



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Feb 24, 2018 – 10:46 AM EST

PDB ID : 6C24
EMDB ID: : EMD-7335
Title : Cryo-EM structure of PRC2 bound to cofactors AEBP2 and JARID2 in the
Extended Active State
Authors : Kasinath, V.; Faini, M.; Poepsel, S.; Reif, D.; Feng, A.; Stjepanovic, G.;
Aebersold, R.; Nogales, E.
Deposited on : 2018-01-06
Resolution : 3.50 Å(reported)

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

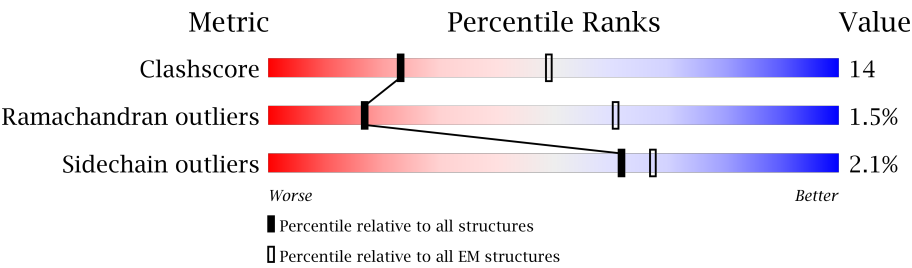
MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	739	13% .. 83%
1	M	739	13% . 83%
1	Q	739	7% . 91%
2	B	345	. 98%
3	E	345	5% .. 92%
4	C	746	17% . 80%
4	K	746	35% 9% 56%
5	L	441	54% 27% . 18%
6	N	425	65% 24% . 9%

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Mol	Chain	Length	Quality of chain
7	O	7	<div><div></div><div>86%</div><div>14%</div></div>
8	P	295	<div><div></div><div>19%</div><div>..</div><div>78%</div></div>
9	Z	135	<div><div></div><div>80%</div><div>20%</div></div>

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 13346 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Polycomb protein SUZ12.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	123	Total	C	N	O	S	0	0
			867	555	157	149	6		
1	M	122	Total	C	N	O	S	0	0
			962	609	169	175	9		
1	Q	66	Total	C	N	O	S	0	0
			496	315	94	85	2		

- Molecule 2 is a protein called Protein Jumonji.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	B	7	Total	C	N	O	0	0
			52	35	9	8		

- Molecule 3 is a protein called Protein Jumonji.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	27	Total	C	N	O	S	0	0
			184	112	32	39	1		

- Molecule 4 is a protein called Histone-lysine N-methyltransferase EZH2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	K	325	Total	C	N	O	S	0	0
			2406	1514	426	436	30		
4	C	148	Total	C	N	O	S	0	0
			1227	779	218	223	7		

- Molecule 5 is a protein called Polycomb protein EED.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	362	Total	C	N	O	S	0	0
			2881	1829	506	526	20		

- Molecule 6 is a protein called Histone-binding protein RBBP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	N	386	Total	C	N	O	S	0	0
			3062	1933	524	595	10		

- Molecule 7 is a protein called JARID2-substrate.

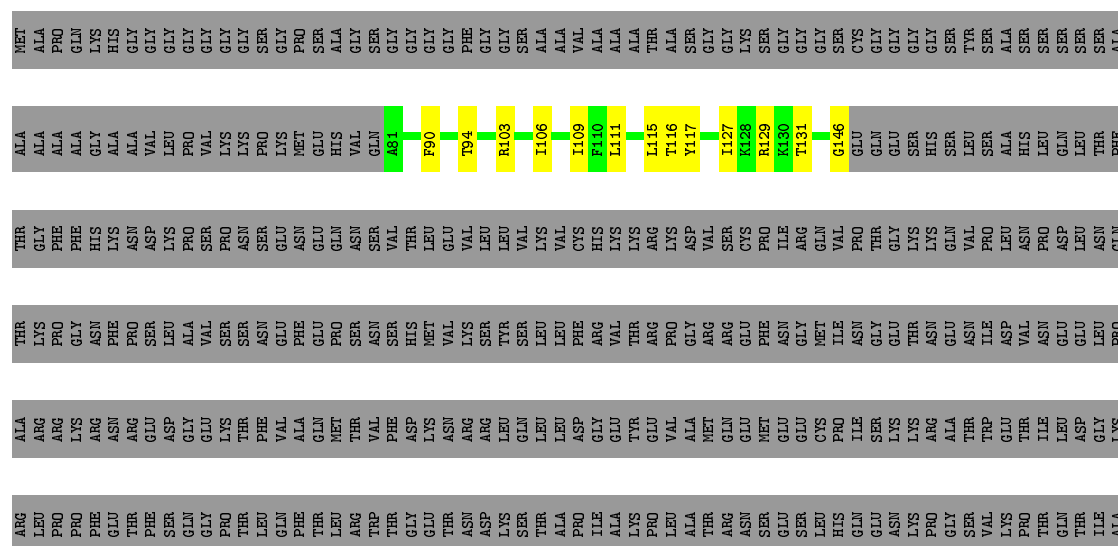
Mol	Chain	Residues	Atoms				AltConf	Trace
7	O	7	Total	C	N	O	0	0
			51	33	11	7		

- Molecule 8 is a protein called Zinc finger protein AEBP2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	P	64	Total	C	N	O	S	0	0
			484	304	91	87	2		

- Molecule 9 is a protein called SUZ12.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	Z	135	Total	C	N	O	0	0
			674	404	135	135		



