

Nov 29, 2022 – 03:59 AM EST

PDB ID	:	7UWK
EMDB ID	:	EMD-26834
Title	:	Structure of the higher-order IL-25-IL-17RB complex
Authors	:	Wilson, S.C.; Caveney, N.A.; Jude, K.M.; Garcia, K.C.
Deposited on	:	2022-05-03
Resolution	:	4.40 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org* A user guide is available at https://www.wwpdb.org/validation/2017/EMValidationReportHelp with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

:	0.0.1. dev 43
:	4.02b-467
:	20191225.v01 (using entries in the PDB archive December 25th 2019)
:	1.9.9
:	Engh & Huber (2001)
:	Parkinson et al. (1996)
:	2.31.2
	: : : : :

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 4.40 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)	${f EM} {f structures} \ (\#{f Entries})$	
Clashscore	158937	4297	
Ramachandran outliers	154571	4023	
Sidechain outliers	154315	3826	

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for $\geq=3, 2, 1$ and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq=5\%$ The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain				
1	А	188	28%	14%	·	49	%
1	В	188	26% 32%	21%		47	%
1	Е	188	32%	18%	•	49%	6
1	F	188	13%	20%		49%	6
1	G	188	29%	24%	•	4	7%
1	Н	188	27%	26%	•	4	7%
2	С	305	39% 48%			33%	19%
2	D	305	599	6		18%	23%



Mol	Chain	Length	Quality of chain				
2	Ι	305	30%	26%	• 18%		
2	J	305	33% 50%	30%	20%		
2	K	305	34% 56%	23%	20%		
2	L	305	26%	25%	17%		



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 16064 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.

Mol	Chain	Residues		Atoms					Trace
1	Δ	96	Total	С	Ν	Ο	S	0	0
1	Π	30	771	475	154	133	9	0	0
1	В	100	Total	С	Ν	Ο	\mathbf{S}	0	0
1	D	100	806	496	161	140	9	0	0
1	F	06	Total	С	Ν	Ο	\mathbf{S}	0	0
1	Ľ	90	780	481	157	133	9	0	0
1	С	100	Total	С	Ν	0	\mathbf{S}	0	0
1	G	100	808	497	161	141	9	0	0
1	F	06	Total	С	Ν	0	\mathbf{S}	0	0
1	Г	г 90	778	480	157	132	9	0	0
1	Ч	100	Total	С	Ν	0	S	0	0
	11	100	803	494	159	141	9		

• Molecule 1 is a protein called Interleukin-25.

There are 240 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	26	ASP	-	expression tag	UNP Q9H293
А	27	ALA	-	expression tag	UNP Q9H293
А	28	SER	-	expression tag	UNP Q9H293
A	29	ALA	-	expression tag	UNP Q9H293
А	178	ALA	-	expression tag	UNP Q9H293
А	179	PRO	-	expression tag	UNP Q9H293
А	180	ALA	-	expression tag	UNP Q9H293
A	181	ALA	-	expression tag	UNP Q9H293
А	182	LEU	-	expression tag	UNP Q9H293
А	183	GLU	-	expression tag	UNP Q9H293
А	184	VAL	-	expression tag	UNP Q9H293
А	185	LEU	-	expression tag	UNP Q9H293
А	186	PHE	-	expression tag	UNP Q9H293
А	187	GLN	-	expression tag	UNP Q9H293
А	188	GLY	-	expression tag	UNP Q9H293
А	189	PRO	-	expression tag	UNP Q9H293
А	190	GLY	-	expression tag	UNP Q9H293
А	191	ALA	-	expression tag	UNP Q9H293



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Chain	Residue	Modelled	Actual	Comment	Reference		
А	192	ALA	-	expression tag	UNP Q9H293		
A	193	GLY	-	expression tag	UNP Q9H293		
A	194	LEU	-	expression tag	UNP Q9H293		
А	195	ASN	-	expression tag	UNP Q9H293		
А	196	ASP	-	expression tag	UNP Q9H293		
А	197	ILE	-	expression tag	UNP Q9H293		
А	198	PHE	-	expression tag	UNP Q9H293		
А	199	GLU	-	expression tag	UNP Q9H293		
А	200	ALA	-	expression tag	UNP Q9H293		
А	201	GLN	-	expression tag	UNP Q9H293		
А	202	LYS	-	expression tag	UNP Q9H293		
А	203	ILE	-	expression tag	UNP Q9H293		
А	204	GLU	-	expression tag	UNP Q9H293		
А	205	TRP	-	expression tag	UNP Q9H293		
А	206	HIS	-	expression tag	UNP Q9H293		
А	207	GLU	-	expression tag	UNP Q9H293		
А	208	HIS	-	expression tag	UNP Q9H293		
А	209	HIS	-	expression tag	UNP Q9H293		
А	210	HIS	-	expression tag	UNP Q9H293		
А	211	HIS	-	expression tag	UNP Q9H293		
А	212	HIS	-	expression tag	UNP Q9H293		
А	213	HIS	-	expression tag	UNP Q9H293		
В	26	ASP	-	expression tag	UNP Q9H293		
В	27	ALA	-	expression tag	UNP Q9H293		
В	28	SER	-	expression tag	UNP Q9H293		
В	29	ALA	-	expression tag	UNP Q9H293		
В	178	ALA	-	expression tag	UNP Q9H293		
В	179	PRO	-	expression tag	UNP Q9H293		
В	180	ALA	-	expression tag	UNP Q9H293		
В	181	ALA	-	expression tag	UNP Q9H293		
В	182	LEU	-	expression tag	UNP Q9H293		
В	183	GLU	-	expression tag	UNP Q9H293		
В	184	VAL	-	expression tag	UNP Q9H293		
В	185	LEU	-	expression tag	UNP Q9H293		
В	186	PHE	-	expression tag	UNP Q9H293		
В	187	GLN	-	expression tag	UNP Q9H293		
В	188	GLY	-	expression tag	UNP Q9H293		
В	189	PRO	-	expression tag	UNP Q9H293		
В	190	GLY	-	expression tag	UNP Q9H293		
В	191	ALA	-	expression tag	UNP Q9H293		
В	192	ALA	-	expression tag	UNP Q9H293		
В	193	GLY	-	expression tag	UNP Q9H293		

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Chain	Residue	Modelled	Actual	Comment	Reference		
В	194	LEU	-	expression tag	UNP Q9H293		
В	195	ASN	-	expression tag	UNP Q9H293		
В	196	ASP	-	expression tag	UNP Q9H293		
В	197	ILE	-	expression tag	UNP Q9H293		
В	198	PHE	-	expression tag	UNP Q9H293		
В	199	GLU	-	expression tag	UNP Q9H293		
В	200	ALA	-	expression tag	UNP Q9H293		
В	201	GLN	-	expression tag	UNP Q9H293		
В	202	LYS	-	expression tag	UNP Q9H293		
В	203	ILE	-	expression tag	UNP Q9H293		
В	204	GLU	-	expression tag	UNP Q9H293		
В	205	TRP	-	expression tag	UNP Q9H293		
В	206	HIS	-	expression tag	UNP Q9H293		
В	207	GLU	-	expression tag	UNP Q9H293		
В	208	HIS	-	expression tag	UNP Q9H293		
В	209	HIS	-	expression tag	UNP Q9H293		
В	210	HIS	-	expression tag	UNP Q9H293		
В	211	HIS	-	expression tag	UNP Q9H293		
В	212	HIS	-	expression tag	UNP Q9H293		
В	213	HIS	-	expression tag	UNP Q9H293		
Е	26	ASP	-	expression tag	UNP Q9H293		
Е	27	ALA	-	expression tag	UNP Q9H293		
Е	28	SER	-	expression tag	UNP Q9H293		
Е	29	ALA	-	expression tag	UNP Q9H293		
Е	178	ALA	-	expression tag	UNP Q9H293		
Е	179	PRO	-	expression tag	UNP Q9H293		
Е	180	ALA	-	expression tag	UNP Q9H293		
Е	181	ALA	-	expression tag	UNP Q9H293		
Е	182	LEU	-	expression tag	UNP Q9H293		
Е	183	GLU	-	expression tag	UNP Q9H293		
Е	184	VAL	-	expression tag	UNP Q9H293		
Е	185	LEU	-	expression tag	UNP Q9H293		
Е	186	PHE	-	expression tag	UNP Q9H293		
Е	187	GLN	-	expression tag	UNP Q9H293		
Е	188	GLY	-	expression tag	UNP Q9H293		
Е	189	PRO	-	expression tag	UNP Q9H293		
Е	190	GLY	-	expression tag	UNP Q9H293		
Е	191	ALA	-	expression tag	UNP Q9H293		
Е	192	ALA	-	expression tag	UNP Q9H293		
Е	193	GLY	-	expression tag	UNP Q9H293		
Е	194	LEU	-	expression tag	UNP Q9H293		
Е	195	ASN	-	expression tag	UNP Q9H293		

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Chain	Residue	Modelled	Actual	Comment	Reference	
E	196	ASP	-	expression tag	UNP Q9H293	
E	197	ILE	-	expression tag	UNP Q9H293	
E	198	PHE	-	expression tag	UNP Q9H293	
Е	199	GLU	-	expression tag	UNP Q9H293	
Е	200	ALA	-	expression tag	UNP Q9H293	
Е	201	GLN	-	expression tag	UNP Q9H293	
Е	202	LYS	-	expression tag	UNP Q9H293	
Е	203	ILE	-	expression tag	UNP Q9H293	
Е	204	GLU	-	expression tag	UNP Q9H293	
Е	205	TRP	-	expression tag	UNP Q9H293	
Е	206	HIS	-	expression tag	UNP Q9H293	
Е	207	GLU	-	expression tag	UNP Q9H293	
Е	208	HIS	-	expression tag	UNP Q9H293	
Е	209	HIS	-	expression tag	UNP Q9H293	
Е	210	HIS	-	expression tag	UNP Q9H293	
Е	211	HIS	-	expression tag	UNP Q9H293	
Е	212	HIS	-	expression tag	UNP Q9H293	
Е	213	HIS	-	expression tag	UNP Q9H293	
G	26	ASP	-	expression tag	UNP Q9H293	
G	27	ALA	-	expression tag	UNP Q9H293	
G	28	SER	-	expression tag	UNP Q9H293	
G	29	ALA	-	expression tag	UNP Q9H293	
G	178	ALA	-	expression tag	UNP Q9H293	
G	179	PRO	-	expression tag	UNP Q9H293	
G	180	ALA	-	expression tag	UNP Q9H293	
G	181	ALA	-	expression tag	UNP Q9H293	
G	182	LEU	-	expression tag	UNP Q9H293	
G	183	GLU	-	expression tag	UNP Q9H293	
G	184	VAL	-	expression tag	UNP Q9H293	
G	185	LEU	-	expression tag	UNP Q9H293	
G	186	PHE	-	expression tag	UNP Q9H293	
G	187	GLN	-	expression tag	UNP Q9H293	
G	188	GLY	-	expression tag	UNP Q9H293	
G	189	PRO	-	expression tag	UNP Q9H293	
G	190	GLY	-	expression tag	UNP Q9H293	
G	191	ALA	-	expression tag	UNP Q9H293	
G	192	ALA	-	expression tag	UNP Q9H293	
G	193	GLY	-	expression tag	UNP Q9H293	
G	194	LEU	-	expression tag	UNP Q9H293	
G	195	ASN	-	expression tag	UNP Q9H293	
G	196	ASP	-	expression tag	UNP Q9H293	
G	197	ILE	-	expression tag	UNP Q9H293	

