	8	28
1	P	143/174 (82%)	131 (92%)	8 (6%)	4 (3%)	4	16
1	Q	142/174 (82%)	132 (93%)	7 (5%)	3 (2%)	5	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	R	129/174 (74%)	122 (95%)	5 (4%)	2 (2%)	7	26
1	S	129/174 (74%)	121 (94%)	6 (5%)	2 (2%)	7	26
1	T	128/174 (74%)	122 (95%)	5 (4%)	1 (1%)	16	42
1	U	129/174 (74%)	118 (92%)	9 (7%)	2 (2%)	7	26
1	V	130/174 (75%)	122 (94%)	6 (5%)	2 (2%)	8	28
1	W	130/174 (75%)	119 (92%)	10 (8%)	1 (1%)	16	42
1	X	127/174 (73%)	117 (92%)	9 (7%)	1 (1%)	16	42
1	Y	128/174 (74%)	118 (92%)	9 (7%)	1 (1%)	16	42
1	Z	130/174 (75%)	123 (95%)	6 (5%)	1 (1%)	16	42
1	a	127/174 (73%)	117 (92%)	8 (6%)	2 (2%)	7	26
1	b	128/174 (74%)	115 (90%)	10 (8%)	3 (2%)	5	19
1	c	132/174 (76%)	120 (91%)	9 (7%)	3 (2%)	5	19
1	d	130/174 (75%)	119 (92%)	10 (8%)	1 (1%)	16	42
1	e	130/174 (75%)	116 (89%)	13 (10%)	1 (1%)	16	42
1	f	130/174 (75%)	121 (93%)	8 (6%)	1 (1%)	16	42
1	h	130/174 (75%)	122 (94%)	6 (5%)	2 (2%)	8	28
1	i	130/174 (75%)	116 (89%)	11 (8%)	3 (2%)	5	19
All	All	4554/5916 (77%)	4208 (92%)	278 (6%)	68 (2%)	8	28

All (68) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	55	SER
1	G	55	SER
1	I	1	SER
1	L	153	THR
1	M	0	HIS
1	N	55	SER
1	O	55	SER
1	P	64	ASP
1	Q	64	ASP
1	S	64	ASP
1	U	0	HIS
1	b	55	SER
1	c	114	VAL
1	e	55	SER

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Mol	Chain	Res	Type
1	h	55	SER
1	i	64	ASP
1	B	55	SER
1	D	55	SER
1	L	55	SER
1	M	55	SER
1	P	0	HIS
1	P	91	ASN
1	Q	55	SER
1	R	55	SER
1	R	64	ASP
1	S	55	SER
1	V	55	SER
1	X	55	SER
1	Z	55	SER
1	a	55	SER
1	b	58	VAL
1	c	55	SER
1	f	55	SER
1	i	55	SER
1	C	55	SER
1	E	55	SER
1	F	55	SER
1	H	55	SER
1	H	64	ASP
1	H	91	ASN
1	I	55	SER
1	J	55	SER
1	K	55	SER
1	P	55	SER
1	Q	91	ASN
1	T	55	SER
1	U	55	SER
1	V	64	ASP
1	W	55	SER
1	Y	55	SER
1	b	64	ASP
1	d	55	SER
1	h	58	VAL
1	A	0	HIS
1	E	64	ASP
1	I	64	ASP

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Mol	Chain	Res	Type
1	M	63	PRO
1	c	64	ASP
1	i	30	ALA
1	E	63	PRO
1	a	64	ASP
1	F	63	PRO
1	K	63	PRO
1	O	63	PRO
1	I	63	PRO
1	G	63	PRO
1	H	77	ASP
1	I	58	VAL