THR	ASN	ASP	ARG	SER	VAL
GLU	TYR	SER	THR	LEU	GLY
GLU	GLY	GLU	PRO	LEU	LYS
GLN	GLN	ASP	ILE	LYS	SER
ASN	GLN	GLU	THR	HIS	LEU
GLY	ILE	LYS	HIS	LEU	THR
THR	ILE	ASP	ILE	LYS	THR
ALA	LYS	PRO	LEU	LEU	ASP
ASN	LYS	GLU	VAL	CYS	LEU
GLY	ASN	TRP	CYS	HIS	GLN
PHE	LEU	LEU	ARG	SER	THR
SER	CYS	ARG	PRO	ARG	ARG
GLU	ARG	GLU	LYS	PHE	LYS
ILE	ASN	LYS	ARG	ILE	GLU
ASN	PHE	THR	THR	PHE	LYS
SER	MET	ILE	LYS	ASN	ASP
LYS	LEU	THR	ALA	TYR	THR
GLU	HIS	GLN	SER	VAL	PRO
LYS	LEU	ILE	MET	TYR	ASN
ALA	VAL	GLU	SER	HIS	GLU
LEU	SER	GLU	GLU	PRO	ASN
GLU	MET	PHE	PHE	LYS	ARG
THR	HIS	SER	LEU	GLY	GLN
ASP	ASP	ASP	GLU	ALA	LYS
SER	PHE	VAL	SER	ARG	LEU
VAL	ASN	ASN	GLU	ILE	ARG
SER	LEU	GLU	ASP	ASP	ILE
GLY	ILE	GLY	GLY	VAL	PHE
VAL	SER	GLU	GLU	SER	TYR
SER	ILE	LYS	VAL	ILE	GLN
LYS	MET	GLU	GLU	ASN	PHE
GLN	SER	VAL	GLN	GLU	LEU
SER	ILE	VAL	GLN	CYS	TYR
LYS	ASP	LYS	ARG	TYR	ASN
LYS	LYS	LEU	THR	ASP	ASN
GLN	ALA	TRP	TYR	GLY	ASN
LYS	VAL	ASN	SER	SER	THR
LEU	LYS	HIS	GLY	ALA	GLN
	ARG	VAL	HIS	GLY	GLN
	ARG	MET	ASN	ASN	THR
	GLU	LYS	ARG	PRO	GLU
	GLY	GLY	TYR	ASP	ALA
	GLN	PHE	PHE	ILE	ARG
	LYS	ILE	HIS	HIS	ASP
	LEU	ALA	SER	ARG	LEU
	LEU	ASP	ASP	GLN	LYS
	GLU	ASN	THR	PRO	HIS
	LYS	ASN	THR	CYS	CYS
	GLY	GLN	CYS	GLY	PRO
	GLU	MET	LEU	PHE	TRP
	SER	ASN	PRO	ALA	CYS
	ALA	HIS	LEU	PHE	THR
	SER	ALA	ARG	SER	LEU
	PRO	CYS	PRO	ARG	ASN
	ALA	MET	GLN	ASN	CYS
	ASN	LEU	GLU	GLY	ARG
	GLU	PHE	MET	PRO	LYS
	VAL	VAL	GLU	VAL	LEU
	THR	THR	THR	THR	THR

- Molecule 2: Protein Jumonji

Chain B: 98%

[illegible]

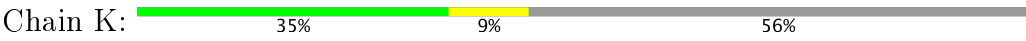
- Molecule 3: Protein Jumonji

Chain E: 5% .. 92%

[illegible]

LYS	ARG	LEU	LEU	VAL	ASP	THR	LYS	LYS	PRO	ASN	HIS	LYS	LYS	PRO	ALA	VAL	ASN	HIS	LYS	THR	ILE	GLY	GLY	LYS	THR	LYS	THR	GLU	ASN	LYS	SER	ARG	ASN	ALA	LYS	THR	ALA	ARG	LYS	GLN	VAL	LEU	SER	LYS	GLY	LEU	ALA
LEU	ASN	PRO	LYS	SER	CYS	THR	LYS	GLU	VAL	GLY	ARG	GLN	LEU	ARG	GLY	LEU	GLN	LEU	GLN	ARG	GLU	THR	GLY	LEU	ARG	ASN	SER	LYS	SER	ARG	ARG	LEU	GLU	GLU	ALA	ALA	GLY	HIS	GLN	VAL	LEU	SER	LYS	GLY	LEU	ALA	

• Molecule 4: Histone-lysine N-methyltransferase EZH2



LYS	HIS	GLU	GLY	ALA	LEU	GLY	ASN	MET	LYS	THR	GLY	VAL	GLN	GLY	THR	GLN	GLY	GLN	LYS	THR	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
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• Molecule 4: Histone-lysine N-methyltransferase EZH2

