



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:55 PM GMT

PDB ID : 4QAE  
Title : Crystal structure of an engineered lipocalin (Anticalin) in complex with human hepcidin  
Authors : Giese, T.; Skerra, A.  
Deposited on : 2014-05-04  
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

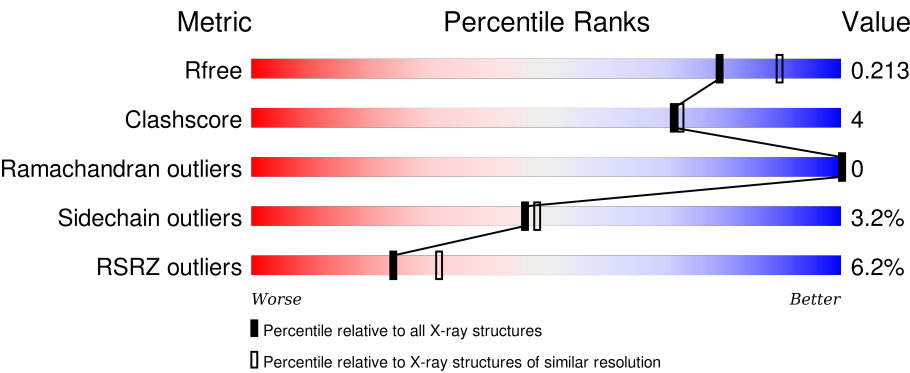
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R <sub>free</sub>	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	P	25	<div><div>12%</div><div><div></div><div>80%</div><div>20%</div></div></div>
1	Q	25	<div><div>16%</div><div><div></div><div>80%</div><div>16%</div><div>•</div></div></div>
1	R	25	<div><div>16%</div><div><div></div><div>84%</div><div>12%</div><div>•</div></div></div>
1	S	25	<div><div>16%</div><div><div></div><div>84%</div><div>8%</div><div>•</div><div>•</div></div></div>
1	T	25	<div><div>12%</div><div><div></div><div>76%</div><div>16%</div><div>8%</div></div></div>

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Mol	Chain	Length	Quality of chain
1	U	25	
2	A	188	
2	B	188	
2	C	188	
2	D	188	
2	E	188	
2	F	188	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MPD	A	201	-	-	-	X
4	MPD	B	202	-	-	-	X
4	MPD	D	202	-	-	-	X
4	MPD	E	201	-	-	-	X
4	MPD	F	201	-	-	-	X
4	MPD	F	203	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9938 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Hepcidin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	P	25	Total	C	N	O	S	0	0	0
			187	113	34	31	9			
1	Q	24	Total	C	N	O	S	0	0	0
			179	109	33	28	9			
1	R	24	Total	C	N	O	S	0	0	0
			179	109	33	28	9			
1	S	24	Total	C	N	O	S	0	0	0
			179	109	33	28	9			
1	T	23	Total	C	N	O	S	0	0	0
			172	105	32	26	9			
1	U	25	Total	C	N	O	S	0	0	0
			187	113	34	31	9			

- Molecule 2 is a protein called Neutrophil gelatinase-associated lipocalin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	172	Total	C	N	O	S	0	0	0
			1391	902	229	254	6			
2	B	175	Total	C	N	O	S	0	0	0
			1408	911	232	259	6			
2	C	163	Total	C	N	O	S	0	0	0
			1331	866	216	243	6			
2	D	164	Total	C	N	O	S	0	0	0
			1338	870	217	245	6			
2	E	166	Total	C	N	O	S	0	0	0
			1351	877	219	249	6			
2	F	164	Total	C	N	O	S	0	0	0
			1338	870	217	245	6			

There are 216 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	HIS	GLN	ENGINEERED MUTATION	UNP P80188