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Chain	Residue	Modelled	Actual	Comment	Reference		
G	198	PHE	-	expression tag	UNP Q9H293		
G	199	GLU	-	expression tag	UNP Q9H293		
G	200	ALA	-	expression tag	UNP Q9H293		
G	201	GLN	-	expression tag	UNP Q9H293		
G	202	LYS	-	expression tag	UNP Q9H293		
G	203	ILE	-	expression tag	UNP Q9H293		
G	204	GLU	-	expression tag	UNP Q9H293		
G	205	TRP	-	expression tag	UNP Q9H293		
G	206	HIS	-	expression tag	UNP Q9H293		
G	207	GLU	-	expression tag	UNP Q9H293		
G	208	HIS	-	expression tag	UNP Q9H293		
G	209	HIS	-	expression tag	UNP Q9H293		
G	210	HIS	-	expression tag	UNP Q9H293		
G	211	HIS	-	expression tag	UNP Q9H293		
G	212	HIS	-	expression tag	UNP Q9H293		
G	213	HIS	-	expression tag	UNP Q9H293		
F	26	ASP	-	expression tag	UNP Q9H293		
F	27	ALA	-	expression tag	UNP Q9H293		
F	28	SER	-	expression tag	UNP Q9H293		
F	29	ALA	-	expression tag	UNP Q9H293		
F	178	ALA	-	expression tag	UNP Q9H293		
F	179	PRO	-	expression tag	UNP Q9H293		
F	180	ALA	-	expression tag	UNP Q9H293		
F	181	ALA	-	expression tag	UNP Q9H293		
F	182	LEU	-	expression tag	UNP Q9H293		
F	183	GLU	-	expression tag	UNP Q9H293		
F	184	VAL	-	expression tag	UNP Q9H293		
F	185	LEU	-	expression tag	UNP Q9H293		
F	186	PHE	-	expression tag	UNP Q9H293		
F	187	GLN	-	expression tag	UNP Q9H293		
F	188	GLY	-	expression tag	UNP Q9H293		
F	189	PRO	-	expression tag	UNP Q9H293		
F	190	GLY	-	expression tag	UNP Q9H293		
F	191	ALA	-	expression tag	UNP Q9H293		
F	192	ALA	-	expression tag	UNP Q9H293		
F	193	GLY	-	expression tag	UNP Q9H293		
F	194	LEU	-	expression tag	UNP Q9H293		
F	195	ASN	-	expression tag	UNP Q9H293		
F	196	ASP	-	expression tag	UNP Q9H293		
F	197	ILE	-	expression tag	UNP Q9H293		
F	198	PHE	-	expression tag	UNP Q9H293		
F	199	GLU	-	expression tag	UNP Q9H293		

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Chain	Residue	Modelled	Actual	Comment	Reference	
F	200	ALA	-	expression tag	UNP Q9H293	
F	201	GLN	-	expression tag	UNP Q9H293	
F	202	LYS	-	expression tag	UNP Q9H293	
F	203	ILE	-	expression tag	UNP Q9H293	
F	204	GLU	-	expression tag	UNP Q9H293	
F	205	TRP	-	expression tag	UNP Q9H293	
F	206	HIS	-	expression tag	UNP Q9H293	
F	207	GLU	-	expression tag	UNP Q9H293	
F	208	HIS	-	expression tag	UNP Q9H293	
F	209	HIS	-	expression tag	UNP Q9H293	
F	210	HIS	-	expression tag	UNP Q9H293	
F	211	HIS	-	expression tag	UNP Q9H293	
F	212	HIS	-	expression tag	UNP Q9H293	
F	213	HIS	-	expression tag	UNP Q9H293	
Н	26	ASP	-	expression tag	UNP Q9H293	
Н	27	ALA	-	expression tag	UNP Q9H293	
Н	28	SER	-	expression tag	UNP Q9H293	
Н	29	ALA	-	expression tag	UNP Q9H293	
Н	178	ALA	-	expression tag	UNP Q9H293	
Н	179	PRO	-	expression tag	UNP Q9H293	
Н	180	ALA	-	expression tag	UNP Q9H293	
Н	181	ALA	-	expression tag	UNP Q9H293	
Н	182	LEU	-	expression tag	UNP Q9H293	
Н	183	GLU	-	expression tag	UNP Q9H293	
Н	184	VAL	-	expression tag	UNP Q9H293	
Н	185	LEU	-	expression tag	UNP Q9H293	
Н	186	PHE	-	expression tag	UNP Q9H293	
Н	187	GLN	-	expression tag	UNP Q9H293	
Н	188	GLY	-	expression tag	UNP Q9H293	
Н	189	PRO	-	expression tag	UNP Q9H293	
Н	190	GLY	-	expression tag	UNP Q9H293	
Н	191	ALA	-	expression tag	UNP Q9H293	
Н	192	ALA	-	expression tag	UNP Q9H293	
Н	193	GLY	-	expression tag	UNP Q9H293	
Н	194	LEU	-	expression tag	UNP Q9H293	
Н	195	ASN	-	expression tag	UNP Q9H293	
Н	196	ASP	-	expression tag	UNP Q9H293	
Н	197	ILE	-	expression tag	UNP Q9H293	
Н	198	PHE	-	expression tag	UNP Q9H293	
Н	199	GLU	-	expression tag	UNP Q9H293	
Н	200	ALA	-	expression tag	UNP Q9H293	
Н	201	GLN	-	expression tag	UNP Q9H293	

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Chain	Residue	Modelled	Actual	Comment	Reference
Н	202	LYS	-	expression tag	UNP Q9H293
Н	203	ILE	-	expression tag	UNP Q9H293
H	204	GLU	-	expression tag	UNP Q9H293
Н	205	TRP	-	expression tag	UNP Q9H293
Н	206	HIS	-	expression tag	UNP Q9H293
Н	207	GLU	-	expression tag	UNP Q9H293
Н	208	HIS	-	expression tag	UNP Q9H293
Н	209	HIS	-	expression tag	UNP Q9H293
Н	210	HIS	-	expression tag	UNP Q9H293
Н	211	HIS	-	expression tag	UNP Q9H293
H	212	HIS	-	expression tag	UNP Q9H293
H	213	HIS	-	expression tag	UNP Q9H293

• Molecule 2 is a protein called Interleukin-17 receptor B.

Mol	Chain	Residues		At	oms			AltConf	Trace
2	С	247	Total	С	Ν	0	S	0	0
	Ŭ	211	1899	1200	325	358	16	0	Ū
2	л	225	Total	\mathbf{C}	Ν	Ο	\mathbf{S}	0	0
	D	230	1804	1145	310	334	15	0	0
9	Т	249	Total	С	Ν	0	S	0	0
	1		1917	1212	326	363	16	0	0
9	K	244	Total	С	Ν	0	S	0	0
	Γ	244	1879	1189	321	353	16	0	0
0	т	244	Total	С	Ν	0	S	0	0
	244	1875	1189	319	351	16	0	0	
0	т	252	Total	С	Ν	0	S	0	0
		232	1944	1230	332	366	16	U	U

There are 204 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
С	289	ALA	-	expression tag	UNP Q9NRM6
С	290	ALA	-	expression tag	UNP Q9NRM6
С	291	ALA	-	expression tag	UNP Q9NRM6
С	292	LEU	-	expression tag	UNP Q9NRM6
С	293	GLU	-	expression tag	UNP Q9NRM6
С	294	VAL	-	expression tag	UNP Q9NRM6
C	295	LEU	-	expression tag	UNP Q9NRM6
С	296	PHE	-	expression tag	UNP Q9NRM6
C	297	GLN	-	expression tag	UNP Q9NRM6
C	298	GLY	_	expression tag	UNP Q9NRM6