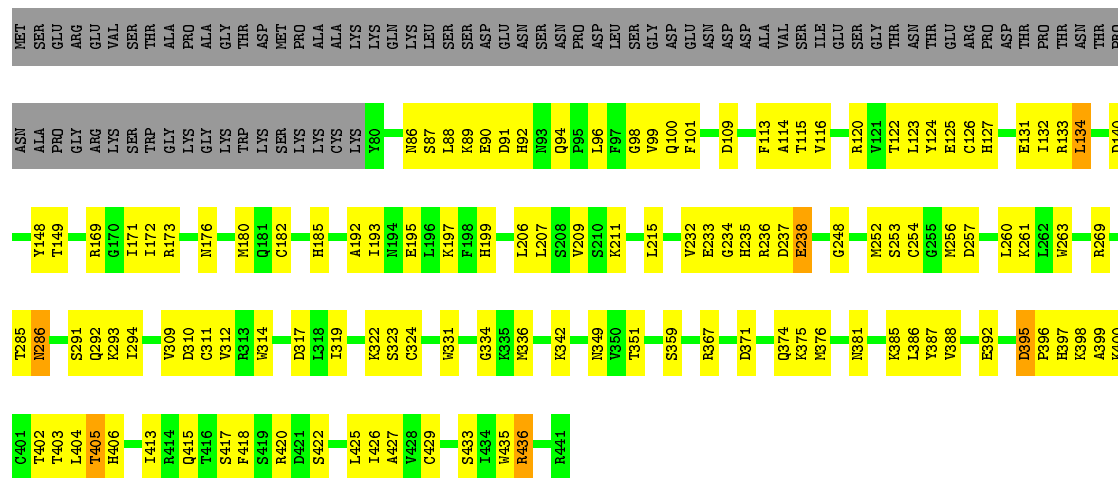


ASN	ILE	PRO	TYR	MET	GLY	ASP	GLU	VAL	LEU	GLY	THR	PHE	ILE	GLU	GLU	LEU	ILE	LYS	ASN	TYR	ASP	GLY	LYS	VAL	HIS	GLY	ASP	ARG	GLY	CYS	GLU	CYS	GLU	THR	PRO	ASN	GLN	ASP	ILE	ASP	GLY	PRO	ASP	LEU	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP	ASP
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HIS	ARG	ILE	LEU	PRO	VAL	SER	PRO
ARG	ILE	GLN	THR	ARG	THR	SER	PRO
GLY	ASP	GLY	CYS	GLN	THR	SER	PRO
ILE	PRO	ALA	GLY	PRO	PHE	GLU	ARG
PHE	ALA	ALA	ASP	ASP	VAL	ASN	GLY
ALA	ASP	ASP	ASP	SER	LYS	SER	GLY
LYS	HIS	ARG	HIS	SER	GLU	ARG	ARG
ARG	ARG	ARG	TRP	CYS	SER	CYS	ARG
ILE	ILE	GLY	ASP	PRO	SER	GLN	ARG
GLN	GLN	VAL	LYS	CYS	ILE	THR	GLY
THR	THR	THR	ASN	ILE	ALA	ILE	ARG
GLY	ASP	GLY	VAL	ALA	PRO	LYS	LEU
GLU	LYS	LYS	SER	ALA	PRO	VAL	PRO
GLU	GLU	THR	THR	CYS	ALA	MET	ASN
GLU	GLU	THR	SER	CYS	ARG	LYS	ASN
ILE	ILE	ILE	TRP	GLN	VAL	GLU	ASN
PRO	PRO	PHE	ILE	CYS	ILE	THR	THR
		ALA	PHE	ASN	GLN	THR	GLU
		ASN	ILE	ASN	LEU	THR	THR
		HIS	LYS	LYS	LYS	THR	GLY
		SER	ASP	GLN	THR	ASN	GLY
		VAL	PRO	CYS	ASP	PHE	GLU
		ASN	VAL	PRO	GLY	CYS	ASN
		ASN	GLN	CYS	SER	ALA	ASN
		ASN	LYS	TYR	SER	ILE	ASP
		CYS	ASN	LEU	ASN	ALA	LYS
		TYR	GLU	ALA	HIS	ARG	GLU
		VAL	PHE	VAL	VAL	LEU	GLU
		LYS	ILE	ARG	TYR	ILE	GLU
		VAL	SER	GLU	ASN	GLY	GLU
		GLU	GLU	CYS	THR	THR	LYS
		MET	TYR	ASP	GLN	LYS	ASP
		VAL	VAL	ASN	PRO	CYS	GLU
		GLY	ILE	THR	ASP	ARG	SER

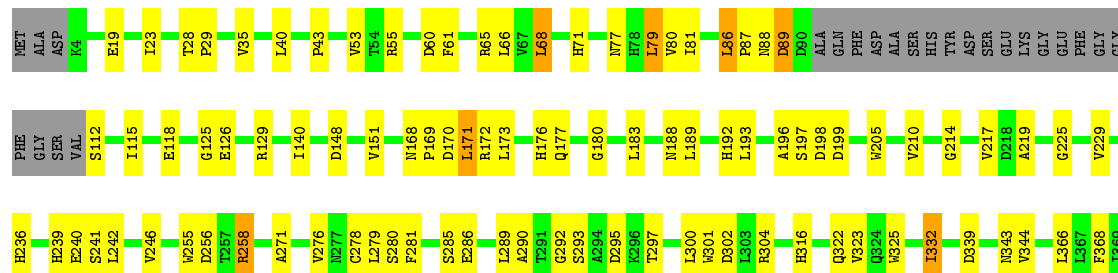
- Molecule 5: Polycomb protein EED

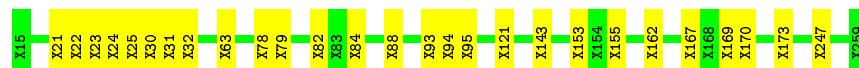
Chain L:  54% 27% • 18%



- Molecule 6: Histone-binding protein RBBP4

Chain N:  65% 24% • 9%





4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	249696	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: M3L

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	$\# Z > 2$	RMSZ	$\# Z > 2$
1	A	0.53	0/890	0.78	1/1219 (0.1%)
1	M	0.48	0/983	0.70	0/1328
1	Q	1.18	3/506 (0.6%)	0.89	1/687 (0.1%)
2	B	0.48	0/40	0.38	0/53
3	E	0.46	0/185	1.04	0/250
4	C	0.42	0/1247	0.69	1/1669 (0.1%)
4	K	0.42	0/2466	0.64	1/3352 (0.0%)
5	L	0.62	0/2956	0.79	1/4012 (0.0%)
6	N	0.64	0/3146	0.77	4/4291 (0.1%)
7	O	0.52	0/51	0.71	0/66
8	P	0.46	0/492	0.79	0/666
All	All	0.59	3/12962 (0.0%)	0.75	9/17593 (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	A	0	4
1	M	0	1
4	K	0	1
5	L	0	1
6	N	0	1
8	P	0	1
9	Z	0	1
All	All	0	10

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Q	146	GLY	C-O	21.12	1.57	1.23
1	Q	146	GLY	CA-C	7.68	1.64	1.51
1	Q	146	GLY	N-CA	6.97	1.56	1.46

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q	146	GLY	CA-C-O	-6.82	108.32	120.60
4	C	73	SER	N-CA-C	-6.73	92.82	111.00
6	N	404	MET	CB-CG-SD	-6.49	92.94	112.40
6	N	79	LEU	CB-CG-CD2	-6.09	100.65	111.00
5	L	405	THR	N-CA-C	5.65	126.25	111.00
6	N	129	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	A	450	CYS	CA-CB-SG	5.05	123.08	114.00
4	K	685	ARG	NE-CZ-NH2	5.01	122.81	120.30
6	N	183	LEU	CB-CA-C	-5.01	100.68	110.20

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	441	GLN	Peptide
1	A	478	TYR	Peptide
1	A	480	TYR	Peptide
1	A	481	HIS	Peptide
4	K	723	PHE	Peptide
5	L	148	TYR	Peptide
1	M	579	MET	Peptide
6	N	219	ALA	Peptide
8	P	239	LEU	Peptide
9	Z	162	UNK	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	867	0	736	21	0
1	M	962	0	898	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Q	496	0	450	10	0
2	B	52	0	49	0	0
3	E	184	0	172	10	0
4	C	1227	0	1249	16	0
4	K	2406	0	2120	70	0
5	L	2881	0	2760	131	0
6	N	3062	0	2908	79	0
7	O	51	0	54	11	0
8	P	484	0	476	6	0
9	Z	674	0	166	19	0
All	All	13346	0	12038	355	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 14.