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Chain	Residue	Modelled	Actual	Comment	Reference
A	40	GLU	ALA	ENGINEERED MUTATION	UNP P80188
A	41	VAL	ILE	ENGINEERED MUTATION	UNP P80188
A	49	MET	GLN	ENGINEERED MUTATION	UNP P80188
A	52	TRP	TYR	ENGINEERED MUTATION	UNP P80188
A	59	GLU	LYS	ENGINEERED MUTATION	UNP P80188
A	68	ILE	SER	ENGINEERED MUTATION	UNP P80188
A	70	MET	LEU	ENGINEERED MUTATION	UNP P80188
A	71	PRO	PHE	ENGINEERED MUTATION	UNP P80188
A	72	LEU	ARG	ENGINEERED MUTATION	UNP P80188
A	73	ALA	LYS	ENGINEERED MUTATION	UNP P80188
A	74	GLU	LYS	ENGINEERED MUTATION	UNP P80188
A	77	GLU	ASP	ENGINEERED MUTATION	UNP P80188
A	79	LEU	TRP	ENGINEERED MUTATION	UNP P80188
A	80	PHE	ILE	ENGINEERED MUTATION	UNP P80188
A	81	GLN	ARG	ENGINEERED MUTATION	UNP P80188
A	87	SER	CYS	ENGINEERED MUTATION	UNP P80188
A	96	GLY	ASN	ENGINEERED MUTATION	UNP P80188
A	100	GLY	TYR	ENGINEERED MUTATION	UNP P80188
A	103	ARG	LEU	ENGINEERED MUTATION	UNP P80188
A	106	GLY	TYR	ENGINEERED MUTATION	UNP P80188
A	125	VAL	LYS	ENGINEERED MUTATION	UNP P80188
A	127	TRP	SER	ENGINEERED MUTATION	UNP P80188
A	132	VAL	TYR	ENGINEERED MUTATION	UNP P80188
A	134	TRP	LYS	ENGINEERED MUTATION	UNP P80188
A	135	VAL	ILE	ENGINEERED MUTATION	UNP P80188
A	179	SER	-	EXPRESSION TAG	UNP P80188
A	180	ALA	-	EXPRESSION TAG	UNP P80188
A	181	TRP	-	EXPRESSION TAG	UNP P80188
A	182	SER	-	EXPRESSION TAG	UNP P80188
A	183	HIS	-	EXPRESSION TAG	UNP P80188
A	184	PRO	-	EXPRESSION TAG	UNP P80188
A	185	GLN	-	EXPRESSION TAG	UNP P80188
A	186	PHE	-	EXPRESSION TAG	UNP P80188
A	187	GLU	-	EXPRESSION TAG	UNP P80188
A	188	LYS	-	EXPRESSION TAG	UNP P80188
B	28	HIS	GLN	ENGINEERED MUTATION	UNP P80188
B	40	GLU	ALA	ENGINEERED MUTATION	UNP P80188
B	41	VAL	ILE	ENGINEERED MUTATION	UNP P80188
B	49	MET	GLN	ENGINEERED MUTATION	UNP P80188
B	52	TRP	TYR	ENGINEERED MUTATION	UNP P80188
B	59	GLU	LYS	ENGINEERED MUTATION	UNP P80188
B	68	ILE	SER	ENGINEERED MUTATION	UNP P80188