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	125/153 (82%)	114 (91%)	11 (9%)	9	30
1	B	123/153 (80%)	107 (87%)	16 (13%)	4	15
1	C	127/153 (83%)	115 (91%)	12 (9%)	8	27
1	D	126/153 (82%)	109 (86%)	17 (14%)	4	14
1	E	123/153 (80%)	110 (89%)	13 (11%)	6	23
1	F	127/153 (83%)	110 (87%)	17 (13%)	4	14
1	G	127/153 (83%)	108 (85%)	19 (15%)	3	11
1	H	127/153 (83%)	104 (82%)	23 (18%)	2	7
1	I	125/153 (82%)	112 (90%)	13 (10%)	7	23
1	J	128/153 (84%)	116 (91%)	12 (9%)	8	27
1	K	127/153 (83%)	112 (88%)	15 (12%)	5	18
1	L	125/153 (82%)	110 (88%)	15 (12%)	5	17
1	M	126/153 (82%)	113 (90%)	13 (10%)	7	24
1	N	126/153 (82%)	111 (88%)	15 (12%)	5	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	O	123/153 (80%)	113 (92%)	10 (8%)	11	33
1	P	130/153 (85%)	121 (93%)	9 (7%)	14	38
1	Q	129/153 (84%)	115 (89%)	14 (11%)	6	21
1	R	118/153 (77%)	101 (86%)	17 (14%)	3	12
1	S	118/153 (77%)	108 (92%)	10 (8%)	10	31
1	T	117/153 (76%)	102 (87%)	15 (13%)	4	15
1	U	118/153 (77%)	109 (92%)	9 (8%)	12	35
1	V	119/153 (78%)	107 (90%)	12 (10%)	7	24
1	W	119/153 (78%)	106 (89%)	13 (11%)	6	21
1	X	116/153 (76%)	105 (90%)	11 (10%)	8	27
1	Y	117/153 (76%)	101 (86%)	16 (14%)	3	13
1	Z	119/153 (78%)	104 (87%)	15 (13%)	4	16
1	a	116/153 (76%)	105 (90%)	11 (10%)	8	27
1	b	117/153 (76%)	104 (89%)	13 (11%)	6	21
1	c	120/153 (78%)	109 (91%)	11 (9%)	8	28
1	d	119/153 (78%)	100 (84%)	19 (16%)	2	10
1	e	119/153 (78%)	106 (89%)	13 (11%)	6	21
1	f	119/153 (78%)	102 (86%)	17 (14%)	3	12
1	h	119/153 (78%)	102 (86%)	17 (14%)	3	12
1	i	119/153 (78%)	107 (90%)	12 (10%)	7	24
All	All	4153/5202 (80%)	3678 (89%)	475 (11%)	5	20

All (475) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	A	6	THR
1	A	19	ASP
1	A	23	LEU
1	A	42	THR
1	A	44	VAL
1	A	107	THR
1	A	112	ARG
1	A	115	ASP
1	A	128	LEU

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Mol	Chain	Res	Type
1	A	153	THR
1	B	-1	SER
1	B	3	SER
1	B	4	ILE
1	B	6	THR
1	B	23	LEU
1	B	26	LEU
1	B	42	THR
1	B	44	VAL
1	B	49	SER
1	B	50	GLU
1	B	64	ASP
1	B	89	THR
1	B	111	THR
1	B	113	ARG
1	B	128	LEU
1	B	136	THR
1	C	0	HIS
1	C	4	ILE
1	C	23	LEU
1	C	26	LEU
1	C	42	THR
1	C	44	VAL
1	C	69	VAL
1	C	89	THR
1	C	107	THR
1	C	123	SER
1	C	128	LEU
1	C	147	SER
1	D	0	HIS
1	D	3	SER
1	D	6	THR
1	D	8	SER
1	D	15	SER
1	D	23	LEU
1	D	26	LEU
1	D	39	GLN
1	D	42	THR
1	D	44	VAL
1	D	89	THR
1	D	91	ASN
1	D	92	ARG

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Mol	Chain	Res	Type
1	D	128	LEU
1	D	136	THR
1	D	142	SER
1	D	146	SER
1	E	0	HIS
1	E	23	LEU
1	E	26	LEU
1	E	39	GLN
1	E	44	VAL
1	E	63	PRO
1	E	89	THR
1	E	113	ARG
1	E	114	VAL
1	E	128	LEU
1	E	129	ILE
1	E	136	THR
1	E	146	SER
1	F	-1	SER
1	F	4	ILE
1	F	21	ILE
1	F	23	LEU
1	F	26	LEU
1	F	42	THR
1	F	44	VAL
1	F	49	SER
1	F	92	ARG
1	F	107	THR
1	F	111	THR
1	F	112	ARG
1	F	114	VAL
1	F	115	ASP
1	F	116	ASP
1	F	128	LEU
1	F	136	THR
1	G	-1	SER
1	G	3	SER
1	G	4	ILE
1	G	5	THR
1	G	23	LEU
1	G	39	GLN
1	G	42	THR
1	G	44	VAL