All (355) 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)
9:Z:25:UNK:CB	9:Z:247:UNK:H	1.19	1.50
4:K:728:TYR:CE1	7:O:25:ALA:HB1	1.52	1.42
9:Z:25:UNK:CB	9:Z:247:UNK:N	1.76	1.37
4:K:440:PHE:O	4:K:444:ILE:HG12	1.23	1.36
4:K:728:TYR:CE1	7:O:25:ALA:CB	2.10	1.33
5:L:125:GLU:O	5:L:133:ARG:N	1.65	1.28
4:K:622:ALA:CB	4:K:735:LYS:HA	1.64	1.25
4:K:728:TYR:CZ	7:O:25:ALA:CB	2.19	1.24
5:L:254:CYS:SG	5:L:309:VAL:CG1	2.29	1.20
5:L:254:CYS:SG	5:L:309:VAL:HG12	1.85	1.14
6:N:246:VAL:CG2	6:N:279:LEU:HB2	1.77	1.13
5:L:125:GLU:HB3	5:L:133:ARG:CB	1.79	1.12
4:K:622:ALA:HB3	4:K:735:LYS:HA	1.32	1.10
4:K:728:TYR:OH	7:O:25:ALA:HB2	1.52	1.10
4:K:728:TYR:CZ	7:O:25:ALA:HB2	1.81	1.09
6:N:246:VAL:HG21	6:N:279:LEU:HB2	1.12	1.08
5:L:123:LEU:O	5:L:124:TYR:CD2	2.11	1.04
5:L:253:SER:HB3	5:L:263:TRP:HZ3	1.18	1.03
5:L:126:CYS:HB3	5:L:436:ARG:HH12	1.21	1.03
5:L:395:ASP:H	5:L:396:PRO:HA	1.23	1.03
6:N:280:SER:O	6:N:289:LEU:HD12	1.60	1.00
4:K:728:TYR:CZ	7:O:25:ALA:HB1	1.89	0.99
5:L:252:MET:CE	5:L:260:LEU:HB3	1.95	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:253:SER:HB3	5:L:263:TRP:CZ3	1.98	0.97
1:A:543:PHE:O	1:A:546:SER:N	1.97	0.97
5:L:253:SER:CB	5:L:263:TRP:HZ3	1.79	0.95
5:L:96:LEU:HD13	5:L:115:THR:CG2	1.98	0.94
5:L:122:THR:HG22	5:L:124:TYR:CE2	2.03	0.93
4:K:440:PHE:O	4:K:444:ILE:CG1	2.17	0.92
5:L:252:MET:HE1	5:L:260:LEU:HB3	1.52	0.91
5:L:113:PHE:HE1	5:L:126:CYS:SG	1.95	0.90
9:Z:153:UNK:O	9:Z:169:UNK:CB	2.21	0.89
1:A:543:PHE:CD1	1:A:546:SER:CB	2.56	0.88
5:L:90:GLU:OE2	5:L:124:TYR:OH	1.92	0.87
5:L:237:ASP:OD2	5:L:256:MET:HB3	1.75	0.86
9:Z:23:UNK:CB	9:Z:31:UNK:O	2.22	0.86
5:L:254:CYS:SG	5:L:309:VAL:HG11	2.16	0.85
5:L:123:LEU:C	5:L:124:TYR:CD2	2.50	0.84
5:L:429:CYS:SG	5:L:433:SER:OG	2.35	0.84
9:Z:25:UNK:CB	9:Z:247:UNK:H2	1.87	0.83
6:N:246:VAL:HG21	6:N:279:LEU:CB	2.05	0.83
5:L:237:ASP:OD2	5:L:256:MET:HG2	1.80	0.82
5:L:395:ASP:N	5:L:396:PRO:HA	1.88	0.82
4:K:622:ALA:HB1	4:K:735:LYS:HA	1.62	0.82
5:L:237:ASP:OD2	5:L:256:MET:CG	2.30	0.80
5:L:237:ASP:OD2	5:L:256:MET:CB	2.30	0.79
9:Z:23:UNK:CB	9:Z:32:UNK:HA	2.13	0.79
5:L:395:ASP:CB	5:L:398:LYS:H	1.95	0.78
1:A:453:CYS:SG	1:A:466:HIS:NE2	2.55	0.78
5:L:96:LEU:HD13	5:L:115:THR:HG23	1.65	0.78
4:C:73:SER:O	4:C:77:LEU:HD11	1.83	0.78
6:N:279:LEU:HD13	6:N:280:SER:N	1.99	0.78
4:K:728:TYR:CD2	4:K:730:GLN:N	2.48	0.77
5:L:96:LEU:HD13	5:L:115:THR:HG21	1.65	0.77
5:L:125:GLU:N	5:L:133:ARG:O	2.17	0.77
4:K:728:TYR:CE1	7:O:25:ALA:HB2	2.00	0.76
6:N:60:ASP:O	6:N:88:ASN:N	2.19	0.75
6:N:88:ASN:O	6:N:89:ASP:HB3	1.86	0.75
4:K:443:LEU:HA	4:K:446:THR:CG2	2.17	0.74
5:L:123:LEU:C	5:L:124:TYR:HD2	1.89	0.73
6:N:86:LEU:HD23	6:N:86:LEU:N	2.03	0.73
1:A:461:TYR:OH	1:A:542:GLU:HA	1.73	0.73
4:K:278:LEU:HD23	1:M:658:LEU:HD21	1.70	0.73
6:N:148:ASP:OD2	6:N:172:ARG:NH2	2.22	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:N:86:LEU:HD23	6:N:86:LEU:H	1.54	0.73
4:K:728:TYR:CD1	7:O:25:ALA:HB1	2.21	0.73
9:Z:24:UNK:O	9:Z:25:UNK:CB	2.37	0.72
3:E:158:LEU:O	3:E:159:THR:HG22	1.90	0.71
1:A:543:PHE:O	1:A:544:LEU:C	2.26	0.71
4:K:446:THR:HG23	4:K:447:TYR:HD1	1.54	0.71
1:A:452:TRP:CH2	3:E:147:LEU:HD22	2.26	0.71
5:L:253:SER:CB	5:L:263:TRP:CZ3	2.67	0.71
6:N:271:ALA:HB1	6:N:301:TRP:CH2	2.25	0.71
1:M:580:GLU:O	1:M:582:ASP:N	2.24	0.70
4:K:728:TYR:HH	7:O:25:ALA:HB2	1.57	0.70
4:K:622:ALA:HB3	4:K:735:LYS:CA	2.16	0.69
1:A:480:TYR:O	1:A:485:ALA:N	2.24	0.69
5:L:113:PHE:CE1	5:L:126:CYS:SG	2.82	0.68
8:P:269:LEU:HD13	9:Z:143:UNK:HA	1.75	0.68
5:L:237:ASP:OD1	5:L:238:GLU:N	2.26	0.68
3:E:145:SER:OG	3:E:162:CYS:SG	2.52	0.68
1:Q:127:ILE:O	1:Q:129:ARG:NH1	2.27	0.68
1:A:452:TRP:CZ3	1:Q:94:THR:HG22	2.29	0.68
5:L:127:HIS:HD2	5:L:131:GLU:O	1.75	0.68
1:M:647:ILE:O	1:M:651:ASN:N	2.27	0.68
5:L:395:ASP:HB3	5:L:398:LYS:H	1.58	0.68
5:L:96:LEU:CD1	5:L:115:THR:HG21	2.23	0.67
5:L:96:LEU:HD22	5:L:115:THR:HG22	1.75	0.67
6:N:241:SER:OG	6:N:256:ASP:OD1	2.11	0.67
5:L:254:CYS:SG	5:L:309:VAL:CB	2.83	0.67
1:A:434:TYR:O	1:A:438:THR:OG1	2.06	0.66
5:L:122:THR:HG22	5:L:124:TYR:HE2	1.61	0.66