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Chain	Residue	Modelled	Actual	Comment	Reference
B	70	MET	LEU	ENGINEERED MUTATION	UNP P80188
B	71	PRO	PHE	ENGINEERED MUTATION	UNP P80188
B	72	LEU	ARG	ENGINEERED MUTATION	UNP P80188
B	73	ALA	LYS	ENGINEERED MUTATION	UNP P80188
B	74	GLU	LYS	ENGINEERED MUTATION	UNP P80188
B	77	GLU	ASP	ENGINEERED MUTATION	UNP P80188
B	79	LEU	TRP	ENGINEERED MUTATION	UNP P80188
B	80	PHE	ILE	ENGINEERED MUTATION	UNP P80188
B	81	GLN	ARG	ENGINEERED MUTATION	UNP P80188
B	87	SER	CYS	ENGINEERED MUTATION	UNP P80188
B	96	GLY	ASN	ENGINEERED MUTATION	UNP P80188
B	100	GLY	TYR	ENGINEERED MUTATION	UNP P80188
B	103	ARG	LEU	ENGINEERED MUTATION	UNP P80188
B	106	GLY	TYR	ENGINEERED MUTATION	UNP P80188
B	125	VAL	LYS	ENGINEERED MUTATION	UNP P80188
B	127	TRP	SER	ENGINEERED MUTATION	UNP P80188
B	132	VAL	TYR	ENGINEERED MUTATION	UNP P80188
B	134	TRP	LYS	ENGINEERED MUTATION	UNP P80188
B	135	VAL	ILE	ENGINEERED MUTATION	UNP P80188
B	179	SER	-	EXPRESSION TAG	UNP P80188
B	180	ALA	-	EXPRESSION TAG	UNP P80188
B	181	TRP	-	EXPRESSION TAG	UNP P80188
B	182	SER	-	EXPRESSION TAG	UNP P80188
B	183	HIS	-	EXPRESSION TAG	UNP P80188
B	184	PRO	-	EXPRESSION TAG	UNP P80188
B	185	GLN	-	EXPRESSION TAG	UNP P80188
B	186	PHE	-	EXPRESSION TAG	UNP P80188
B	187	GLU	-	EXPRESSION TAG	UNP P80188
B	188	LYS	-	EXPRESSION TAG	UNP P80188
C	28	HIS	GLN	ENGINEERED MUTATION	UNP P80188
C	40	GLU	ALA	ENGINEERED MUTATION	UNP P80188
C	41	VAL	ILE	ENGINEERED MUTATION	UNP P80188
C	49	MET	GLN	ENGINEERED MUTATION	UNP P80188
C	52	TRP	TYR	ENGINEERED MUTATION	UNP P80188
C	59	GLU	LYS	ENGINEERED MUTATION	UNP P80188
C	68	ILE	SER	ENGINEERED MUTATION	UNP P80188
C	70	MET	LEU	ENGINEERED MUTATION	UNP P80188
C	71	PRO	PHE	ENGINEERED MUTATION	UNP P80188
C	72	LEU	ARG	ENGINEERED MUTATION	UNP P80188
C	73	ALA	LYS	ENGINEERED MUTATION	UNP P80188
C	74	GLU	LYS	ENGINEERED MUTATION	UNP P80188
C	77	GLU	ASP	ENGINEERED MUTATION	UNP P80188

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Chain	Residue	Modelled	Actual	Comment	Reference
C	79	LEU	TRP	ENGINEERED MUTATION	UNP P80188
C	80	PHE	ILE	ENGINEERED MUTATION	UNP P80188
C	81	GLN	ARG	ENGINEERED MUTATION	UNP P80188
C	87	SER	CYS	ENGINEERED MUTATION	UNP P80188
C	96	GLY	ASN	ENGINEERED MUTATION	UNP P80188
C	100	GLY	TYR	ENGINEERED MUTATION	UNP P80188
C	103	ARG	LEU	ENGINEERED MUTATION	UNP P80188
C	106	GLY	TYR	ENGINEERED MUTATION	UNP P80188
C	125	VAL	LYS	ENGINEERED MUTATION	UNP P80188
C	127	TRP	SER	ENGINEERED MUTATION	UNP P80188
C	132	VAL	TYR	ENGINEERED MUTATION	UNP P80188
C	134	TRP	LYS	ENGINEERED MUTATION	UNP P80188
C	135	VAL	ILE	ENGINEERED MUTATION	UNP P80188
C	179	SER	-	EXPRESSION TAG	UNP P80188
C	180	ALA	-	EXPRESSION TAG	UNP P80188
C	181	TRP	-	EXPRESSION TAG	UNP P80188
C	182	SER	-	EXPRESSION TAG	UNP P80188
C	183	HIS	-	EXPRESSION TAG	UNP P80188
C	184	PRO	-	EXPRESSION TAG	UNP P80188
C	185	GLN	-	EXPRESSION TAG	UNP P80188
C	186	PHE	-	EXPRESSION TAG	UNP P80188
C	187	GLU	-	EXPRESSION TAG	UNP P80188
C	188	LYS	-	EXPRESSION TAG	UNP P80188
D	28	HIS	GLN	ENGINEERED MUTATION	UNP P80188
D	40	GLU	ALA	ENGINEERED MUTATION	UNP P80188
D	41	VAL	ILE	ENGINEERED MUTATION	UNP P80188
D	49	MET	GLN	ENGINEERED MUTATION	UNP P80188
D	52	TRP	TYR	ENGINEERED MUTATION	UNP P80188
D	59	GLU	LYS	ENGINEERED MUTATION	UNP P80188
D	68	ILE	SER	ENGINEERED MUTATION	UNP P80188
D	70	MET	LEU	ENGINEERED MUTATION	UNP P80188
D	71	PRO	PHE	ENGINEERED MUTATION	UNP P80188
D	72	LEU	ARG	ENGINEERED MUTATION	UNP P80188
D	73	ALA	LYS	ENGINEERED MUTATION	UNP P80188
D	74	GLU	LYS	ENGINEERED MUTATION	UNP P80188
D	77	GLU	ASP	ENGINEERED MUTATION	UNP P80188
D	79	LEU	TRP	ENGINEERED MUTATION	UNP P80188
D	80	PHE	ILE	ENGINEERED MUTATION	UNP P80188
D	81	GLN	ARG	ENGINEERED MUTATION	UNP P80188
D	87	SER	CYS	ENGINEERED MUTATION	UNP P80188
D	96	GLY	ASN	ENGINEERED MUTATION	UNP P80188
D	100	GLY	TYR	ENGINEERED MUTATION	UNP P80188