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Mol	Chain	Res	Type
1	G	63	PRO
1	G	89	THR
1	G	92	ARG
1	G	93	ILE
1	G	113	ARG
1	G	114	VAL
1	G	128	LEU
1	G	136	THR
1	G	146	SER
1	G	153	THR
1	G	154	SER
1	H	0	HIS
1	H	3	SER
1	H	6	THR
1	H	21	ILE
1	H	22	GLU
1	H	23	LEU
1	H	26	LEU
1	H	33	ASN
1	H	39	GLN
1	H	44	VAL
1	H	49	SER
1	H	63	PRO
1	H	92	ARG
1	H	106	GLU
1	H	107	THR
1	H	111	THR
1	H	112	ARG
1	H	113	ARG
1	H	128	LEU
1	H	136	THR
1	H	146	SER
1	H	153	THR
1	H	154	SER
1	I	0	HIS
1	I	1	SER
1	I	4	ILE
1	I	23	LEU
1	I	26	LEU
1	I	44	VAL
1	I	107	THR
1	I	113	ARG

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Mol	Chain	Res	Type
1	I	114	VAL
1	I	128	LEU
1	I	136	THR
1	I	147	SER
1	I	153	THR
1	J	4	ILE
1	J	21	ILE
1	J	23	LEU
1	J	26	LEU
1	J	39	GLN
1	J	44	VAL
1	J	89	THR
1	J	92	ARG
1	J	107	THR
1	J	108	LEU
1	J	128	LEU
1	J	154	SER
1	K	3	SER
1	K	4	ILE
1	K	15	SER
1	K	22	GLU
1	K	23	LEU
1	K	26	LEU
1	K	39	GLN
1	K	42	THR
1	K	44	VAL
1	K	64	ASP
1	K	92	ARG
1	K	111	THR
1	K	128	LEU
1	K	136	THR
1	K	146	SER
1	L	0	HIS
1	L	3	SER
1	L	4	ILE
1	L	23	LEU
1	L	24	ILE
1	L	39	GLN
1	L	42	THR
1	L	44	VAL
1	L	49	SER
1	L	64	ASP

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Mol	Chain	Res	Type
1	L	114	VAL
1	L	128	LEU
1	L	136	THR
1	L	153	THR
1	L	154	SER
1	M	0	HIS
1	M	4	ILE
1	M	6	THR
1	M	23	LEU
1	M	26	LEU
1	M	39	GLN
1	M	42	THR
1	M	44	VAL
1	M	92	ARG
1	M	115	ASP
1	M	128	LEU
1	M	136	THR
1	M	154	SER
1	N	0	HIS
1	N	4	ILE
1	N	6	THR
1	N	23	LEU
1	N	26	LEU
1	N	42	THR
1	N	43	VAL
1	N	44	VAL
1	N	89	THR
1	N	92	ARG
1	N	107	THR
1	N	112	ARG
1	N	128	LEU
1	N	136	THR
1	N	153	THR
1	O	0	HIS
1	O	3	SER
1	O	6	THR
1	O	23	LEU
1	O	44	VAL
1	O	49	SER
1	O	89	THR
1	O	111	THR
1	O	128	LEU

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Mol	Chain	Res	Type
1	O	153	THR
1	P	22	GLU
1	P	23	LEU
1	P	26	LEU
1	P	44	VAL
1	P	92	ARG
1	P	103	THR
1	P	104	THR
1	P	113	ARG
1	P	128	LEU
1	Q	0	HIS
1	Q	3	SER
1	Q	4	ILE
1	Q	23	LEU
1	Q	26	LEU
1	Q	44	VAL
1	Q	50	GLU
1	Q	89	THR
1	Q	91	ASN
1	Q	92	ARG
1	Q	112	ARG
1	Q	114	VAL
1	Q	128	LEU
1	Q	153	THR
1	R	-1	SER
1	R	0	HIS
1	R	6	THR
1	R	22	GLU
1	R	23	LEU
1	R	39	GLN
1	R	42	THR
1	R	44	VAL
1	R	89	THR
1	R	114	VAL
1	R	118	THR
1	R	123	SER
1	R	128	LEU
1	R	133	ILE
1	R	136	THR
1	R	153	THR
1	R	154	SER
1	S	6	THR