6:N:65:ARG:NH1	6:N:118:GLU:OE2	2.28	0.66
5:L:237:ASP:CG	5:L:256:MET:HB3	2.15	0.65
6:N:171:LEU:HD23	6:N:172:ARG:N	2.11	0.65
4:K:565:GLN:NE2	4:K:600:SER:O	2.29	0.65
4:K:647:SER:OG	4:K:649:ASP:OD1	2.08	0.65
1:M:601:GLU:OE2	1:M:615:LYS:NZ	2.30	0.65
5:L:310:ASP:OD2	5:L:322:LYS:NZ	2.30	0.65
4:K:732:ASP:OD1	4:K:732:ASP:N	2.28	0.65
4:K:593:HIS:CE1	4:K:598:ASN:O	2.50	0.64
6:N:61:PHE:HB2	6:N:86:LEU:O	1.97	0.64
5:L:124:TYR:HA	5:L:133:ARG:O	1.98	0.64
6:N:279:LEU:HD13	6:N:279:LEU:C	2.19	0.64
4:K:594:TRP:HB3	1:M:631:GLN:HG2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:254:CYS:SG	5:L:309:VAL:HB	2.38	0.63
6:N:61:PHE:CB	6:N:86:LEU:O	2.45	0.63
5:L:96:LEU:CD1	5:L:115:THR:CG2	2.74	0.63
5:L:405:THR:O	5:L:406:HIS:CG	2.52	0.63
5:L:413:ILE:HG21	5:L:427:ALA:HB1	1.80	0.62
5:L:395:ASP:HB2	5:L:399:ALA:H	1.64	0.62
6:N:344:VAL:HG22	6:N:368:PHE:HB3	1.82	0.62
4:K:622:ALA:CB	4:K:735:LYS:CA	2.60	0.61
5:L:126:CYS:HB3	5:L:436:ARG:NH1	2.05	0.61
5:L:134:LEU:C	5:L:134:LEU:HD12	2.21	0.61
4:K:593:HIS:HB3	4:K:596:SER:O	2.00	0.61
6:N:278:CYS:SG	6:N:323:VAL:HB	2.41	0.61
1:A:452:TRP:CH2	1:Q:94:THR:HG22	2.35	0.61
3:E:159:THR:HG23	3:E:159:THR:O	2.01	0.60
9:Z:25:UNK:O	9:Z:30:UNK:CB	2.48	0.60
6:N:280:SER:O	6:N:289:LEU:CD1	2.43	0.60
6:N:246:VAL:HG23	6:N:279:LEU:HB2	1.78	0.60
6:N:279:LEU:HD11	6:N:281:PHE:CE1	2.36	0.60
6:N:168:ASN:HB2	6:N:170:ASP:OD1	2.02	0.60
3:E:155:GLU:O	3:E:156:ASP:HB2	2.01	0.60
4:K:594:TRP:HA	1:M:631:GLN:HE21	1.66	0.60
1:Q:90:PHE:O	1:Q:94:THR:HG23	2.02	0.60
4:K:442:VAL:O	4:K:446:THR:HG22	2.02	0.60
5:L:252:MET:SD	5:L:261:LYS:O	2.59	0.59
5:L:413:ILE:CG2	5:L:427:ALA:HB1	2.32	0.59
6:N:71:HIS:ND1	6:N:126:GLU:OE1	2.32	0.59
4:K:670:ASN:OD1	4:K:673:PHE:N	2.35	0.59
4:K:662:MET:SD	4:K:732:ASP:HB3	2.43	0.58
6:N:151:VAL:O	6:N:169:PRO:O	2.21	0.58
5:L:359:SER:O	5:L:381:ASN:ND2	2.36	0.58
6:N:173:LEU:HD12	6:N:205:TRP:CD2	2.38	0.58
5:L:122:THR:CG2	5:L:124:TYR:CE2	2.83	0.58
5:L:211:LYS:HA	5:L:238:GLU:HB2	1.86	0.58
9:Z:153:UNK:CB	9:Z:170:UNK:N	2.67	0.57
4:K:627:PHE:CE2	1:M:563:ARG:HD3	2.39	0.57
9:Z:25:UNK:CA	9:Z:247:UNK:N	2.64	0.57
4:K:728:TYR:HD2	4:K:730:GLN:H	1.42	0.57
5:L:207:LEU:HD11	5:L:215:LEU:HD23	1.86	0.57
5:L:319:ILE:HG21	5:L:331:TRP:CZ2	2.40	0.57
3:E:155:GLU:O	3:E:155:GLU:HG3	2.04	0.57
4:K:588:CYS:SG	4:K:589:GLY:N	2.78	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:83:CYS:SG	4:C:84:SER:N	2.78	0.56
4:K:278:LEU:CD2	1:M:658:LEU:HD21	2.36	0.56
5:L:140:ASP:OD1	4:C:101:LEU:HB2	2.05	0.56
5:L:96:LEU:HD22	5:L:116:VAL:O	2.05	0.56
4:K:597:LYS:NZ	4:K:608:ARG:O	2.39	0.56
4:K:728:TYR:HE1	7:O:25:ALA:CB	2.05	0.56
5:L:395:ASP:HB3	5:L:396:PRO:C	2.26	0.55
5:L:176:ASN:O	5:L:180:MET:N	2.39	0.55
4:C:73:SER:HB2	4:C:75:SER:O	2.07	0.55
1:A:525:ILE:HG13	6:N:397:ASN:HD22	1.72	0.55
3:E:155:GLU:HA	3:E:155:GLU:OE1	2.07	0.54
4:K:443:LEU:HA	4:K:446:THR:HG21	1.89	0.54
4:K:728:TYR:OH	7:O:25:ALA:CB	2.32	0.54
6:N:302:ASP:OD2	6:N:304:ARG:NH1	2.40	0.54
5:L:395:ASP:CB	5:L:399:ALA:H	2.20	0.54
5:L:417:SER:O	5:L:425:LEU:HD12	2.07	0.54
4:K:592:ASP:O	4:K:608:ARG:NH2	2.41	0.54
4:C:19:VAL:HG21	4:C:223:ILE:HG22	1.90	0.54
1:M:562:ASN:OD1	1:M:565:TYR:OH	2.24	0.54
5:L:96:LEU:CD2	5:L:116:VAL:O	2.56	0.54
5:L:100:GLN:OE1	5:L:415:GLN:NE2	2.41	0.53
5:L:253:SER:OG	5:L:263:TRP:HZ3	1.90	0.53
6:N:290:ALA:HB2	6:N:325:TRP:CZ2	2.43	0.53
6:N:188:ASN:HB3	6:N:240:GLU:HG2	1.89	0.53
4:K:443:LEU:C	4:K:446:THR:HG22	2.30	0.52
5:L:126:CYS:HA	5:L:132:ILE:HA	1.89	0.52
6:N:177:GLN:N	6:N:199:ASP:OD2	2.42	0.52
5:L:99:VAL:HA	5:L:114:ALA:O	2.10	0.52
9:Z:93:UNK:O	9:Z:94:UNK:CB	2.58	0.52
4:K:728:TYR:CG	4:K:729:SER:N	2.77	0.52
6:N:188:ASN:ND2	6:N:239:HIS:O	2.43	0.52
5:L:403:THR:C	5:L:404:LEU:HD23	2.30	0.52
9:Z:155:UNK:N	9:Z:167:UNK:O	2.43	0.52
5:L:323:SER:OG	5:L:324:CYS:N	2.43	0.51
3:E:151:LYS:CB	3:E:152:PRO:HD3	2.40	0.51
3:E:158:LEU:HD12	3:E:158:LEU:O	2.10	0.51
5:L:195:GLU:OE2	5:L:367:ARG:NH1	2.44	0.51
6:N:66:LEU:HB3	6:N:68:LEU:HD13	1.91	0.51
5:L:199:HIS:NE2	5:L:248:GLY:O	2.43	0.51