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Chain	Residue	Modelled	Actual	Comment	Reference
D	103	ARG	LEU	ENGINEERED MUTATION	UNP P80188
D	106	GLY	TYR	ENGINEERED MUTATION	UNP P80188
D	125	VAL	LYS	ENGINEERED MUTATION	UNP P80188
D	127	TRP	SER	ENGINEERED MUTATION	UNP P80188
D	132	VAL	TYR	ENGINEERED MUTATION	UNP P80188
D	134	TRP	LYS	ENGINEERED MUTATION	UNP P80188
D	135	VAL	ILE	ENGINEERED MUTATION	UNP P80188
D	179	SER	-	EXPRESSION TAG	UNP P80188
D	180	ALA	-	EXPRESSION TAG	UNP P80188
D	181	TRP	-	EXPRESSION TAG	UNP P80188
D	182	SER	-	EXPRESSION TAG	UNP P80188
D	183	HIS	-	EXPRESSION TAG	UNP P80188
D	184	PRO	-	EXPRESSION TAG	UNP P80188
D	185	GLN	-	EXPRESSION TAG	UNP P80188
D	186	PHE	-	EXPRESSION TAG	UNP P80188
D	187	GLU	-	EXPRESSION TAG	UNP P80188
D	188	LYS	-	EXPRESSION TAG	UNP P80188
E	28	HIS	GLN	ENGINEERED MUTATION	UNP P80188
E	40	GLU	ALA	ENGINEERED MUTATION	UNP P80188
E	41	VAL	ILE	ENGINEERED MUTATION	UNP P80188
E	49	MET	GLN	ENGINEERED MUTATION	UNP P80188
E	52	TRP	TYR	ENGINEERED MUTATION	UNP P80188
E	59	GLU	LYS	ENGINEERED MUTATION	UNP P80188
E	68	ILE	SER	ENGINEERED MUTATION	UNP P80188
E	70	MET	LEU	ENGINEERED MUTATION	UNP P80188
E	71	PRO	PHE	ENGINEERED MUTATION	UNP P80188
E	72	LEU	ARG	ENGINEERED MUTATION	UNP P80188
E	73	ALA	LYS	ENGINEERED MUTATION	UNP P80188
E	74	GLU	LYS	ENGINEERED MUTATION	UNP P80188
E	77	GLU	ASP	ENGINEERED MUTATION	UNP P80188
E	79	LEU	TRP	ENGINEERED MUTATION	UNP P80188
E	80	PHE	ILE	ENGINEERED MUTATION	UNP P80188
E	81	GLN	ARG	ENGINEERED MUTATION	UNP P80188
E	87	SER	CYS	ENGINEERED MUTATION	UNP P80188
E	96	GLY	ASN	ENGINEERED MUTATION	UNP P80188
E	100	GLY	TYR	ENGINEERED MUTATION	UNP P80188
E	103	ARG	LEU	ENGINEERED MUTATION	UNP P80188
E	106	GLY	TYR	ENGINEERED MUTATION	UNP P80188
E	125	VAL	LYS	ENGINEERED MUTATION	UNP P80188
E	127	TRP	SER	ENGINEERED MUTATION	UNP P80188
E	132	VAL	TYR	ENGINEERED MUTATION	UNP P80188
E	134	TRP	LYS	ENGINEERED MUTATION	UNP P80188