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Chain	Residue	Modelled	Actual	Comment	Reference
C	299	PRO	-	expression tag	UNP Q9NRM6
C	300	GLY	-	expression tag	UNP Q9NRM6
C	301	ALA	-	expression tag	UNP Q9NRM6
С	302	ALA	-	expression tag	UNP Q9NRM6
C	303	GLU	-	expression tag	UNP Q9NRM6
C	304	ASP	-	expression tag	UNP Q9NRM6
С	305	GLN	-	expression tag	UNP Q9NRM6
C	306	VAL	-	expression tag	UNP Q9NRM6
С	307	ASP	-	expression tag	UNP Q9NRM6
С	308	PRO	-	expression tag	UNP Q9NRM6
C	309	ARG	-	expression tag	UNP Q9NRM6
С	310	LEU	-	expression tag	UNP Q9NRM6
С	311	ILE	-	expression tag	UNP Q9NRM6
С	312	ASP	-	expression tag	UNP Q9NRM6
С	313	GLY	-	expression tag	UNP Q9NRM6
С	314	LYS	-	expression tag	UNP Q9NRM6
С	315	HIS	-	expression tag	UNP Q9NRM6
С	316	HIS	-	expression tag	UNP Q9NRM6
С	317	HIS	-	expression tag	UNP Q9NRM6
С	318	HIS	-	expression tag	UNP Q9NRM6
С	319	HIS	-	expression tag	UNP Q9NRM6
С	320	HIS	-	expression tag	UNP Q9NRM6
С	321	HIS	-	expression tag	UNP Q9NRM6
С	322	HIS	-	expression tag	UNP Q9NRM6
D	289	ALA	-	expression tag	UNP Q9NRM6
D	290	ALA	-	expression tag	UNP Q9NRM6
D	291	ALA	-	expression tag	UNP Q9NRM6
D	292	LEU	-	expression tag	UNP Q9NRM6
D	293	GLU	-	expression tag	UNP Q9NRM6
D	294	VAL	-	expression tag	UNP Q9NRM6
D	295	LEU	-	expression tag	UNP Q9NRM6
D	296	PHE	-	expression tag	UNP Q9NRM6
D	297	GLN	-	expression tag	UNP Q9NRM6
D	298	GLY	-	expression tag	UNP Q9NRM6
D	299	PRO	-	expression tag	UNP Q9NRM6
D	300	GLY	-	expression tag	UNP Q9NRM6
D	301	ALA	-	expression tag	UNP Q9NRM6
D	302	ALA	-	expression tag	UNP Q9NRM6
D	303	GLU	-	expression tag	UNP Q9NRM6
D	304	ASP	-	expression tag	UNP Q9NRM6
D	305	GLN	-	expression tag	UNP Q9NRM6
D	306	VAL	-	expression tag	UNP Q9NRM6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	307	ASP	-	expression tag	UNP Q9NRM6
D	308	PRO	-	expression tag	UNP Q9NRM6
D	309	ARG	-	expression tag	UNP Q9NRM6
D	310	LEU	-	expression tag	UNP Q9NRM6
D	311	ILE	-	expression tag	UNP Q9NRM6
D	312	ASP	-	expression tag	UNP Q9NRM6
D	313	GLY	-	expression tag	UNP Q9NRM6
D	314	LYS	-	expression tag	UNP Q9NRM6
D	315	HIS	-	expression tag	UNP Q9NRM6
D	316	HIS	-	expression tag	UNP Q9NRM6
D	317	HIS	-	expression tag	UNP Q9NRM6
D	318	HIS	-	expression tag	UNP Q9NRM6
D	319	HIS	-	expression tag	UNP Q9NRM6
D	320	HIS	-	expression tag	UNP Q9NRM6
D	321	HIS	-	expression tag	UNP Q9NRM6
D	322	HIS	-	expression tag	UNP Q9NRM6
Ι	289	ALA	-	expression tag	UNP Q9NRM6
Ι	290	ALA	-	expression tag	UNP Q9NRM6
Ι	291	ALA	-	expression tag	UNP Q9NRM6
Ι	292	LEU	-	expression tag	UNP Q9NRM6
Ι	293	GLU	-	expression tag	UNP Q9NRM6
Ι	294	VAL	-	expression tag	UNP Q9NRM6
Ι	295	LEU	-	expression tag	UNP Q9NRM6
Ι	296	PHE	-	expression tag	UNP Q9NRM6
Ι	297	GLN	-	expression tag	UNP Q9NRM6
Ι	298	GLY	-	expression tag	UNP Q9NRM6
Ι	299	PRO	-	expression tag	UNP Q9NRM6
Ι	300	GLY	-	expression tag	UNP Q9NRM6
Ι	301	ALA	-	expression tag	UNP Q9NRM6
Ι	302	ALA	-	expression tag	UNP Q9NRM6
Ι	303	GLU	-	expression tag	UNP Q9NRM6
Ι	304	ASP	-	expression tag	UNP Q9NRM6
Ι	305	GLN	-	expression tag	UNP Q9NRM6
Ι	306	VAL	-	expression tag	UNP Q9NRM6
Ι	307	ASP	-	expression tag	UNP Q9NRM6
Ι	308	PRO	-	expression tag	UNP Q9NRM6
Ι	309	ARG	-	expression tag	UNP Q9NRM6
Ι	310	LEU	-	expression tag	UNP Q9NRM6
Ι	311	ILE	-	expression tag	UNP Q9NRM6
Ι	312	ASP	-	expression tag	UNP Q9NRM6
Ι	313	GLY	-	expression tag	UNP Q9NRM6
Ι	314	LYS	-	expression tag	UNP Q9NRM6



Chain	Degidue	Madallad	Actual	Commont	Deference
Unain	nesidue	widdelled	Actual	· · ·	LIND COMPACE
	315	HIS	-	expression tag	UNP Q9NRM6
	316	HIS	-	expression tag	UNP Q9NRM6
	317	HIS	-	expression tag	UNP Q9NRM6
	318	HIS	-	expression tag	UNP Q9NRM6
	319	HIS	-	expression tag	UNP Q9NRM6
	320	HIS	-	expression tag	UNP Q9NRM6
I	321	HIS	-	expression tag	UNP Q9NRM6
I	322	HIS	-	expression tag	UNP Q9NRM6
K	289	ALA	-	expression tag	UNP Q9NRM6
K	290	ALA	-	expression tag	UNP Q9NRM6
K	291	ALA	-	expression tag	UNP Q9NRM6
K	292	LEU	-	expression tag	UNP Q9NRM6
K	293	GLU	-	expression tag	UNP Q9NRM6
K	294	VAL	-	expression tag	UNP Q9NRM6
K	295	LEU	-	expression tag	UNP Q9NRM6
K	296	PHE	-	expression tag	UNP Q9NRM6
K	297	GLN	-	expression tag	UNP Q9NRM6
K	298	GLY	-	expression tag	UNP Q9NRM6
K	299	PRO	-	expression tag	UNP Q9NRM6
K	300	GLY	-	expression tag	UNP Q9NRM6
K	301	ALA	-	expression tag	UNP Q9NRM6
K	302	ALA	-	expression tag	UNP Q9NRM6
K	303	GLU	-	expression tag	UNP Q9NRM6
K	304	ASP	-	expression tag	UNP Q9NRM6
K	305	GLN	-	expression tag	UNP Q9NRM6
K	306	VAL	-	expression tag	UNP Q9NRM6
K	307	ASP	-	expression tag	UNP Q9NRM6
K	308	PRO	-	expression tag	UNP Q9NRM6
К	309	ARG	-	expression tag	UNP Q9NRM6
K	310	LEU	-	expression tag	UNP Q9NRM6
K	311	ILE	-	expression tag	UNP Q9NRM6
K	312	ASP	-	expression tag	UNP Q9NRM6
K	313	GLY	-	expression tag	UNP Q9NRM6
K	314	LYS	-	expression tag	UNP Q9NRM6
K	315	HIS	_	expression tag	UNP Q9NRM6
K	316	HIS	_	expression tag	UNP Q9NRM6
K	317	HIS	-	expression tag	UNP Q9NRM6
K	318	HIS	-	expression tag	UNP Q9NRM6
K	319	HIS	-	expression tag	UNP Q9NRM6
K	320	HIS	_	expression tag	UNP Q9NRM6
K	321	HIS	_	expression tag	UNP Q9NRM6
K	322	HIS	_	expression tag	UNP Q9NRM6



	Besidue	Modelled	Actual	Comment	Reference
I			Actual		IND OONDM6
J	209		-	expression tag	UNF Q9NRMO
J	290		-	expression tag	UNF Q9NRMO
J	291		-	expression tag	UNI Q9NRMO
J	292		-	expression tag	UNI Q9NRMO
J	295		-	expression tag	UNF Q9NGMO
J	294	VAL LEU	-	expression tag	UNF Q9NRMO
J	293		-	expression tag	UNF Q9NRMO
J	290		-	expression tag	UNI Q9NRMO
J	297	GLN	-	expression tag	UNF Q9NRMO
J	298	BDO	-	expression tag	UNF Q9NRMO
J	299		-	expression tag	UNP Q9NRM0
J	300	GLY	-	expression tag	UNP Q9NRMO
J	301	ALA	-	expression tag	UNP Q9NRM0
J	302	ALA	-	expression tag	UNP Q9NRM0
J	303		-	expression tag	UNP Q9NRM6
J	304	ASP	-	expression tag	UNP Q9NRM0
J	303		-	expression tag	UNP Q9NRM6
J	300		-	expression tag	UNP Q9NRM6
J	307	ASP	-	expression tag	UNP Q9NRM6
J	308	PRO	-	expression tag	UNP Q9NRM6
J	309	ARG	-	expression tag	UNP Q9NRM6
J	310		-	expression tag	UNP Q9NRM6
J	311	ILE	-	expression tag	UNP Q9NRM6
J	312	ASP	-	expression tag	UNP Q9NRM6
J	313	GLY	-	expression tag	UNP Q9NRM6
J	314		-	expression tag	UNP Q9NRM6
J	315	HIS	-	expression tag	UNP Q9NRM6
J	316	HIS	-	expression tag	UNP Q9NRM6
J	317	HIS	-	expression tag	UNP Q9NRM6
J	318	HIS	-	expression tag	UNP Q9NRM6
J	319	HIS	-	expression tag	UNP Q9NRM6
J	320	HIS	-	expression tag	UNP Q9NRM6
J	321	HIS	-	expression tag	UNP Q9NRM6
J	322	HIS	-	expression tag	UNP Q9NRM6
L	289	ALA	-	expression tag	UNP Q9NRM6
	290	ALA	-	expression tag	UNP Q9NRM6
L	291	ALA	-	expression tag	UNP Q9NRM6
L	292	LEU	-	expression tag	UNP Q9NRM6
L	293	GLU	-	expression tag	UNP Q9NRM6
L	294	VAL	-	expression tag	UNP Q9NRM6
L	295	LEU	-	expression tag	UNP Q9NRM6
L	296	PHE	-	expression tag	UNP Q9NRM6



	Decidina	Madallad	Actual	Commont	Defenence
Chain	Residue	Modelled	Actual	Comment	Reference
L	297	GLN	-	expression tag	UNP Q9NRM6
L	298	GLY	-	expression tag	UNP Q9NRM6
L	299	PRO	-	expression tag	UNP Q9NRM6
L	300	GLY	-	expression tag	UNP Q9NRM6
L	301	ALA	-	expression tag	UNP Q9NRM6
L	302	ALA	-	expression tag	UNP Q9NRM6
L	303	GLU	-	expression tag	UNP Q9NRM6
L	304	ASP	-	expression tag	UNP Q9NRM6
L	305	GLN	-	expression tag	UNP Q9NRM6
L	306	VAL	-	expression tag	UNP Q9NRM6
L	307	ASP	-	expression tag	UNP Q9NRM6
L	308	PRO	-	expression tag	UNP Q9NRM6
L	309	ARG	-	expression tag	UNP Q9NRM6
L	310	LEU	-	expression tag	UNP Q9NRM6
L	311	ILE	-	expression tag	UNP Q9NRM6
L	312	ASP	-	expression tag	UNP Q9NRM6
L	313	GLY	-	expression tag	UNP Q9NRM6
L	314	LYS	-	expression tag	UNP Q9NRM6
L	315	HIS	-	expression tag	UNP Q9NRM6
L	316	HIS	-	expression tag	UNP Q9NRM6
L	317	HIS	-	expression tag	UNP Q9NRM6
L	318	HIS	-	expression tag	UNP Q9NRM6
L	319	HIS	-	expression tag	UNP Q9NRM6
L	320	HIS	-	expression tag	UNP Q9NRM6
L	321	HIS	-	expression tag	UNP Q9NRM6
L	322	HIS	-	expression tag	UNP Q9NRM6



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Interleukin-25











HIS HIS HIS HIS HIS HIS HIS

• Molecule 2: Interleukin-17 receptor B







 \bullet Molecule 2: Interleukin-17 receptor B





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	297300	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{\AA}^2)$	53	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 $(6k \ge 4k)$	Depositor
Maximum map value	1.484	Depositor
Minimum map value	-0.070	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	500.976, 500.976, 500.976	wwPDB
Map dimensions	294, 294, 294	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.704, 1.704, 1.704	Depositor



5 Model quality (i)

5.1 Standard geometry (i)

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).