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Mol	Chain	Res	Type
1	S	15	SER
1	S	23	LEU
1	S	26	LEU
1	S	39	GLN
1	S	42	THR
1	S	128	LEU
1	S	136	THR
1	S	153	THR
1	S	154	SER
1	T	0	HIS
1	T	6	THR
1	T	23	LEU
1	T	39	GLN
1	T	43	VAL
1	T	53	LYS
1	T	81	THR
1	T	89	THR
1	T	90	ARG
1	T	118	THR
1	T	123	SER
1	T	128	LEU
1	T	134	ARG
1	T	136	THR
1	T	153	THR
1	U	23	LEU
1	U	39	GLN
1	U	44	VAL
1	U	57	GLN
1	U	114	VAL
1	U	128	LEU
1	U	146	SER
1	U	153	THR
1	U	154	SER
1	V	23	LEU
1	V	26	LEU
1	V	36	GLN
1	V	39	GLN
1	V	42	THR
1	V	44	VAL
1	V	58	VAL
1	V	63	PRO
1	V	119	VAL

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Mol	Chain	Res	Type
1	V	128	LEU
1	V	142	SER
1	V	151	VAL
1	W	0	HIS
1	W	3	SER
1	W	4	ILE
1	W	23	LEU
1	W	26	LEU
1	W	39	GLN
1	W	44	VAL
1	W	90	ARG
1	W	116	ASP
1	W	123	SER
1	W	128	LEU
1	W	136	THR
1	W	147	SER
1	X	1	SER
1	X	4	ILE
1	X	22	GLU
1	X	23	LEU
1	X	36	GLN
1	X	37	THR
1	X	39	GLN
1	X	49	SER
1	X	89	THR
1	X	128	LEU
1	X	146	SER
1	Y	0	HIS
1	Y	4	ILE
1	Y	6	THR
1	Y	23	LEU
1	Y	26	LEU
1	Y	39	GLN
1	Y	50	GLU
1	Y	64	ASP
1	Y	115	ASP
1	Y	123	SER
1	Y	128	LEU
1	Y	143	SER
1	Y	146	SER
1	Y	147	SER
1	Y	153	THR

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Mol	Chain	Res	Type
1	Y	154	SER
1	Z	3	SER
1	Z	4	ILE
1	Z	23	LEU
1	Z	26	LEU
1	Z	39	GLN
1	Z	44	VAL
1	Z	50	GLU
1	Z	65	SER
1	Z	89	THR
1	Z	91	ASN
1	Z	114	VAL
1	Z	128	LEU
1	Z	134	ARG
1	Z	136	THR
1	Z	146	SER
1	a	0	HIS
1	a	6	THR
1	a	23	LEU
1	a	26	LEU
1	a	39	GLN
1	a	44	VAL
1	a	50	GLU
1	a	76	LEU
1	a	116	ASP
1	a	119	VAL
1	a	128	LEU
1	b	-1	SER
1	b	0	HIS
1	b	4	ILE
1	b	14	SER
1	b	23	LEU
1	b	39	GLN
1	b	44	VAL
1	b	47	GLN
1	b	49	SER
1	b	59	THR
1	b	115	ASP
1	b	128	LEU
1	b	146	SER
1	c	3	SER
1	c	6	THR

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Mol	Chain	Res	Type
1	c	23	LEU
1	c	39	GLN
1	c	42	THR
1	c	44	VAL
1	c	113	ARG
1	c	115	ASP
1	c	128	LEU
1	c	136	THR
1	c	154	SER
1	d	0	HIS
1	d	3	SER
1	d	4	ILE
1	d	23	LEU
1	d	26	LEU
1	d	39	GLN
1	d	42	THR
1	d	44	VAL
1	d	49	SER
1	d	57	GLN
1	d	59	THR
1	d	89	THR
1	d	90	ARG
1	d	115	ASP
1	d	123	SER
1	d	128	LEU
1	d	136	THR
1	d	142	SER
1	d	153	THR
1	e	0	HIS
1	e	6	THR
1	e	23	LEU
1	e	26	LEU
1	e	44	VAL
1	e	89	THR
1	e	115	ASP
1	e	119	VAL
1	e	128	LEU
1	e	134	ARG
1	e	136	THR
1	e	146	SER
1	e	153	THR
1	f	3	SER