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Chain	Residue	Modelled	Actual	Comment	Reference
E	135	VAL	ILE	ENGINEERED MUTATION	UNP P80188
E	179	SER	-	EXPRESSION TAG	UNP P80188
E	180	ALA	-	EXPRESSION TAG	UNP P80188
E	181	TRP	-	EXPRESSION TAG	UNP P80188
E	182	SER	-	EXPRESSION TAG	UNP P80188
E	183	HIS	-	EXPRESSION TAG	UNP P80188
E	184	PRO	-	EXPRESSION TAG	UNP P80188
E	185	GLN	-	EXPRESSION TAG	UNP P80188
E	186	PHE	-	EXPRESSION TAG	UNP P80188
E	187	GLU	-	EXPRESSION TAG	UNP P80188
E	188	LYS	-	EXPRESSION TAG	UNP P80188
F	28	HIS	GLN	ENGINEERED MUTATION	UNP P80188
F	40	GLU	ALA	ENGINEERED MUTATION	UNP P80188
F	41	VAL	ILE	ENGINEERED MUTATION	UNP P80188
F	49	MET	GLN	ENGINEERED MUTATION	UNP P80188
F	52	TRP	TYR	ENGINEERED MUTATION	UNP P80188
F	59	GLU	LYS	ENGINEERED MUTATION	UNP P80188
F	68	ILE	SER	ENGINEERED MUTATION	UNP P80188
F	70	MET	LEU	ENGINEERED MUTATION	UNP P80188
F	71	PRO	PHE	ENGINEERED MUTATION	UNP P80188
F	72	LEU	ARG	ENGINEERED MUTATION	UNP P80188
F	73	ALA	LYS	ENGINEERED MUTATION	UNP P80188
F	74	GLU	LYS	ENGINEERED MUTATION	UNP P80188
F	77	GLU	ASP	ENGINEERED MUTATION	UNP P80188
F	79	LEU	TRP	ENGINEERED MUTATION	UNP P80188
F	80	PHE	ILE	ENGINEERED MUTATION	UNP P80188
F	81	GLN	ARG	ENGINEERED MUTATION	UNP P80188
F	87	SER	CYS	ENGINEERED MUTATION	UNP P80188
F	96	GLY	ASN	ENGINEERED MUTATION	UNP P80188
F	100	GLY	TYR	ENGINEERED MUTATION	UNP P80188
F	103	ARG	LEU	ENGINEERED MUTATION	UNP P80188
F	106	GLY	TYR	ENGINEERED MUTATION	UNP P80188
F	125	VAL	LYS	ENGINEERED MUTATION	UNP P80188
F	127	TRP	SER	ENGINEERED MUTATION	UNP P80188
F	132	VAL	TYR	ENGINEERED MUTATION	UNP P80188
F	134	TRP	LYS	ENGINEERED MUTATION	UNP P80188
F	135	VAL	ILE	ENGINEERED MUTATION	UNP P80188
F	179	SER	-	EXPRESSION TAG	UNP P80188
F	180	ALA	-	EXPRESSION TAG	UNP P80188
F	181	TRP	-	EXPRESSION TAG	UNP P80188
F	182	SER	-	EXPRESSION TAG	UNP P80188
F	183	HIS	-	EXPRESSION TAG	UNP P80188