Mal	Chain	Bond	lengths	Bond angles	
IVIOI	Ullaill	$\operatorname{RMSZ} \mid \# Z > 5$		RMSZ	# Z > 5
1	А	0.25	0/790	0.60	0/1068
1	В	0.25	0/826	0.61	0/1116
1	Ε	0.29	0/799	0.64	0/1079
1	F	0.28	0/797	0.65	0/1076
1	G	0.29	0/828	0.63	0/1119
1	Н	0.28	0/822	0.64	0/1111
2	С	0.27	0/1944	0.55	0/2644
2	D	0.26	0/1843	0.52	0/2500
2	Ι	0.28	0/1961	0.54	0/2667
2	J	0.26	0/1917	0.55	0/2605
2	Κ	0.27	0/1921	0.54	0/2610
2	L	0.28	0/1991	0.55	0/2710
All	All	0.27	0/16439	0.57	0/22305

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (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	А	771	0	742	26	0
1	В	806	0	777	43	0
1	Е	780	0	762	35	0
1	F	778	0	757	34	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	808	0	782	43	0
1	Н	803	0	777	48	0
2	С	1899	0	1841	83	0
2	D	1804	0	1759	36	0
2	Ι	1917	0	1876	64	0
2	J	1875	0	1832	62	0
2	Κ	1879	0	1831	62	0
2	L	1944	0	1907	68	0
All	All	16064	0	15643	548	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 17.

All (548) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom-2	Interatomic	Clash
Atom-1		distance (Å)	overlap (Å)
1:G:142:ARG:HH22	2:K:34:TRP:HB3	1.17	1.04
2:L:85:LYS:NZ	2:L:99:CYS:SG	2.42	0.92
1:G:81:PRO:HG2	2:K:133:VAL:HG23	1.61	0.83
2:C:21:THR:H	2:C:105:THR:HG22	1.44	0.82
1:B:132:LEU:HD12	1:B:165:SER:HB2	1.61	0.82
2:J:49:ARG:NH1	2:J:50:VAL:O	2.13	0.81
2:C:49:ARG:NH1	2:C:50:VAL:O	2.13	0.80
2:K:85:LYS:NZ	2:K:87:CYS:SG	2.55	0.80
2:L:207:TYR:HB2	2:L:222:VAL:HB	1.63	0.79
2:I:49:ARG:NH1	2:I:50:VAL:O	2.16	0.78
1:F:95:ASP:O	1:F:100:ARG:NH2	2.17	0.78
1:H:114:HIS:ND1	1:H:128:GLY:O	2.17	0.76
2:J:249:GLN:HG2	2:J:263:ARG:HE	1.50	0.76
2:K:43:GLY:O	2:K:140:ASN:ND2	2.18	0.75
1:B:107:HIS:HB2	1:B:109:ARG:NH1	2.02	0.75
2:C:262:ILE:HA	1:B:174:ARG:HH22	1.52	0.75
2:I:43:GLY:O	2:I:140:ASN:ND2	2.19	0.74
2:I:201:THR:HG22	2:I:203:LEU:H	1.53	0.74
2:C:82:LYS:HG2	2:C:142:PRO:HD3	1.70	0.74
2:L:140:ASN:O	2:L:143:ASN:ND2	2.21	0.74
2:C:57:VAL:HB	2:C:62:TYR:HB2	1.68	0.73
1:G:142:ARG:NH2	2:K:34:TRP:HB3	2.00	0.73
1:A:118:LEU:HD21	1:B:127:ARG:HB3	1.70	0.73
2:J:211:ILE:HG23	2:J:217:ILE:HG13	1.71	0.73
2:D:92:SER:O	2:D:95:GLN:NE2	2.22	0.72



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
2:C:105:THR:HG23	2:C:106:GLU:HG3	1.72	0.72
1:G:158:GLU:OE1	1:G:160:ARG:NH1	2.18	0.71
1:E:107:HIS:O	1:E:109:ARG:NH1	2.22	0.71
1:A:163:ARG:NH2	2:D:95:GLN:OE1	2.24	0.71
1:B:100:ARG:NH2	1:B:103:GLN:O	2.24	0.71
2:J:105:THR:HG23	2:J:106:GLU:HG3	1.72	0.71
2:I:216:ILE:HD11	1:G:127:ARG:HH22	1.55	0.70
2:L:83:ALA:HB3	2:L:141:ILE:HB	1.72	0.70
2:I:88:VAL:HG21	2:I:134:TYR:HB3	1.73	0.70
2:I:76:ALA:O	2:I:79:ARG:NH1	2.23	0.70
1:B:107:HIS:HB2	1:B:109:ARG:HH12	1.57	0.69
2:K:85:LYS:NZ	2:K:99:CYS:SG	2.67	0.68
1:A:110:CYS:SG	1:A:130:SER:OG	2.52	0.68
2:C:189:LYS:HG3	2:C:195:GLU:HB3	1.75	0.68
1:B:92:TYR:HB3	1:B:106:TYR:HB3	1.76	0.68
2:D:85:LYS:HG2	2:D:101:ARG:HB2	1.76	0.68
1:H:91:ARG:HH12	1:H:111:LEU:H	1.43	0.67
2:J:21:THR:H	2:J:105:THR:HG22	1.58	0.67
1:F:119:GLN:NE2	2:J:214:SER:O	2.28	0.66
2:D:250:LEU:HD23	2:D:252:PRO:HD3	1.77	0.66
2:J:165:HIS:O	2:J:168:LYS:NZ	2.27	0.66
2:L:92:SER:O	2:L:95:GLN:NE2	2.28	0.66
2:C:95:GLN:HE22	1:B:135:HIS:HA	1.60	0.66
2:C:112:THR:OG1	2:C:117:GLY:O	2.14	0.66
2:I:82:LYS:HZ1	2:I:142:PRO:HD3	1.61	0.66
2:L:182:PRO:HB2	2:L:184:ILE:HG13	1.77	0.66
1:B:90:TRP:HA	1:B:110:CYS:HA	1.78	0.66
1:F:97:ASP:O	1:F:103:GLN:NE2	2.27	0.65
2:I:180:TRP:NE1	2:I:201:THR:OG1	2.28	0.65
2:J:109:GLN:HG2	2:J:110:THR:HG23	1.79	0.65
2:C:129:GLU:HG3	2:C:130:LEU:H	1.61	0.64
1:H:140:PHE:HA	1:H:159:ARG:HH21	1.62	0.64
2:C:168:LYS:HG3	2:C:178:SER:HB2	1.77	0.64
2:K:62:TYR:O	2:K:170:LYS:NZ	2.31	0.64
1:F:174:ARG:NH1	2:L:131:ASN:OD1	2.30	0.64
1:B:142:ARG:NH2	1:B:143:ARG:O	2.24	0.64
1:F:172:ARG:O	1:H:85:ARG:NH1	2.31	0.64
1:B:93:GLU:HB2	1:B:109:ARG:HH21	1.63	0.64
2:D:78:ILE:HD12	2:D:111:GLN:HA	1.80	0.64
1:H:135:HIS:ND1	1:H:166:LEU:HD21	2.13	0.64
1:H:141:TYR:HB3	1:H:143:ARG:HH12	1.63	0.64



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:E:126:PRO:HG2	2:K:210:LEU:HD21	1.81	0.63
1:F:101:LEU:O	1:F:140:PHE:N	2.24	0.63
2:L:87:CYS:HA	2:L:99:CYS:HB2	1.81	0.63
1:G:79:ASP:HA	1:G:85:ARG:HD3	1.81	0.63
2:C:93:ASN:OD1	2:C:94:PHE:N	2.32	0.62
1:B:89:PRO:O	1:B:91:ARG:NH1	2.32	0.62
2:K:79:ARG:O	2:K:79:ARG:NH1	2.32	0.62
2:I:129:GLU:HB2	2:I:132:THR:HG21	1.82	0.62
1:E:91:ARG:NH1	1:E:109:ARG:O	2.33	0.62
2:I:86:ILE:HD13	2:I:138:ALA:HB2	1.81	0.62
2:L:47:ASP:OD1	2:L:49:ARG:NH2	2.30	0.62
1:G:97:ASP:HB3	1:G:100:ARG:HH11	1.64	0.62
2:J:45:LEU:HD11	2:J:70:TRP:HB2	1.82	0.62
2:J:101:ARG:NH1	2:J:103:ASN:OD1	2.33	0.62
1:H:144:PRO:HA	1:H:155:TYR:HA	1.82	0.62
1:E:98:LEU:O	1:E:142:ARG:NH1	2.28	0.61
2:D:227:GLN:O	2:D:230:GLN:NE2	2.34	0.61
2:I:24:CYS:HA	2:I:102:CYS:HB3	1.82	0.61
1:F:135:HIS:ND1	1:F:166:LEU:HD11	2.14	0.61
2:J:81:LEU:HD23	2:J:108:PHE:HE2	1.66	0.61
2:I:263:ARG:HB2	1:G:175:VAL:HG13	1.83	0.61
2:L:206:ARG:HD2	2:L:223:PHE:HD1	1.66	0.61
2:C:182:PRO:HB2	2:C:184:ILE:HG13	1.82	0.60
2:C:208:MET:HB3	2:C:251:THR:HB	1.83	0.60
1:F:114:HIS:HA	1:F:129:ASN:HA	1.81	0.60
2:L:62:TYR:OH	2:L:166:ILE:O	2.19	0.60
1:G:114:HIS:HB2	1:G:124:MET:HE3	1.83	0.60
1:G:119:GLN:NE2	2:K:214:SER:O	2.35	0.60
2:J:208:MET:HG3	2:J:221:GLN:HG2	1.83	0.60
2:C:46:ARG:HB3	2:C:71:VAL:HG12	1.84	0.60
2:C:229:LYS:HE3	2:C:229:LYS:HA	1.81	0.60
2:K:249:GLN:HE21	2:K:263:ARG:NH2	1.99	0.60
2:C:189:LYS:H	2:C:194:VAL:HA	1.65	0.60
2:I:105:THR:HG23	2:I:106:GLU:HG3	1.84	0.60
1:H:96:ARG:NH2	2:L:152:SER:O	2.35	0.60
2:J:249:GLN:NE2	2:J:251:THR:OG1	2.25	0.59
2:K:41:ILE:HG21	2:K:144:ALA:HA	1.84	0.59
2:J:189:LYS:HD2	2:J:195:GLU:HB3	1.84	0.59
1:H:92:TYR:HE2	2:L:91:LYS:HD3	1.68	0.59
1:H:99:ASN:HA	2:L:34:TRP:HZ2	1.68	0.59
2:C:66:MET:HE2	2:C:128:VAL:HG21	1.85	0.59