5:L:387:TYR:CE1	5:L:403:THR:HG22	2.45	0.50
4:K:619:SER:OG	4:K:620:ASP:N	2.43	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:K:627:PHE:HE2	1:M:563:ARG:HD3	1.76	0.50
5:L:209:VAL:HG22	5:L:215:LEU:HG	1.94	0.50
6:N:370:HIS:NE2	6:N:400:GLN:OE1	2.43	0.50
5:L:96:LEU:HD22	5:L:115:THR:CG2	2.41	0.50
6:N:170:ASP:O	6:N:171:LEU:CB	2.59	0.50
4:K:272:VAL:O	4:K:441:ARG:NH1	2.45	0.50
5:L:317:ASP:OD1	4:C:52:ARG:NH1	2.43	0.50
5:L:371:ASP:OD1	5:L:374:GLN:N	2.45	0.50
6:N:86:LEU:N	6:N:86:LEU:CD2	2.73	0.50
6:N:246:VAL:CG1	6:N:276:VAL:HG12	2.42	0.49
1:A:543:PHE:O	1:A:545:GLU:N	2.45	0.49
5:L:314:TRP:CH2	5:L:319:ILE:HD11	2.47	0.49
6:N:87:PRO:HD3	6:N:112:SER:N	2.27	0.49
4:K:523:CYS:O	4:K:548:GLN:N	2.45	0.49
5:L:253:SER:OG	5:L:263:TRP:CZ3	2.64	0.49
6:N:171:LEU:HD23	6:N:172:ARG:H	1.75	0.49
6:N:295:ASP:OD1	6:N:297:THR:OG1	2.30	0.49
4:K:717:GLN:OE1	4:K:717:GLN:N	2.46	0.49
5:L:371:ASP:OD2	5:L:422:SER:OG	2.31	0.49
5:L:386:LEU:CD1	5:L:425:LEU:HD21	2.42	0.49
9:Z:82:UNK:O	9:Z:84:UNK:N	2.45	0.49
4:K:443:LEU:CA	4:K:446:THR:CG2	2.90	0.49
5:L:173:ARG:HD3	5:L:182:CYS:SG	2.53	0.49
6:N:198:ASP:HA	6:N:229:VAL:HG23	1.95	0.49
5:L:86:ASN:OD1	5:L:87:SER:N	2.46	0.49
4:K:658:TYR:O	4:K:662:MET:N	2.46	0.49
5:L:292:GLN:O	5:L:294:ILE:HD12	2.13	0.49
5:L:405:THR:O	5:L:406:HIS:CD2	2.65	0.49
5:L:98:GLY:H	5:L:116:VAL:CG2	2.26	0.49
6:N:151:VAL:HB	6:N:171:LEU:HB3	1.95	0.49
1:A:452:TRP:HZ3	1:Q:94:THR:HG22	1.75	0.48
4:C:71:LEU:HD21	4:C:96:ILE:CG2	2.43	0.48
6:N:170:ASP:O	6:N:171:LEU:HB2	2.13	0.48
6:N:197:SER:OG	6:N:198:ASP:N	2.46	0.48
6:N:173:LEU:HD13	6:N:217:VAL:HG13	1.95	0.48
4:K:614:LEU:HD13	4:K:626:ILE:HD11	1.95	0.48
5:L:233:GLU:OE1	5:L:233:GLU:HA	2.14	0.48
1:A:510:PRO:O	1:A:512:PHE:N	2.43	0.48
5:L:172:ILE:HG13	5:L:193:ILE:HD13	1.96	0.48
5:L:395:ASP:HB3	5:L:397:HIS:N	2.28	0.48
5:L:404:LEU:C	5:L:405:THR:HG23	2.34	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:607:ASN:OD1	1:M:608:GLU:N	2.46	0.48
5:L:185:HIS:CD2	4:C:104:VAL:HG11	2.49	0.48
6:N:366:LEU:CD1	1:Q:111:LEU:HD11	2.44	0.48
4:K:296:LEU:HD23	4:K:296:LEU:H	1.77	0.48
4:K:687:ALA:O	4:K:726:TYR:OH	2.14	0.48
5:L:417:SER:OG	5:L:418:PHE:N	2.47	0.48
8:P:272:LEU:HD12	8:P:272:LEU:N	2.29	0.48
5:L:311:CYS:SG	5:L:312:VAL:N	2.83	0.47
4:K:279:HIS:O	4:K:283:THR:HG22	2.13	0.47
5:L:334:GLY:N	5:L:349:ASN:O	2.48	0.47
6:N:322:GLN:NE2	6:N:379:ASP:OD1	2.46	0.47
6:N:332:ILE:HD13	6:N:388:TRP:CH2	2.49	0.47
6:N:394:SER:OG	6:N:395:GLU:N	2.48	0.47
4:K:649:ASP:OD1	4:K:650:GLU:N	2.47	0.47
6:N:389:VAL:HG22	6:N:403:GLN:HB2	1.96	0.47
5:L:127:HIS:HB2	5:L:131:GLU:CB	2.44	0.47
4:K:648:GLN:O	4:K:651:ALA:HB3	2.14	0.47
4:K:728:TYR:HD2	4:K:730:GLN:N	2.07	0.47
6:N:316:HIS:NE2	6:N:343:ASN:OD1	2.48	0.47
6:N:373:HIS:CD2	6:N:377:ILE:HD11	2.50	0.47
5:L:252:MET:HE2	5:L:260:LEU:HD22	1.97	0.47
6:N:339:ASP:HA	8:P:286:ARG:NH2	2.30	0.46
6:N:176:HIS:NE2	6:N:196:ALA:O	2.49	0.46
5:L:88:LEU:HD23	5:L:89:LYS:N	2.31	0.46
6:N:189:LEU:HD23	6:N:192:HIS:CD2	2.51	0.46
6:N:285:SER:OG	6:N:286:GLU:N	2.48	0.46
4:K:611:LYS:HE3	1:M:585:ASP:HB3	1.98	0.46
6:N:246:VAL:HG13	6:N:276:VAL:HG12	1.98	0.46
5:L:215:LEU:HD11	5:L:253:SER:HB2	1.97	0.46
5:L:101:PHE:CE1	5:L:426:ILE:HD13	2.51	0.46
5:L:387:TYR:HA	5:L:402:THR:O	2.16	0.45
1:Q:115:LEU:HD21	1:Q:117:TYR:CE2	2.50	0.45
4:K:593:HIS:HB3	4:K:596:SER:C	2.36	0.45
5:L:405:THR:HB	5:L:406:HIS:H	1.54	0.45
4:K:691:VAL:O	4:K:691:VAL:HG12	2.16	0.45
6:N:225:GLY:HA3	6:N:255:TRP:HZ2	1.82	0.45
4:K:523:CYS:N	4:K:547:CYS:SG	2.86	0.45
5:L:336:MET:HG2	5:L:351:THR:HG23	1.98	0.45
4:K:592:ASP:O	4:K:593:HIS:HB2	2.17	0.45
4:K:451:PHE:HD2	4:K:452:CYS:HG	1.63	0.45
4:K:695:CYS:SG	4:K:722:LEU:HD22	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:Z:93:UNK:C	9:Z:95:UNK:N	2.78	0.45
5:L:234:GLY:O	5:L:235:HIS:CG	2.70	0.45
1:M:610:GLU:O	1:M:613:VAL:HG12	2.17	0.45
1:A:492:ASN:OD1	1:A:493:GLU:N	2.50	0.45
5:L:404:LEU:N	5:L:404:LEU:HD23	2.31	0.45
5:L:92:HIS:ND1	5:L:94:GLN:OE1	2.47	0.45
6:N:271:ALA:HB1	6:N:301:TRP:CZ2	2.52	0.44