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Mol	Chain	Res	Type
1	f	4	ILE
1	f	5	THR
1	f	23	LEU
1	f	26	LEU
1	f	37	THR
1	f	39	GLN
1	f	44	VAL
1	f	88	ASP
1	f	89	THR
1	f	115	ASP
1	f	118	THR
1	f	128	LEU
1	f	136	THR
1	f	146	SER
1	f	151	VAL
1	f	153	THR
1	h	-1	SER
1	h	1	SER
1	h	4	ILE
1	h	6	THR
1	h	23	LEU
1	h	26	LEU
1	h	44	VAL
1	h	59	THR
1	h	89	THR
1	h	114	VAL
1	h	118	THR
1	h	128	LEU
1	h	136	THR
1	h	146	SER
1	h	147	SER
1	h	151	VAL
1	h	153	THR
1	i	0	HIS
1	i	4	ILE
1	i	23	LEU
1	i	39	GLN
1	i	42	THR
1	i	44	VAL
1	i	58	VAL
1	i	89	THR
1	i	115	ASP

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Mol	Chain	Res	Type
1	i	128	LEU
1	i	147	SER
1	i	153	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (163) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	A	34	GLN
1	A	36	GLN
1	A	38	GLN
1	A	91	ASN
1	A	126	ASN
1	B	34	GLN
1	B	38	GLN
1	B	91	ASN
1	B	126	ASN
1	C	34	GLN
1	C	126	ASN
1	D	34	GLN
1	D	38	GLN
1	D	57	GLN
1	D	91	ASN
1	D	126	ASN
1	E	29	ASN
1	E	34	GLN
1	E	38	GLN
1	E	39	GLN
1	E	126	ASN
1	F	34	GLN
1	F	38	GLN
1	F	39	GLN
1	F	47	GLN
1	F	57	GLN
1	F	91	ASN
1	F	126	ASN
1	G	29	ASN
1	G	34	GLN
1	G	38	GLN
1	G	47	GLN
1	G	91	ASN
1	G	126	ASN

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Mol	Chain	Res	Type
1	H	0	HIS
1	H	34	GLN
1	H	38	GLN
1	H	57	GLN
1	H	126	ASN
1	I	38	GLN
1	I	39	GLN
1	I	91	ASN
1	J	29	ASN
1	J	34	GLN
1	J	57	GLN
1	J	91	ASN
1	K	0	HIS
1	K	34	GLN
1	K	38	GLN
1	K	57	GLN
1	K	91	ASN
1	K	126	ASN
1	L	0	HIS
1	L	36	GLN
1	L	47	GLN
1	L	57	GLN
1	L	126	ASN
1	M	0	HIS
1	M	38	GLN
1	M	57	GLN
1	M	91	ASN
1	N	29	ASN
1	N	34	GLN
1	N	38	GLN
1	N	39	GLN
1	N	57	GLN
1	N	91	ASN
1	N	126	ASN
1	O	25	ASN
1	O	29	ASN
1	O	57	GLN
1	O	126	ASN
1	P	36	GLN
1	P	38	GLN
1	P	39	GLN
1	P	57	GLN

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Mol	Chain	Res	Type
1	P	91	ASN
1	P	126	ASN
1	Q	29	ASN
1	Q	38	GLN
1	Q	91	ASN
1	Q	126	ASN
1	R	34	GLN
1	R	36	GLN
1	R	38	GLN
1	R	126	ASN
1	S	34	GLN
1	S	38	GLN
1	S	126	ASN
1	T	34	GLN
1	T	38	GLN
1	U	29	ASN
1	U	34	GLN
1	U	38	GLN
1	U	39	GLN
1	U	57	GLN
1	U	126	ASN
1	V	0	HIS
1	V	29	ASN
1	V	34	GLN
1	V	36	GLN
1	V	38	GLN
1	V	57	GLN
1	V	126	ASN
1	W	29	ASN
1	W	38	GLN
1	W	57	GLN
1	W	91	ASN
1	W	126	ASN
1	X	0	HIS
1	X	29	ASN
1	X	34	GLN
1	X	38	GLN
1	X	126	ASN
1	Y	0	HIS
1	Y	29	ASN
1	Y	34	GLN
1	Y	38	GLN