	lous page	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:H:87:ILE:HG12	1:H:118:LEU:HD21	1.85	0.59
1:A:172:ARG:NH1	1:B:78:GLU:O	2.36	0.58
2:D:74:ALA:HA	2:D:78:ILE:HD11	1.85	0.58
1:E:114:HIS:ND1	1:E:128:GLY:O	2.29	0.58
1:F:108:ALA:N	1:F:165:SER:OG	2.24	0.58
2:L:227:GLN:OE1	2:L:230:GLN:NE2	2.36	0.58
2:C:228:LYS:HD2	2:C:229:LYS:HZ2	1.69	0.58
2:J:47:ASP:HB3	2:J:71:VAL:HB	1.84	0.58
2:C:66:MET:HB2	2:C:126:PHE:HB2	1.86	0.58
1:B:142:ARG:HH12	1:B:155:TYR:HA	1.68	0.58
2:D:229:LYS:HB3	2:D:231:THR:HG23	1.86	0.58
2:I:227:GLN:O	2:I:230:GLN:NE2	2.31	0.58
1:B:93:GLU:HB2	1:B:109:ARG:NH2	2.19	0.58
2:K:47:ASP:HB3	2:K:71:VAL:HB	1.86	0.58
2:J:67:ASN:HD21	2:J:122:SER:HB2	1.67	0.57
2:J:140:ASN:OD1	2:J:141:ILE:N	2.37	0.57
1:B:134:TYR:HD2	1:B:163:ARG:HH21	1.52	0.57
2:D:165:HIS:HA	2:D:168:LYS:HD2	1.87	0.57
2:K:83:ALA:HB3	2:K:141:ILE:HB	1.86	0.57
2:D:43:GLY:O	2:D:140:ASN:ND2	2.36	0.57
2:C:188:LYS:HA	2:C:194:VAL:HG22	1.87	0.57
1:E:159:ARG:HH12	1:E:161:LEU:HD13	1.70	0.57
2:L:197:ASN:OD1	2:L:232:ARG:HB3	2.05	0.57
1:E:143:ARG:HG2	1:E:158:GLU:OE2	2.05	0.56
1:H:97:ASP:OD1	1:H:98:LEU:N	2.37	0.56
1:E:97:ASP:OD1	1:E:98:LEU:N	2.38	0.56
1:E:174:ARG:NH2	2:K:260:ASP:O	2.38	0.56
1:A:99:ASN:HA	1:A:142:ARG:NH1	2.20	0.56
2:C:79:ARG:O	2:C:79:ARG:NE	2.37	0.56
2:K:112:THR:OG1	2:K:117:GLY:O	2.23	0.56
2:L:113:ARG:NH1	2:L:117:GLY:O	2.38	0.56
2:D:24:CYS:HB2	2:D:123:TYR:CE1	2.40	0.56
2:L:85:LYS:NZ	2:L:87:CYS:SG	2.76	0.56
2:K:184:ILE:HD11	2:K:264:HIS:CE1	2.41	0.56
1:F:159:ARG:NH2	1:F:160:ARG:O	2.38	0.56
2:I:265:LYS:NZ	1:G:175:VAL:HG12	2.21	0.56
2:K:139:HIS:ND1	2:K:140:ASN:O	2.35	0.56
1:A:134:TYR:HB3	1:A:163:ARG:HG3	1.87	0.56
1:H:81:PRO:HB2	2:L:133:VAL:HG23	1.88	0.56
1:E:99:ASN:HA	1:E:142:ARG:NH1	2.21	0.56
2:D:67:ASN:HD22	2:D:124:ILE:HG12	1.70	0.56



	hi o	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
2:D:269:VAL:HG22	2:D:270:LEU:H	1.71	0.56
1:G:100:ARG:HG2	1:G:141:TYR:CE1	2.40	0.56
1:E:92:TYR:OH	2:I:91:LYS:NZ	2.22	0.55
1:H:130:SER:HA	1:H:170:CYS:HA	1.87	0.55
2:L:206:ARG:HH11	2:L:223:PHE:HB3	1.72	0.55
2:C:113:ARG:NH1	2:C:119:TRP:HA	2.22	0.55
2:L:254:PHE:HB2	2:L:257:CYS:SG	2.46	0.55
1:G:132:LEU:HD23	1:G:165:SER:HB3	1.88	0.55
2:J:129:GLU:O	2:J:134:TYR:OH	2.23	0.55
2:J:137:GLY:HA2	2:J:154:SER:HA	1.88	0.55
2:K:209:ALA:HB3	2:K:220:SER:H	1.72	0.55
2:K:206:ARG:HH22	2:K:222:VAL:H	1.53	0.55
1:F:127:ARG:HH21	1:H:119:GLN:HG3	1.72	0.55
1:A:152:HIS:CE1	2:C:37:GLN:H	2.25	0.55
2:C:67:ASN:HB2	2:C:124:ILE:HD13	1.89	0.55
2:D:183:ASN:O	2:D:232:ARG:NH1	2.40	0.55
2:K:50:VAL:HG22	2:K:68:VAL:HG23	1.88	0.55
1:H:90:TRP:HE1	1:H:92:TYR:HH	1.55	0.55
2:L:189:LYS:HG3	2:L:195:GLU:HB2	1.88	0.55
2:D:206:ARG:NH2	2:D:221:GLN:OE1	2.40	0.54
2:I:86:ILE:HD11	2:I:136:ILE:HG22	1.90	0.54
2:I:165:HIS:O	2:I:168:LYS:NZ	2.29	0.54
1:A:98:LEU:O	1:A:142:ARG:NH1	2.31	0.54
1:A:152:HIS:CD2	1:A:154:GLY:H	2.26	0.54
2:C:129:GLU:HG3	2:C:130:LEU:HD23	1.88	0.54
1:B:80:GLY:H	1:B:85:ARG:HD3	1.72	0.54
1:B:96:ARG:NH1	2:D:152:SER:OG	2.41	0.54
2:I:39:ASP:O	2:L:111:GLN:NE2	2.40	0.54
2:I:90:GLY:N	2:I:96:SER:O	2.40	0.54
2:L:46:ARG:NH2	2:L:74:ALA:H	2.05	0.54
1:G:114:HIS:ND1	1:G:128:GLY:O	2.35	0.54
1:H:94:LEU:HD21	1:H:96:ARG:HG3	1.89	0.54
2:K:249:GLN:HE21	2:K:263:ARG:HH22	1.55	0.54
2:L:38:HIS:O	2:L:145:ASN:ND2	2.33	0.54
2:D:74:ALA:O	2:D:111:GLN:NE2	2.38	0.54
2:I:24:CYS:HB2	2:I:123:TYR:CE1	2.43	0.54
1:G:120:THR:HG21	1:G:123:HIS:HB2	1.90	0.54
2:K:206:ARG:HB3	2:K:253:TYR:HB2	1.89	0.54
2:C:212:GLN:OE1	1:B:127:ARG:NH2	2.33	0.53
2:K:73:ARG:NH1	2:K:75:ASP:H	2.05	0.53
2:J:264:HIS:ND1	1:H:176:MET:O	2.41	0.53



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:118:LEU:HD23	1:B:127:ARG:HD2	1.91	0.53
2:I:67:ASN:HA	2:I:123:TYR:O	2.07	0.53
1:A:133:LEU:O	1:A:166:LEU:N	2.37	0.53
2:C:20:PRO:HG3	2:C:106:GLU:HB2	1.91	0.53
2:D:254:PHE:HB2	2:D:257:CYS:SG	2.49	0.53
2:I:24:CYS:HB2	2:I:123:TYR:CZ	2.44	0.53
1:G:130:SER:HB2	1:G:168:CYS:HB3	1.91	0.53
2:K:188:LYS:HA	2:K:194:VAL:HG22	1.91	0.53
1:F:152:HIS:CE1	2:J:37:GLN:H	2.27	0.53
2:J:210:LEU:HD13	2:J:219:PHE:HB3	1.90	0.53
2:L:68:VAL:O	2:L:122:SER:HA	2.09	0.53
2:D:83:ALA:HB3	2:D:141:ILE:HD12	1.90	0.53
1:F:91:ARG:NH1	1:F:93:GLU:OE2	2.42	0.53
2:J:85:LYS:HD3	2:J:101:ARG:HB2	1.89	0.53
1:H:115:CYS:O	1:H:125:ASP:HB3	2.09	0.53
1:F:91:ARG:NH1	1:F:92:TYR:O	2.42	0.53
2:C:70:TRP:NE1	2:C:121:PHE:HB2	2.25	0.53
2:J:88:VAL:HG21	2:J:134:TYR:HB3	1.91	0.53
2:I:88:VAL:HB	2:I:136:ILE:HG12	1.91	0.52
2:K:166:ILE:HG13	2:K:167:MET:HG2	1.91	0.52
2:K:208:MET:HE1	2:K:210:LEU:HD13	1.91	0.52
2:J:83:ALA:HB3	2:J:141:ILE:HD11	1.91	0.52
2:C:254:PHE:HB2	2:C:257:CYS:SG	2.50	0.52
1:B:96:ARG:NH2	1:B:103:GLN:HB3	2.24	0.52
2:D:134:TYR:HB2	2:D:157:PHE:HB3	1.91	0.52
2:C:83:ALA:HB3	2:C:141:ILE:HB	1.92	0.52
1:E:136:ASN:OD1	1:E:161:LEU:HD12	2.08	0.52
2:I:21:THR:H	2:I:105:THR:HG22	1.75	0.52
2:L:88:VAL:HG22	2:L:136:ILE:HD12	1.92	0.52
2:L:130:LEU:HD22	2:L:161:GLY:HA2	1.92	0.52
1:G:90:TRP:HA	1:G:110:CYS:HA	1.91	0.52
1:F:104:ASP:OD1	1:F:105:LEU:N	2.43	0.52
1:G:125:ASP:OD1	1:G:127:ARG:NH2	2.43	0.52
1:F:91:ARG:HG2	1:F:92:TYR:H	1.73	0.52
2:C:46:ARG:HA	2:C:73:ARG:NH2	2.25	0.52
2:D:188:LYS:HA	2:D:194:VAL:HG22	1.91	0.51
2:I:167:MET:HE1	2:I:170:LYS:HE3	1.92	0.51
2:K:73:ARG:CZ	2:K:75:ASP:HB2	2.40	0.51
1:E:107:HIS:HB2	1:E:109:ARG:NH1	2.26	0.51
1:H:129:ASN:O	1:H:171:VAL:N	2.32	0.51
1:F:127:ARG:NH2	1:H:118:LEU:HB2	2.25	0.51