1:Q:103:ARG:O	1:Q:106:ILE:N	2.47	0.44
5:L:395:ASP:N	5:L:396:PRO:CA	2.71	0.44
6:N:279:LEU:CD1	6:N:279:LEU:C	2.86	0.44
6:N:271:ALA:HB1	6:N:301:TRP:HH2	1.77	0.44
9:Z:78:UNK:N	9:Z:173:UNK:O	2.50	0.44
9:Z:63:UNK:N	9:Z:88:UNK:O	2.51	0.44
5:L:237:ASP:O	5:L:238:GLU:O	2.36	0.44
5:L:234:GLY:O	5:L:235:HIS:CD2	2.70	0.44
6:N:77:ASN:ND2	6:N:125:GLY:O	2.50	0.44
4:K:588:CYS:SG	4:K:590:ALA:N	2.90	0.44
5:L:134:LEU:HG	4:C:96:ILE:HG13	2.00	0.44
6:N:292:GLY:O	6:N:293:SER:OG	2.34	0.44
1:A:442:THR:OG1	1:A:443:GLU:N	2.50	0.44
8:P:267:VAL:HG22	8:P:269:LEU:O	2.18	0.44
6:N:236:HIS:CB	6:N:242:LEU:HD12	2.48	0.44
5:L:122:THR:O	5:L:124:TYR:CE2	2.71	0.43
6:N:180:GLY:HA3	6:N:197:SER:HA	2.00	0.43
5:L:98:GLY:CA	5:L:116:VAL:HG22	2.48	0.43
5:L:127:HIS:CD2	5:L:131:GLU:O	2.64	0.43
1:A:442:THR:O	1:A:443:GLU:CB	2.66	0.43
6:N:19:GLU:HG3	8:P:239:LEU:HD11	2.01	0.43
5:L:376:MET:HE1	5:L:388:VAL:HG11	2.00	0.43
4:C:73:SER:C	4:C:75:SER:N	2.69	0.43
5:L:232:VAL:HG13	5:L:233:GLU:N	2.34	0.43
5:L:404:LEU:C	5:L:405:THR:CG2	2.87	0.43
6:N:53:VAL:HG21	6:N:385:ASN:CB	2.48	0.43
4:C:72:THR:O	4:C:72:THR:HG22	2.19	0.43
4:K:639:SER:OG	4:K:640:GLU:N	2.52	0.42
5:L:234:GLY:O	5:L:261:LYS:HE3	2.19	0.42
4:K:617:ALA:HB3	4:K:627:PHE:CE2	2.54	0.42
6:N:88:ASN:O	6:N:89:ASP:CB	2.60	0.42
4:C:61:LYS:O	4:C:64:ARG:NH1	2.53	0.42
5:L:395:ASP:CG	5:L:399:ALA:H	2.21	0.42
1:Q:116:THR:OG1	1:Q:117:TYR:N	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:481:HIS:CB	1:A:485:ALA:H	2.33	0.42
5:L:252:MET:HE3	5:L:260:LEU:HB3	1.89	0.42
6:N:173:LEU:HD12	6:N:205:TRP:CG	2.55	0.42
6:N:40:LEU:N	6:N:397:ASN:O	2.53	0.42
4:K:689:HIS:NE2	4:K:730:GLN:OE1	2.51	0.42
4:C:49:ILE:O	4:C:53:THR:HG22	2.20	0.42
5:L:91:ASP:OD1	5:L:120:ARG:NH1	2.53	0.42
5:L:91:ASP:OD2	4:C:84:SER:N	2.53	0.42
1:M:647:ILE:HG23	1:M:652:LEU:HB2	2.01	0.42
9:Z:79:UNK:N	9:Z:121:UNK:O	2.53	0.42
1:M:606:VAL:HG23	1:M:611:LYS:HE3	2.01	0.41
1:A:461:TYR:CE1	1:A:465:LYS:HD2	2.55	0.41
5:L:197:LYS:O	5:L:206:LEU:HD12	2.20	0.41
4:K:679:ARG:NH2	5:L:236:ARG:NH2	2.68	0.41
6:N:246:VAL:HG13	6:N:276:VAL:CG1	2.49	0.41
4:K:593:HIS:NE2	4:K:598:ASN:O	2.53	0.41
5:L:285:THR:OG1	5:L:286:ASN:N	2.54	0.41
5:L:375:LYS:HG2	5:L:392:GLU:OE2	2.21	0.41
5:L:397:HIS:ND1	5:L:398:LYS:HG3	2.35	0.41
4:C:176:ASN:O	4:C:180:GLN:N	2.54	0.41
4:K:443:LEU:CA	4:K:446:THR:HG22	2.51	0.41
5:L:385:LYS:HZ1	5:L:403:THR:HG21	1.84	0.41
6:N:210:VAL:HG13	6:N:210:VAL:O	2.21	0.41
1:A:450:CYS:SG	1:A:471:HIS:NE2	2.92	0.41
5:L:122:THR:HG21	5:L:124:TYR:OH	2.21	0.41
3:E:158:LEU:HD12	3:E:158:LEU:C	2.40	0.41
6:N:28:THR:N	6:N:29:PRO:CD	2.84	0.41
1:M:574:LEU:HD23	1:M:575:ARG:O	2.21	0.41
6:N:53:VAL:HG21	6:N:385:ASN:HB3	2.03	0.41
6:N:80:VAL:O	6:N:81:ILE:HD13	2.21	0.41
8:P:281:ASP:N	8:P:281:ASP:OD1	2.54	0.41
9:Z:21:UNK:O	9:Z:22:UNK:CB	2.69	0.41
1:A:448:LEU:HD23	1:A:448:LEU:O	2.21	0.41
4:C:15:TRP:O	4:C:19:VAL:HG23	2.21	0.41
4:K:443:LEU:C	4:K:446:THR:CG2	2.90	0.41
5:L:122:THR:CG2	5:L:124:TYR:HE2	2.25	0.41
5:L:291:SER:O	5:L:293:LYS:N	2.54	0.41
5:L:171:ILE:HG22	5:L:172:ILE:N	2.36	0.40
5:L:237:ASP:HB3	5:L:257:ASP:HB3	2.04	0.40
5:L:433:SER:OG	5:L:435:TRP:NE1	2.47	0.40
6:N:256:ASP:OD2	6:N:258:ARG:NH1	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:N:23:ILE:HD11	1:Q:109:ILE:HD12	2.03	0.40
6:N:140:ILE:HD13	6:N:140:ILE:HG21	1.89	0.40
5:L:122:THR:HG22	5:L:124:TYR:CZ	2.50	0.40
6:N:43:PRO:HD2	6:N:71:HIS:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	121/739 (16%)	85 (70%)	30 (25%)	6 (5%)	2	24
1	M	120/739 (16%)	105 (88%)	13 (11%)	2 (2%)	11	49
1	Q	64/739 (9%)	45 (70%)	18 (28%)	1 (2%)	11	50
2	B	4/345 (1%)	4 (100%)	0	0	100	100
3	E	25/345 (7%)	15 (60%)	6 (24%)	4 (16%)	0	3
4	C	140/746 (19%)	128 (91%)	12 (9%)	0	100	100
4	K	319/746 (43%)	275 (86%)	41 (13%)	3 (1%)	20	63
5	L	360/441 (82%)	299 (83%)	57 (16%)	4 (1%)	17	59
6	N	382/425 (90%)	326 (85%)	53 (14%)	3 (1%)	22	65
7	O	5/7 (71%)	4 (80%)	1 (20%)	0	100	100
8	P	62/295 (21%)	43 (69%)	18 (29%)	1 (2%)	11	50
All	All	1602/5567 (29%)	1329 (83%)	249 (16%)	24 (2%)	17	52