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Mol	Chain	Res	Type
1	Y	39	GLN
1	Y	126	ASN
1	Z	29	ASN
1	Z	34	GLN
1	Z	57	GLN
1	Z	91	ASN
1	Z	126	ASN
1	a	34	GLN
1	a	38	GLN
1	a	39	GLN
1	a	57	GLN
1	a	127	ASN
1	b	29	ASN
1	b	38	GLN
1	b	45	GLN
1	b	126	ASN
1	c	38	GLN
1	c	91	ASN
1	c	126	ASN
1	d	0	HIS
1	d	34	GLN
1	d	36	GLN
1	d	38	GLN
1	d	91	ASN
1	d	126	ASN
1	e	34	GLN
1	e	38	GLN
1	e	91	ASN
1	e	126	ASN
1	f	0	HIS
1	f	29	ASN
1	f	34	GLN
1	f	38	GLN
1	f	126	ASN
1	h	0	HIS
1	h	29	ASN
1	h	34	GLN
1	h	38	GLN
1	h	91	ASN
1	i	34	GLN
1	i	47	GLN
1	i	57	GLN

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Mol	Chain	Res	Type
1	i	91	ASN
1	i	126	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	142/174 (81%)	-0.11	9 (6%) 26 13	35, 41, 84, 113	0
1	B	139/174 (79%)	-0.30	4 (2%) 53 31	34, 41, 76, 107	0
1	C	144/174 (82%)	-0.11	9 (6%) 26 13	33, 41, 105, 128	0
1	D	143/174 (82%)	-0.12	10 (6%) 22 11	31, 40, 87, 111	0
1	E	140/174 (80%)	-0.24	7 (5%) 34 17	33, 40, 80, 108	0
1	F	143/174 (82%)	-0.04	11 (7%) 19 10	35, 44, 92, 121	0
1	G	143/174 (82%)	-0.07	11 (7%) 19 10	36, 42, 101, 117	0
1	H	144/174 (82%)	-0.03	10 (6%) 23 11	35, 45, 93, 116	0
1	I	141/174 (81%)	-0.18	7 (4%) 34 17	35, 44, 88, 114	0
1	J	145/174 (83%)	-0.00	11 (7%) 20 10	34, 44, 105, 124	0
1	K	143/174 (82%)	-0.11	7 (4%) 35 17	32, 40, 90, 116	0
1	L	141/174 (81%)	-0.08	7 (4%) 34 17	35, 43, 84, 112	0
1	M	142/174 (81%)	-0.16	5 (3%) 47 26	34, 43, 90, 112	0
1	N	142/174 (81%)	-0.20	5 (3%) 47 26	35, 44, 88, 106	0
1	O	140/174 (80%)	-0.16	6 (4%) 40 21	37, 45, 79, 107	0
1	P	147/174 (84%)	-0.01	14 (9%) 14 7	36, 45, 114, 130	0
1	Q	146/174 (83%)	0.02	10 (6%) 23 11	36, 44, 110, 129	0
1	R	133/174 (76%)	-0.26	5 (3%) 44 24	32, 40, 65, 86	0
1	S	133/174 (76%)	-0.34	3 (2%) 61 38	33, 42, 63, 87	0
1	T	132/174 (75%)	-0.27	4 (3%) 52 30	36, 44, 62, 83	0
1	U	133/174 (76%)	-0.13	5 (3%) 44 24	36, 47, 69, 89	0
1	V	134/174 (77%)	-0.30	5 (3%) 45 25	29, 40, 65, 86	0
1	W	134/174 (77%)	-0.24	6 (4%) 38 20	35, 42, 67, 88	0
1	X	131/174 (75%)	-0.31	3 (2%) 61 38	36, 44, 59, 81	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	Y	132/174 (75%)	-0.31	2 (1%)	72 50	33, 43, 61, 85	0
1	Z	134/174 (77%)	-0.24	5 (3%)	45 25	34, 42, 69, 87	0
1	a	131/174 (75%)	-0.20	4 (3%)	51 29	37, 47, 64, 89	0
1	b	132/174 (75%)	-0.18	5 (3%)	44 24	37, 47, 67, 83	0
1	c	136/174 (78%)	-0.11	6 (4%)	39 20	36, 45, 76, 95	0
1	d	134/174 (77%)	-0.21	5 (3%)	45 25	30, 41, 68, 85	0
1	e	134/174 (77%)	-0.19	5 (3%)	45 25	37, 46, 68, 88	0
1	f	134/174 (77%)	-0.23	5 (3%)	45 25	30, 41, 65, 84	0
1	h	134/174 (77%)	-0.16	6 (4%)	38 20	35, 45, 69, 88	0
1	i	134/174 (77%)	-0.18	7 (5%)	33 16	34, 43, 68, 86	0
All	All	4690/5916 (79%)	-0.17	224 (4%)	35 18	29, 43, 82, 130	0