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
2:I:87:CYS:CB	2:I:99:CYS:HA	2.40	0.51
1:G:83:ASN:HD22	1:G:83:ASN:N	2.08	0.51
1:G:97:ASP:HB3	1:G:100:ARG:HD3	1.93	0.51
2:J:89:THR:HG23	2:J:97:TYR:HB2	1.92	0.51
2:C:47:ASP:HB3	2:C:71:VAL:HB	1.93	0.50
1:E:159:ARG:NH1	1:E:160:ARG:O	2.43	0.50
1:G:126:PRO:HD2	1:G:127:ARG:NH2	2.26	0.50
2:L:26:SER:HA	2:L:100:VAL:HG23	1.93	0.50
2:C:47:ASP:OD1	2:C:48:LEU:N	2.43	0.50
1:B:115:CYS:O	1:B:125:ASP:N	2.45	0.50
1:E:175:VAL:HG23	2:K:263:ARG:HG3	1.93	0.50
1:G:97:ASP:CB	1:G:100:ARG:HD3	2.41	0.50
2:I:46:ARG:CG	2:I:73:ARG:HA	2.42	0.50
2:L:157:PHE:CG	2:L:158:THR:N	2.80	0.50
1:G:100:ARG:HH21	1:G:105:LEU:HD23	1.77	0.50
2:L:46:ARG:NE	2:L:73:ARG:HA	2.27	0.50
2:L:91:LYS:HG3	2:L:95:GLN:HE21	1.77	0.50
2:L:206:ARG:HD3	2:L:223:PHE:HA	1.93	0.50
2:C:119:TRP:HB3	2:C:121:PHE:HE1	1.76	0.50
1:A:90:TRP:HA	1:A:110:CYS:HA	1.94	0.49
2:L:54:THR:HG22	2:L:64:ILE:HD12	1.94	0.49
2:C:171:LYS:HA	2:C:174:VAL:HB	1.94	0.49
2:C:212:GLN:O	2:C:247:THR:OG1	2.24	0.49
1:B:142:ARG:HD2	2:D:34:TRP:CH2	2.48	0.49
2:L:49:ARG:O	2:L:69:SER:N	2.45	0.49
1:H:107:HIS:HE1	1:H:164:VAL:HG22	1.77	0.49
1:H:141:TYR:HB3	1:H:143:ARG:NH1	2.25	0.49
2:L:85:LYS:HB3	2:L:139:HIS:CE1	2.48	0.49
1:E:107:HIS:HB2	1:E:109:ARG:HH11	1.76	0.49
2:L:171:LYS:H	2:L:171:LYS:HD2	1.77	0.49
1:E:158:GLU:HG3	1:E:160:ARG:HH12	1.77	0.49
2:I:188:LYS:HB3	2:I:270:LEU:HD23	1.94	0.49
1:B:152:HIS:CD2	1:B:153:LYS:H	2.31	0.49
1:F:108:ALA:HB3	1:F:165:SER:HB2	1.94	0.49
2:D:249:GLN:NE2	2:D:263:ARG:HG2	2.28	0.48
2:K:250:LEU:HD23	2:K:252:PRO:HD3	1.94	0.48
2:C:62:TYR:OH	2:C:166:ILE:O	2.18	0.48
2:C:101:ARG:HD2	2:C:101:ARG:C	2.34	0.48
1:E:102:PRO:HG2	1:E:104:ASP:O	2.13	0.48
2:C:24:CYS:HA	2:C:102:CYS:CB	2.44	0.48
2:K:85:LYS:HB2	2:K:141:ILE:HD11	1.95	0.48



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:F:101:LEU:N	1:F:140:PHE:O	2.29	0.48
1:E:99:ASN:HA	1:E:142:ARG:HH11	1.79	0.48
1:E:138:THR:HA	1:E:159:ARG:NH2	2.29	0.48
2:I:265:LYS:NZ	1:G:176:MET:O	2.46	0.48
2:L:48:LEU:HD13	2:L:70:TRP:HB3	1.95	0.48
2:L:87:CYS:HA	2:L:99:CYS:CB	2.44	0.48
1:A:172:ARG:HH12	1:B:79:ASP:HA	1.78	0.48
1:B:160:ARG:HD3	1:B:161:LEU:O	2.13	0.48
2:K:206:ARG:NH2	2:K:222:VAL:O	2.46	0.48
1:B:89:PRO:HG2	1:B:91:ARG:HH12	1.78	0.48
1:G:97:ASP:OD1	1:G:98:LEU:HD23	2.13	0.48
2:J:27:GLU:OE2	2:J:101:ARG:N	2.47	0.48
1:A:175:VAL:HA	2:D:263:ARG:NH1	2.28	0.48
2:C:46:ARG:HD3	2:C:73:ARG:HH21	1.79	0.48
2:C:130:LEU:H	2:C:130:LEU:HD23	1.77	0.48
2:D:253:TYR:O	2:D:254:PHE:C	2.50	0.48
2:J:70:TRP:CD1	2:J:84:THR:HG21	2.49	0.48
2:C:119:TRP:HB3	2:C:121:PHE:CE1	2.48	0.48
2:C:172:LYS:HA	2:C:172:LYS:HE2	1.96	0.48
1:E:99:ASN:OD1	1:E:142:ARG:NH1	2.46	0.48
2:I:87:CYS:HB3	2:I:99:CYS:HA	1.94	0.48
2:I:171:LYS:HG3	2:I:172:LYS:HD3	1.96	0.48
2:I:182:PRO:HB2	2:I:184:ILE:HG13	1.95	0.48
1:G:94:LEU:HD12	1:G:95:ASP:H	1.78	0.48
1:G:142:ARG:O	1:G:143:ARG:HD2	2.14	0.48
2:J:212:GLN:O	2:J:247:THR:N	2.47	0.48
1:B:134:TYR:HE1	1:B:165:SER:HB3	1.78	0.47
2:L:179:LEU:HD23	2:L:179:LEU:H	1.79	0.47
2:C:24:CYS:HA	2:C:102:CYS:HB3	1.96	0.47
1:B:136:ASN:HB3	1:B:161:LEU:HB2	1.95	0.47
2:I:83:ALA:HB2	2:I:103:ASN:ND2	2.29	0.47
2:I:171:LYS:O	2:I:175:LYS:HG2	2.15	0.47
2:J:23:GLN:O	2:J:102:CYS:HB2	2.14	0.47
1:H:91:ARG:NH1	1:H:111:LEU:H	2.10	0.47
1:B:136:ASN:HA	1:B:162:TYR:O	2.13	0.47
2:K:186:ALA:HB2	2:K:196:VAL:HG13	1.95	0.47
2:J:85:LYS:NZ	2:J:100:VAL:O	2.44	0.47
1:E:174:ARG:HG3	1:G:85:ARG:NH1	2.29	0.47
1:A:143:ARG:HD2	1:A:144:PRO:O	2.15	0.47
2:C:188:LYS:HE2	2:C:191:GLU:HA	1.97	0.47
2:D:32:PRO:HD2	2:D:101:ARG:NH1	2.29	0.47



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Atom-1	Atom-2	distance (Å)	overlap (Å)
1:E:136:ASN:HD21	1:E:161:LEU:HB3	1.80	0.47
2:I:28:THR:OG1	2:I:99:CYS:N	2.38	0.47
1:H:91:ARG:HH22	1:H:111:LEU:HB3	1.79	0.47
1:B:136:ASN:OD1	1:B:161:LEU:HD13	2.15	0.47
1:E:158:GLU:HG3	1:E:160:ARG:NH1	2.30	0.47
2:K:48:LEU:HA	2:K:70:TRP:HA	1.96	0.47
1:F:88:SER:OG	1:F:168:CYS:O	2.23	0.47
2:L:208:MET:CE	2:L:210:LEU:HD23	2.45	0.47
2:L:49:ARG:N	2:L:69:SER:O	2.46	0.47
1:A:160:ARG:NH1	1:A:161:LEU:O	2.48	0.47
2:I:82:LYS:NZ	2:I:142:PRO:HD3	2.29	0.47
2:K:208:MET:SD	2:K:250:LEU:HA	2.55	0.47
2:J:43:GLY:HA3	2:J:77:SER:HB3	1.97	0.47
1:E:95:ASP:O	1:E:100:ARG:NH2	2.47	0.46
1:F:117:SER:HB2	1:F:123:HIS:HB3	1.97	0.46
1:F:159:ARG:HH21	1:F:160:ARG:C	2.19	0.46
2:C:92:SER:OG	2:C:94:PHE:O	2.19	0.46
1:G:88:SER:OG	1:G:168:CYS:O	2.25	0.46
2:K:206:ARG:HE	2:K:207:TYR:H	1.62	0.46
1:A:136:ASN:HA	1:A:162:TYR:O	2.15	0.46
2:I:101:ARG:NH1	2:I:103:ASN:OD1	2.48	0.46
1:F:91:ARG:HH12	1:F:93:GLU:HG2	1.80	0.46
2:C:185:THR:HG23	2:C:197:ASN:HB3	1.97	0.46
1:H:91:ARG:HH12	1:H:111:LEU:HG	1.80	0.46
2:C:31:SER:HB2	2:C:34:TRP:HB2	1.98	0.46
2:C:70:TRP:CE2	2:C:121:PHE:HB2	2.51	0.46
1:F:114:HIS:ND1	1:F:128:GLY:O	2.40	0.46
1:F:175:VAL:HG23	2:L:263:ARG:HH11	1.81	0.46
2:J:24:CYS:HA	2:J:102:CYS:CB	2.46	0.46
1:E:138:THR:HG23	1:E:159:ARG:NE	2.30	0.46
2:I:20:PRO:HG2	2:I:119:TRP:HZ3	1.80	0.46
2:C:145:ASN:N	2:C:148:GLU:OE1	2.45	0.46
1:B:94:LEU:HA	1:B:106:TYR:CE1	2.51	0.46
1:G:136:ASN:HB3	1:G:161:LEU:HD12	1.96	0.46
2:K:26:SER:HA	2:K:100:VAL:HG13	1.98	0.46
1:B:99:ASN:HB3	1:B:142:ARG:HB3	1.98	0.46
1:G:135:HIS:HE2	1:G:137:GLN:HB2	1.80	0.46
2:K:229:LYS:HB3	2:K:231:THR:HG23	1.98	0.46
2:J:88:VAL:HB	2:J:136:ILE:HG12	1.98	0.46
2:I:186:ALA:HB3	2:I:267:THR:O	2.16	0.45
2:K:208:MET:HG3	2:K:251:THR:H	1.81	0.45