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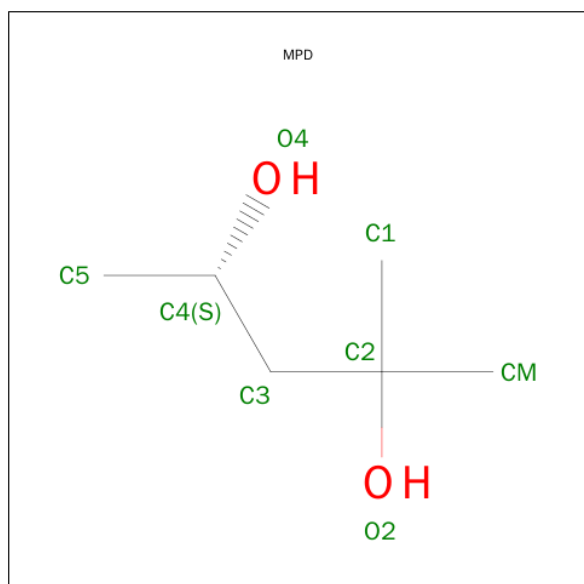
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Chain	Residue	Modelled	Actual	Comment	Reference
F	184	PRO	-	EXPRESSION TAG	UNP P80188
F	185	GLN	-	EXPRESSION TAG	UNP P80188
F	186	PHE	-	EXPRESSION TAG	UNP P80188
F	187	GLU	-	EXPRESSION TAG	UNP P80188
F	188	LYS	-	EXPRESSION TAG	UNP P80188

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	P	1	Total Cl 1 1	0	0
3	B	1	Total Cl 1 1	0	0
3	D	1	Total Cl 1 1	0	0
3	S	1	Total Cl 1 1	0	0
3	U	1	Total Cl 1 1	0	0

- Molecule 4 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: C<sub>6</sub>H<sub>14</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 8 6 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			8	6	2		
4	D	1	Total	C	O	0	0
			8	6	2		
4	E	1	Total	C	O	0	0
			8	6	2		
4	E	1	Total	C	O	0	0
			8	6	2		
4	F	1	Total	C	O	0	0
			8	6	2		
4	F	1	Total	C	O	0	0
			8	6	2		
4	F	1	Total	C	O	0	0
			8	6	2		

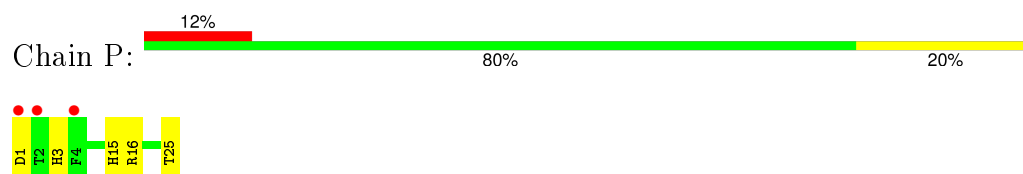
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	P	11	Total	O	0	0
			11	11		
5	Q	10	Total	O	0	0
			10	10		
5	R	11	Total	O	0	0
			11	11		
5	S	8	Total	O	0	0
			8	8		
5	T	8	Total	O	0	0
			8	8		
5	U	9	Total	O	0	0
			9	9		
5	A	126	Total	O	0	0
			126	126		
5	B	117	Total	O	0	0
			117	117		
5	C	66	Total	O	0	0
			66	66		
5	D	76	Total	O	0	0
			76	76		
5	E	107	Total	O	0	0
			107	107		
5	F	80	Total	O	0	0
			80	80		

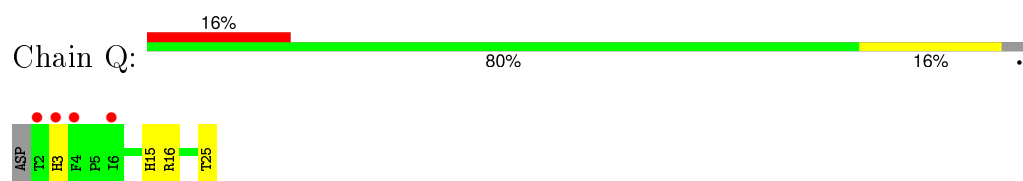
### 3 Residue-property plots [i](#)