All (224) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	U	114	VAL	7.3
1	Y	114	VAL	7.3
1	L	108	LEU	6.6
1	H	108	LEU	6.4
1	c	114	VAL	6.4
1	f	114	VAL	6.4
1	J	108	LEU	6.2
1	R	114	VAL	6.2
1	I	108	LEU	6.1
1	i	114	VAL	5.9
1	P	105	ALA	5.8
1	K	108	LEU	5.8
1	d	114	VAL	5.5
1	P	108	LEU	5.5
1	a	114	VAL	5.5
1	G	94	ILE	5.5
1	G	93	ILE	5.5
1	J	105	ALA	5.4
1	Q	108	LEU	5.4
1	W	114	VAL	5.3
1	S	114	VAL	5.3
1	D	108	LEU	5.3
1	F	108	LEU	5.2

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Mol	Chain	Res	Type	RSRZ
1	M	108	LEU	5.2
1	G	108	LEU	5.1
1	e	114	VAL	5.0
1	U	90	ARG	4.8
1	A	108	LEU	4.7
1	Q	105	ALA	4.7
1	L	107	THR	4.7
1	A	-2	GLY	4.6
1	A	110	ALA	4.6
1	I	107	THR	4.6
1	H	-2	GLY	4.5
1	E	110	ALA	4.5
1	Q	109	ASP	4.5
1	C	108	LEU	4.5
1	C	105	ALA	4.4
1	a	89	THR	4.4
1	L	91	ASN	4.4
1	h	114	VAL	4.4
1	N	108	LEU	4.3
1	G	109	ASP	4.3
1	X	115	ASP	4.2
1	P	104	THR	4.2
1	C	110	ALA	4.2
1	K	107	THR	4.2
1	A	91	ASN	4.1
1	R	90	ARG	4.1
1	e	-1	SER	4.1
1	F	107	THR	4.1
1	c	90	ARG	4.0
1	e	90	ARG	4.0
1	D	110	ALA	4.0
1	c	-2	GLY	4.0
1	O	109	ASP	3.9
1	P	110	ALA	3.9
1	P	107	THR	3.8
1	h	89	THR	3.8
1	f	91	ASN	3.8
1	Q	91	ASN	3.8
1	A	107	THR	3.8
1	Q	103	THR	3.8
1	O	-2	GLY	3.8
1	h	115	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
1	H	110	ALA	3.7
1	N	91	ASN	3.7
1	W	-1	SER	3.7
1	T	90	ARG	3.7
1	K	91	ASN	3.7
1	E	-2	GLY	3.7
1	F	92	ARG	3.6
1	b	89	THR	3.6
1	M	92	ARG	3.6
1	J	109	ASP	3.6
1	O	110	ALA	3.6
1	E	109	ASP	3.6
1	V	91	ASN	3.6
1	Q	104	THR	3.6
1	R	115	ASP	3.5
1	L	110	ALA	3.5
1	i	115	ASP	3.5
1	G	-1	SER	3.5
1	M	91	ASN	3.5
1	P	102	PRO	3.5
1	Z	115	ASP	3.5
1	D	92	ARG	3.4
1	F	106	GLU	3.4
1	b	114	VAL	3.4
1	U	89	THR	3.4
1	Z	91	ASN	3.3
1	D	-2	GLY	3.3
1	V	90	ARG	3.3
1	Z	114	VAL	3.3
1	A	111	THR	3.3
1	O	91	ASN	3.3
1	C	107	THR	3.2
1	d	-1	SER	3.2
1	R	89	THR	3.2
1	i	89	THR	3.2
1	B	110	ALA	3.1
1	I	110	ALA	3.1
1	N	92	ARG	3.1
1	d	90	ARG	3.1
1	J	-1	SER	3.1
1	K	92	ARG	3.1
1	P	92	ARG	3.1