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
2:L:81:LEU:HD11	2:L:140:ASN:HB2	1.97	0.45
2:K:31:SER:HB2	2:K:34:TRP:CD1	2.51	0.45
2:K:49:ARG:O	2:K:69:SER:N	2.39	0.45
2:J:170:LYS:HZ2	2:J:172:LYS:HB3	1.81	0.45
2:L:46:ARG:CZ	2:L:73:ARG:HA	2.46	0.45
2:D:20:PRO:HG3	2:D:106:GLU:HB2	1.98	0.45
1:E:152:HIS:CD2	1:E:154:GLY:H	2.34	0.45
2:I:40:LEU:HA	2:L:111:GLN:NE2	2.31	0.45
2:K:73:ARG:O	2:K:77:SER:OG	2.33	0.45
2:C:50:VAL:HA	2:C:68:VAL:HA	1.98	0.45
2:C:187:CYS:HB3	2:C:269:VAL:HG23	1.97	0.45
2:C:211:ILE:HD12	2:C:218:GLY:HA3	1.99	0.45
1:E:113:PRO:HD2	1:E:124:MET:HE1	1.99	0.45
1:E:159:ARG:HH22	1:E:161:LEU:HD13	1.81	0.45
2:L:171:LYS:HD2	2:L:171:LYS:N	2.32	0.45
2:C:45:LEU:HA	2:C:72:LEU:HA	1.99	0.45
1:F:142:ARG:HG2	2:J:34:TRP:HZ2	1.81	0.45
2:J:182:PRO:O	2:J:199:THR:N	2.41	0.45
2:I:78:ILE:O	2:I:80:LEU:N	2.50	0.45
1:G:104:ASP:O	1:G:105:LEU:HD22	2.17	0.45
1:F:100:ARG:HG3	1:F:102:PRO:O	2.17	0.45
2:L:263:ARG:CZ	2:L:265:LYS:HA	2.46	0.45
2:K:87:CYS:HB3	2:K:99:CYS:HB2	1.59	0.45
1:F:114:HIS:HB2	1:F:124:MET:HE1	1.99	0.45
2:K:70:TRP:HE1	2:K:104:TYR:HH	1.65	0.45
2:K:227:GLN:O	2:K:230:GLN:NE2	2.46	0.45
2:C:21:THR:H	2:C:105:THR:CG2	2.24	0.45
2:I:94:PHE:HB3	1:G:163:ARG:NH2	2.32	0.45
1:H:160:ARG:HD3	1:H:161:LEU:O	2.17	0.45
1:G:120:THR:HG23	1:G:122:SER:H	1.82	0.44
2:I:259:SER:O	1:G:129:ASN:ND2	2.51	0.44
2:J:254:PHE:HB2	2:J:257:CYS:SG	2.57	0.44
1:A:94:LEU:HD12	1:A:106:TYR:HE1	1.82	0.44
2:K:139:HIS:CE1	2:K:143:ASN:HD21	2.36	0.44
1:H:114:HIS:HB3	1:H:126:PRO:HA	2.00	0.44
2:L:47:ASP:OD1	2:L:48:LEU:N	2.51	0.44
1:G:100:ARG:HH21	1:G:105:LEU:HB2	1.83	0.44
2:K:185:THR:HG1	2:K:197:ASN:HB2	1.82	0.44
2:J:72:LEU:HD23	2:J:73:ARG:O	2.17	0.44
2:J:185:THR:OG1	2:J:197:ASN:HB3	2.17	0.44
1:H:94:LEU:HD23	1:H:95:ASP:N	2.33	0.44



	lous page	Interatomic	Clash
Atom-1	Atom-2	distance $(Å)$	overlap (Å)
2:L:181:ASP:OD1	2:L:181:ASP:N	2.47	0.44
2:L:208:MET:SD	2:L:251:THR:N	2.90	0.44
1:E:114:HIS:HB2	1:E:124:MET:HE3	2.00	0.44
2:J:26:SER:HA	2:J:100:VAL:HG23	1.99	0.44
2:J:196:VAL:O	2:J:234:SER:HA	2.18	0.44
1:A:143:ARG:HG2	1:A:144:PRO:HD2	2.00	0.44
2:C:48:LEU:HA	2:C:70:TRP:HA	1.99	0.44
1:G:93:GLU:OE2	1:G:93:GLU:HA	2.17	0.44
1:F:91:ARG:HG2	1:F:91:ARG:HH11	1.83	0.44
2:J:48:LEU:HA	2:J:70:TRP:HA	2.00	0.44
2:J:170:LYS:HZ2	2:J:173:CYS:N	2.16	0.44
2:L:208:MET:HG3	2:L:251:THR:O	2.18	0.44
2:C:180:TRP:O	2:C:264:HIS:NE2	2.51	0.43
2:J:95:GLN:HE22	1:H:135:HIS:HB2	1.83	0.43
1:H:160:ARG:NH1	1:H:161:LEU:O	2.51	0.43
2:I:92:SER:HB3	2:I:132:THR:HG22	1.99	0.43
1:H:96:ARG:NH2	2:L:152:SER:OG	2.51	0.43
1:B:147:GLY:HA3	1:B:149:LYS:HE2	2.00	0.43
1:H:100:ARG:HH21	1:H:105:LEU:HD23	1.83	0.43
2:D:145:ASN:N	2:D:148:GLU:OE1	2.50	0.43
2:K:70:TRP:NE1	2:K:104:TYR:OH	2.48	0.43
2:J:180:TRP:CZ2	2:J:201:THR:HB	2.52	0.43
2:C:111:GLN:O	2:C:119:TRP:NE1	2.32	0.43
2:D:205:ASN:N	2:D:205:ASN:OD1	2.52	0.43
1:F:139:VAL:H	1:F:159:ARG:HH12	1.66	0.43
2:L:48:LEU:HD12	2:L:69:SER:O	2.17	0.43
1:B:90:TRP:CD1	1:B:92:TYR:CE1	3.07	0.43
1:E:133:LEU:HD11	1:E:169:VAL:HG12	2.00	0.43
2:L:66:MET:O	2:L:124:ILE:HD12	2.19	0.43
1:B:93:GLU:OE1	1:B:109:ARG:NH2	2.46	0.43
1:B:152:HIS:CG	1:B:153:LYS:H	2.37	0.43
1:E:135:HIS:ND1	1:E:166:LEU:HD11	2.34	0.43
2:I:85:LYS:HE3	2:I:139:HIS:CE1	2.53	0.43
1:H:135:HIS:HE2	1:H:137:GLN:HG3	1.83	0.43
1:H:141:TYR:HB3	1:H:143:ARG:HH22	1.83	0.43
2:C:184:ILE:HA	2:C:198:PHE:HB3	1.99	0.43
2:I:265:LYS:HZ1	1:G:175:VAL:HG12	1.84	0.43
2:J:66:MET:HG2	2:J:128:VAL:HG21	2.01	0.43
1:H:157:LEU:CD1	1:H:159:ARG:HH12	2.31	0.43
1:A:169:VAL:HG23	1:B:169:VAL:HG12	1.99	0.42
2:C:206:ARG:NH1	2:C:207:TYR:O	2.51	0.42



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:136:ASN:HB3	1:A:161:LEU:HD22	2.01	0.42
2:I:87:CYS:HB2	2:I:98:SER:O	2.19	0.42
2:C:171:LYS:HZ3	2:C:175:LYS:HD3	1.84	0.42
2:D:164:ASP:OD1	2:D:164:ASP:N	2.53	0.42
2:I:73:ARG:O	2:I:78:ILE:HD11	2.20	0.42
2:K:48:LEU:HD12	2:K:69:SER:O	2.20	0.42
2:L:78:ILE:HD12	2:L:111:GLN:HA	2.01	0.42
2:J:79:ARG:HH11	2:J:80:LEU:HD23	1.84	0.42
2:C:46:ARG:N	2:C:71:VAL:O	2.52	0.42
2:C:46:ARG:H	2:C:72:LEU:HA	1.84	0.42
2:C:81:LEU:C	2:C:82:LYS:HD2	2.40	0.42
2:I:46:ARG:HH12	2:I:73:ARG:CZ	2.33	0.42
1:F:158:GLU:HG3	1:F:160:ARG:HH12	1.83	0.42
2:J:216:ILE:HG13	1:H:127:ARG:NH2	2.35	0.42
2:L:48:LEU:CD1	2:L:70:TRP:HB3	2.49	0.42
2:C:196:VAL:HG12	2:C:198:PHE:HD1	1.85	0.42
2:I:187:CYS:SG	2:I:271:CYS:N	2.92	0.42
2:C:262:ILE:HG23	1:B:174:ARG:HH12	1.84	0.42
2:J:113:ARG:HA	2:J:113:ARG:HD2	1.74	0.42
2:J:180:TRP:HD1	2:J:181:ASP:N	2.17	0.42
2:C:111:GLN:NE2	2:K:40:LEU:HD23	2.35	0.42
2:C:129:GLU:HG3	2:C:130:LEU:N	2.33	0.42
2:I:86:ILE:HD12	2:I:137:GLY:O	2.19	0.42
1:H:140:PHE:HA	1:H:159:ARG:NH2	2.33	0.42
2:D:55:THR:HG1	2:D:63:SER:H	1.67	0.42
2:I:46:ARG:HG2	2:I:73:ARG:HA	2.02	0.42
1:H:136:ASN:CG	1:H:161:LEU:HB3	2.40	0.42
1:B:96:ARG:HH22	1:B:103:GLN:HB3	1.84	0.41
2:D:46:ARG:HH12	2:D:73:ARG:CZ	2.33	0.41
2:J:67:ASN:HA	2:J:123:TYR:O	2.20	0.41
2:J:86:ILE:HG23	2:J:138:ALA:HB2	2.02	0.41
1:H:93:GLU:N	1:H:93:GLU:OE1	2.52	0.41
2:D:153:MET:SD	2:D:153:MET:N	2.93	0.41
2:J:70:TRP:NE1	2:J:84:THR:HG21	2.35	0.41
2:J:113:ARG:CZ	2:J:114:PRO:HD2	2.50	0.41
1:H:102:PRO:HD2	1:H:105:LEU:HD21	2.03	0.41
1:H:137:GLN:O	1:H:139:VAL:HG13	2.20	0.41
2:L:208:MET:HE2	2:L:210:LEU:HD23	2.01	0.41
2:C:101:ARG:HD2	2:C:101:ARG:O	2.20	0.41
2:C:119:TRP:HE3	2:C:121:PHE:HZ	1.68	0.41
1:E:92:TYR:CE1	1:E:108:ALA:HB2	2.55	0.41