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	442	THR
1	A	481	HIS

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Mol	Chain	Res	Type
3	E	160	PHE
5	L	238	GLU
1	M	581	VAL
1	A	443	GLU
1	A	511	GLY
3	E	144	ILE
3	E	156	ASP
5	L	192	ALA
1	M	580	GLU
6	N	171	LEU
6	N	214	GLY
1	Q	131	THR
5	L	400	LYS
6	N	89	ASP
1	A	533	PRO
3	E	159	THR
1	A	544	LEU
8	P	273	PRO
4	K	459	GLY
4	K	580	CYS
5	L	395	ASP
4	K	558	PRO

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	73/646 (11%)	72 (99%)	1 (1%)	71	89
1	M	101/646 (16%)	100 (99%)	1 (1%)	80	91
1	Q	45/646 (7%)	45 (100%)	0	100	100
2	B	2/294 (1%)	2 (100%)	0	100	100
3	E	19/295 (6%)	18 (95%)	1 (5%)	26	63
4	C	138/667 (21%)	138 (100%)	0	100	100
4	K	233/667 (35%)	231 (99%)	2 (1%)	82	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	L	311/392 (79%)	302 (97%)	9 (3%)	48	78
6	N	341/375 (91%)	329 (96%)	12 (4%)	41	75
7	O	3/3 (100%)	3 (100%)	0	100	100
8	P	50/263 (19%)	49 (98%)	1 (2%)	60	84
All	All	1316/4894 (27%)	1289 (98%)	27 (2%)	62	84

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	494	CYS
3	E	158	LEU
4	K	653	ARG
4	K	732	ASP
5	L	109	ASP
5	L	134	LEU
5	L	149	THR
5	L	169	ARG
5	L	269	ARG
5	L	286	ASN
5	L	342	LYS
5	L	420	ARG
5	L	436	ARG
1	M	563	ARG
6	N	35	VAL
6	N	55	ARG
6	N	68	LEU
6	N	79	LEU
6	N	86	LEU
6	N	115	ILE
6	N	193	LEU
6	N	258	ARG
6	N	300	LEU
6	N	332	ILE
6	N	393	VAL
6	N	401	VAL
8	P	286	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
4	K	593	HIS
5	L	127	HIS
6	N	88	ASN
6	N	192	HIS
6	N	226	HIS
6	N	328	HIS
8	P	290	GLN
4	C	117	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	M3L	B	116	2	11,11,12	0.54	0	11,14,16	0.91	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	M3L	B	116	2	-	0/8/10/12	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
9	Z	6

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	Z	182:UNK	C	247:UNK	N	39.28
1	Z	45:UNK	C	55:UNK	N	34.04
1	Z	67:UNK	C	77:UNK	N	29.09
1	Z	138:UNK	C	143:UNK	N	26.06
1	Z	99:UNK	C	120:UNK	N	9.78
1	Z	25:UNK	C	30:UNK	N	2.87