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Mol	Chain	Res	Type	RSRZ
1	e	91	ASN	3.1
1	J	107	THR	3.1
1	F	109	ASP	3.1
1	V	114	VAL	3.1
1	f	90	ARG	3.1
1	U	154	SER	3.1
1	Z	90	ARG	3.0
1	Q	92	ARG	3.0
1	P	103	THR	3.0
1	e	89	THR	3.0
1	F	-1	SER	3.0
1	G	92	ARG	3.0
1	E	91	ASN	3.0
1	F	91	ASN	3.0
1	X	89	THR	3.0
1	J	92	ARG	2.9
1	C	91	ASN	2.9
1	C	104	THR	2.9
1	c	91	ASN	2.9
1	K	110	ALA	2.9
1	S	90	ARG	2.9
1	i	90	ARG	2.9
1	A	109	ASP	2.9
1	L	109	ASP	2.9
1	A	-1	SER	2.9
1	c	115	ASP	2.9
1	c	89	THR	2.9
1	N	107	THR	2.8
1	D	91	ASN	2.8
1	h	91	ASN	2.8
1	H	92	ARG	2.8
1	h	90	ARG	2.8
1	D	111	THR	2.8
1	J	110	ALA	2.8
1	M	-1	SER	2.8
1	F	110	ALA	2.8
1	V	89	THR	2.8
1	D	109	ASP	2.8
1	S	115	ASP	2.8
1	I	109	ASP	2.7
1	h	-1	SER	2.7
1	H	107	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	J	104	THR	2.7
1	d	89	THR	2.7
1	P	-1	SER	2.7
1	N	110	ALA	2.7
1	G	110	ALA	2.6
1	L	114	VAL	2.6
1	i	-1	SER	2.6
1	I	91	ASN	2.6
1	M	109	ASP	2.6
1	W	91	ASN	2.6
1	E	114	VAL	2.6
1	G	112	ARG	2.6
1	J	106	GLU	2.6
1	Q	110	ALA	2.6
1	Z	89	THR	2.6
1	K	-1	SER	2.5
1	H	114	VAL	2.5
1	G	91	ASN	2.5
1	W	89	THR	2.5
1	Q	-1	SER	2.4
1	f	89	THR	2.4
1	Y	115	ASP	2.4
1	f	115	ASP	2.4
1	O	112	ARG	2.4
1	H	106	GLU	2.4
1	T	-1	SER	2.4
1	H	109	ASP	2.3
1	W	115	ASP	2.3
1	d	91	ASN	2.3
1	C	109	ASP	2.3
1	U	115	ASP	2.3
1	a	115	ASP	2.3
1	b	36	GLN	2.3
1	L	113	ARG	2.3
1	C	-1	SER	2.3
1	O	111	THR	2.3
1	b	-1	SER	2.3
1	D	113	ARG	2.3
1	D	107	THR	2.3
1	H	-1	SER	2.3
1	Q	111	THR	2.3
1	a	154	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	i	91	ASN	2.3
1	B	115	ASP	2.3
1	J	115	ASP	2.3
1	A	112	ARG	2.3
1	P	112	ARG	2.3
1	T	36	GLN	2.3
1	F	154	SER	2.2
1	H	115	ASP	2.2
1	P	106	GLU	2.2
1	G	113	ARG	2.2
1	J	111	THR	2.2
1	I	-1	SER	2.2
1	b	154	SER	2.2
1	P	109	ASP	2.2
1	F	112	ARG	2.2
1	D	154	SER	2.2
1	R	-1	SER	2.2
1	E	115	ASP	2.1
1	F	111	THR	2.1
1	V	115	ASP	2.1
1	T	89	THR	2.1
1	G	154	SER	2.1
1	I	115	ASP	2.1
1	X	-1	SER	2.1
1	i	154	SER	2.1
1	W	90	ARG	2.1
1	B	111	THR	2.1
1	E	111	THR	2.0
1	K	109	ASP	2.0
1	P	115	ASP	2.0
1	P	154	SER	2.0
1	B	109	ASP	2.0
1	C	114	VAL	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.