	lous page	Interatomic	Clash
Atom-1	Atom-2	distance $(Å)$	overlap(Å)
1.G.108.ALA.N	1.G.165.SEB.OG	2.52	0.41
1:H:131:GLU:OE1	1:H:131:GLU:N	2.53	0.41
2:L:185:THR:OG1	2:L:197:ASN:HB3	2.20	0.41
1:B:90:TRP:HB3	1:B:110:CYS:HB3	2.03	0.41
1:G:106:TYR:HE2	2:K:135:PHE:CE2	2.38	0.41
2:J:24:CYS:HA	2:J:102:CYS:HB2	2.02	0.41
1:H:100:ARG:HA	1:H:140:PHE:O	2.21	0.41
2:L:46:ARG:NH1	2:L:73:ARG:HG2	2.35	0.41
2:L:48:LEU:HD22	2:L:138:ALA:HB2	2.02	0.41
1:A:82:LEU:HD13	2:C:93:ASN:H	1.85	0.41
2:C:170:LYS:HE3	2:C:170:LYS:HA	2.01	0.41
2:D:49:ARG:O	2:D:69:SER:OG	2.31	0.41
2:K:184:ILE:HD11	2:K:264:HIS:HE1	1.82	0.41
2:J:180:TRP:CH2	2:J:201:THR:HB	2.56	0.41
2:C:89:THR:O	2:C:134:TYR:HA	2.20	0.41
2:I:206:ARG:NH2	2:I:253:TYR:HB2	2.36	0.41
2:K:83:ALA:HB2	2:K:103:ASN:OD1	2.21	0.41
2:K:86:ILE:HG12	2:K:138:ALA:HB1	2.02	0.41
2:K:110:THR:HG23	2:K:119:TRP:HZ2	1.86	0.41
1:F:91:ARG:HG2	1:F:92:TYR:N	2.35	0.41
2:J:265:LYS:HD3	2:J:266:GLY:N	2.35	0.41
1:A:134:TYR:O	1:A:163:ARG:NH2	2.54	0.41
2:C:27:GLU:CD	2:C:101:ARG:HE	2.23	0.41
2:C:88:VAL:HG22	2:C:136:ILE:HD12	2.03	0.41
2:L:88:VAL:HG22	2:L:136:ILE:CD1	2.49	0.41
2:L:186:ALA:HB2	2:L:196:VAL:HG13	2.01	0.41
2:C:26:SER:HA	2:C:100:VAL:HG12	2.03	0.41
2:D:45:LEU:HD11	2:D:84:THR:HG21	2.03	0.41
1:E:82:LEU:HD21	2:I:93:ASN:N	2.35	0.41
2:I:94:PHE:HB3	1:G:163:ARG:HH21	1.86	0.41
1:G:97:ASP:OD1	1:G:98:LEU:N	2.54	0.41
1:F:172:ARG:NH1	1:H:121:GLY:HA3	2.36	0.41
2:C:153:MET:SD	2:C:153:MET:N	2.94	0.41
2:C:180:TRP:HZ3	2:C:252:PRO:HG3	1.86	0.41
1:E:136:ASN:OD1	1:E:137:GLN:N	2.53	0.41
2:I:66:MET:O	2:I:124:ILE:HD12	2.21	0.41
2:1:229:LYS:HG2	2:1:231:THR:HG23	2.02	0.41
2:K:254:PHE:HB2	2:K:257:CYS:SG	2.61	0.41
1:F':89:PRO:O	1:F:110:CYS:HB2	2.21	0.41
2:J:88:VAL:HG23	2:J:135:PHE:C	2.41	0.41
2:J:210:LEU:HB2	2:J:249:GLN:HB3	2.02	0.41



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:H:143:ARG:O	1:H:156:CYS:N	2.54	0.41
2:L:70:TRP:HZ2	2:L:104:TYR:HH	1.68	0.41
1:A:95:ASP:HB3	1:A:105:LEU:O	2.21	0.41
1:A:99:ASN:HA	1:A:142:ARG:HH12	1.85	0.41
2:C:84:THR:HA	2:C:140:ASN:HA	2.03	0.41
2:C:159:SER:HA	2:C:160:PRO:HD3	1.95	0.41
1:B:107:HIS:HB3	1:B:165:SER:OG	2.21	0.41
2:I:40:LEU:HA	2:L:111:GLN:HE21	1.86	0.41
2:K:64:ILE:HD11	2:K:167:MET:SD	2.60	0.41
2:I:48:LEU:HD12	2:I:69:SER:O	2.21	0.40
2:J:113:ARG:HB2	2:J:117:GLY:O	2.21	0.40
2:L:209:ALA:O	2:L:210:LEU:HD22	2.21	0.40
2:C:111:GLN:NE2	2:K:40:LEU:HA	2.36	0.40
2:C:87:CYS:HA	2:C:99:CYS:HA	2.02	0.40
2:I:44:ASP:O	2:I:73:ARG:HG3	2.21	0.40
2:I:148:GLU:N	2:I:148:GLU:OE1	2.54	0.40
2:K:206:ARG:HE	2:K:207:TYR:N	2.19	0.40
2:J:227:GLN:H	2:J:230:GLN:NE2	2.19	0.40
1:H:97:ASP:OD2	1:H:100:ARG:HB2	2.21	0.40
2:L:164:ASP:OD1	2:L:167:MET:HB2	2.21	0.40
2:I:168:LYS:HE2	2:I:168:LYS:HB2	1.91	0.40
1:G:140:PHE:CD1	1:G:159:ARG:HG2	2.56	0.40
2:K:119:TRP:CD1	2:K:119:TRP:N	2.88	0.40
1:H:140:PHE:HD1	1:H:159:ARG:NE	2.19	0.40
2:L:112:THR:HA	2:L:119:TRP:HE1	1.86	0.40
1:A:99:ASN:OD1	1:A:142:ARG:HG3	2.22	0.40
1:B:107:HIS:CE1	1:B:164:VAL:HG23	2.56	0.40
2:D:72:LEU:HD23	2:D:73:ARG:N	2.37	0.40
2:I:44:ASP:O	2:I:45:LEU:HD23	2.22	0.40
2:K:206:ARG:NH2	2:K:222:VAL:H	2.18	0.40
2:K:250:LEU:HB3	2:K:264:HIS:CE1	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Perce	entiles
1	А	94/188~(50%)	92~(98%)	2(2%)	0	100	100
1	В	98/188~(52%)	95~(97%)	3~(3%)	0	100	100
1	Ε	94/188~(50%)	92~(98%)	2(2%)	0	100	100
1	F	94/188~(50%)	93~(99%)	1 (1%)	0	100	100
1	G	98/188~(52%)	95~(97%)	3~(3%)	0	100	100
1	Н	98/188~(52%)	94~(96%)	4 (4%)	0	100	100
2	\mathbf{C}	241/305~(79%)	227~(94%)	14~(6%)	0	100	100
2	D	223/305~(73%)	214 (96%)	9~(4%)	0	100	100
2	Ι	245/305~(80%)	223~(91%)	22 (9%)	0	100	100
2	J	236/305~(77%)	219~(93%)	17 (7%)	0	100	100
2	Κ	236/305~(77%)	224~(95%)	12~(5%)	0	100	100
2	L	248/305~(81%)	236~(95%)	12(5%)	0	100	100
All	All	$200\overline{5/2958}~(68\%)$	1904 (95%)	101 (5%)	0	100	100

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

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	Perce	ntiles
1	А	84/164~(51%)	83~(99%)	1 (1%)	71	84
1	В	88/164~(54%)	88 (100%)	0	100	100
1	Е	86/164~(52%)	84 (98%)	2(2%)	50	70
1	F	85/164~(52%)	84 (99%)	1 (1%)	71	84
1	G	89/164~(54%)	88 (99%)	1 (1%)	73	85
1	Н	88/164~(54%)	87~(99%)	1 (1%)	73	85
2	С	213/265~(80%)	212 (100%)	1 (0%)	88	93



Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	D	201/265~(76%)	200 (100%)	1 (0%)	88 93
2	Ι	217/265~(82%)	215~(99%)	2(1%)	78 88
2	J	211/265~(80%)	210 (100%)	1 (0%)	88 93
2	Κ	211/265~(80%)	210 (100%)	1 (0%)	88 93
2	L	221/265~(83%)	220 (100%)	1 (0%)	88 93
All	All	1794/2574 (70%)	1781 (99%)	13 (1%)	84 90

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	160	ARG
2	С	23	GLN
2	D	263	ARG
1	Ε	91	ARG
1	Ε	142	ARG
2	Ι	79	ARG
2	Ι	85	LYS
1	G	83	ASN
2	Κ	73	ARG
1	F	96	ARG
2	J	170	LYS
1	Н	160	ARG
2	L	113	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	152	HIS
2	С	111	GLN
2	D	205	ASN
2	D	249	GLN
2	Ι	143	ASN
1	F	152	HIS
1	Н	103	GLN
1	Н	107	HIS
2	L	95	GLN
2	L	111	GLN
2	L	139	HIS
2	L	143	ASN



Continued from previous page...

Mol	Chain	\mathbf{Res}	Type
2	L	230	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides 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 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-26834. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections (i)

6.1.1 Primary map



6.1.2 Raw map



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



6.2 Central slices (i)

6.2.1 Primary map



X Index: 147



Y Index: 147



Z Index: 147

6.2.2 Raw map



X Index: 147

Y Index: 147

Z Index: 147

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



6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 173



Y Index: 142



Z Index: 135

6.3.2 Raw map



X Index: 173

Y Index: 142



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



6.4 Orthogonal surface views (i)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.



Mask visualisation (i) 6.5

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

$emd_{26834}msk_{1.map}$ (i) 6.5.1





7 Map analysis (i)

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

7.1 Map-value distribution (i)



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



7.2 Volume estimate (i)



The volume at the recommended contour level is 100 nm^3 ; this corresponds to an approximate mass of 91 kDa.

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



7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.227 ${\rm \AA^{-1}}$



8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.227 ${\rm \AA^{-1}}$



8.2 Resolution estimates (i)

$\begin{bmatrix} Bosolution ostimato (Å) \end{bmatrix}$	Estimation criterion (FSC cut-off)			
Resolution estimate (A)	0.143	0.5	Half-bit	
Reported by author	4.40	-	-	
Author-provided FSC curve	4.37	5.89	4.54	
Unmasked-calculated*	6.96	9.34	7.41	

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.96 differs from the reported value 4.4 by more than 10 %



9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-26834 and PDB model 7UWK. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay (i)



The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.



9.2 Q-score mapped to coordinate model (i)



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

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).



9.4 Atom inclusion (i)



At the recommended contour level, 61% of all backbone atoms, 48% of all non-hydrogen atoms, are inside the map.



9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

	Q-score	Atom inclusion	Chain
10	0.1650	0.4816	All
1.0	0.1210	0.3954	А
	0.0780	0.4561	В
	0.1220	0.4494	С
	0.0650	0.2086	D
	0.2410	0.5856	Е
	0.2330	0.6542	F
	0.2480	0.6211	G
	0.2300	0.6291	Н
0.0	0.1990	0.5432	Ι
<0.0	0.1490	0.4558	J
	0.1790	0.4711	K
	0.2020	0.5606	L