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

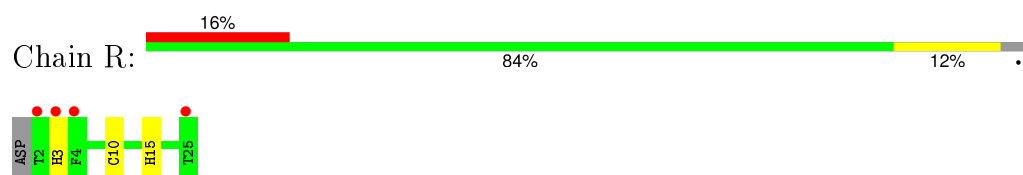
#### • Molecule 1: Hepcidin



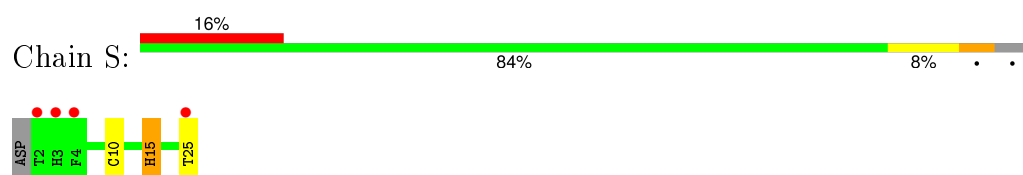
#### • Molecule 1: Hepcidin



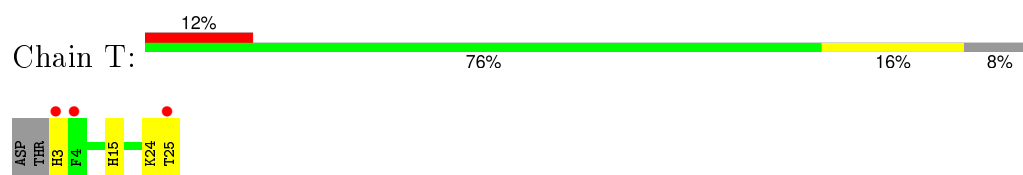
#### • Molecule 1: Hepcidin



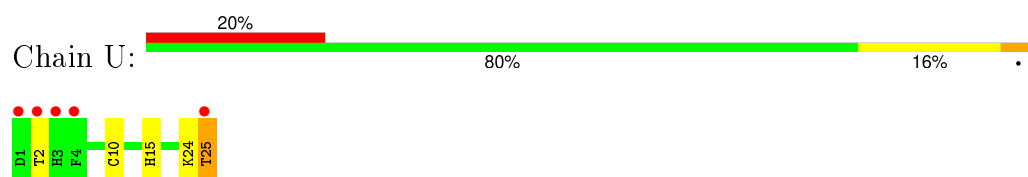
#### • Molecule 1: Hepcidin



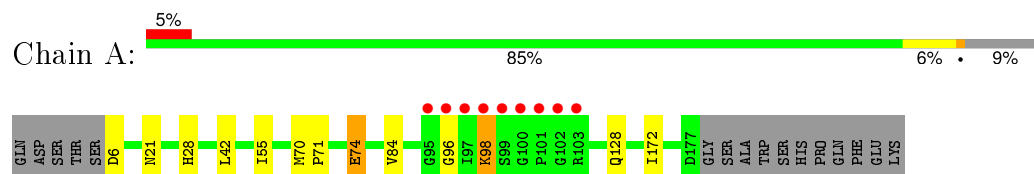
#### • Molecule 1: Hepcidin



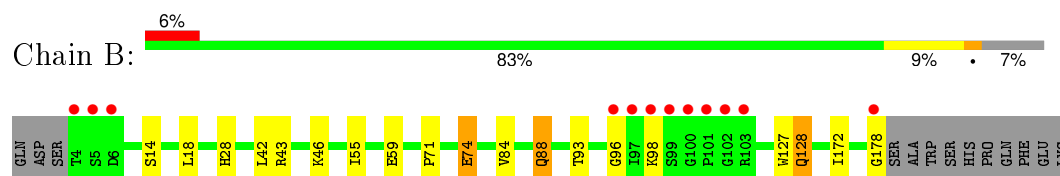
#### • Molecule 1: Hepcidin



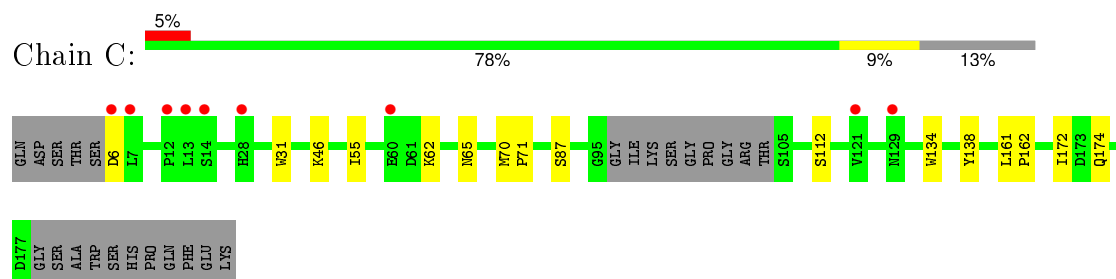
- Molecule 2: Neutrophil gelatinase-associated lipocalin



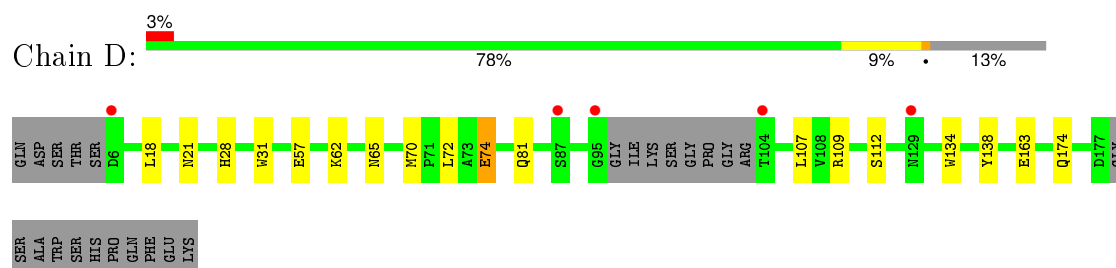
- Molecule 2: Neutrophil gelatinase-associated lipocalin



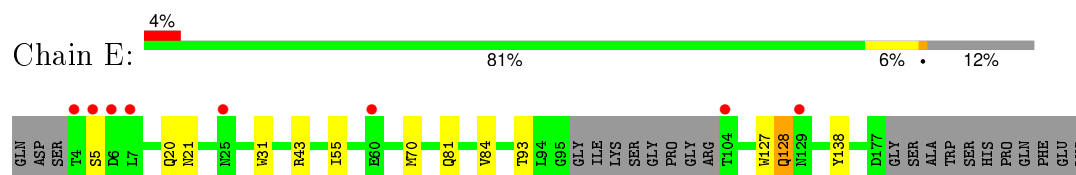
- Molecule 2: Neutrophil gelatinase-associated lipocalin



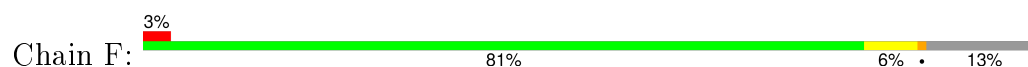
- Molecule 2: Neutrophil gelatinase-associated lipocalin

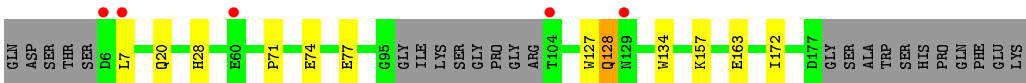


- Molecule 2: Neutrophil gelatinase-associated lipocalin



- Molecule 2: Neutrophil gelatinase-associated lipocalin





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	126.89Å 126.89Å 156.71Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.18 – 2.10 33.18 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (33.18-2.10) 99.8 (33.18-2.10)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.28 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.166 , 0.206 0.175 , 0.213	Depositor DCC
$R_{free}$ test set	4267 reflections (5.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	29.0	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 53.5	EDS
Estimated twinning fraction	0.000 for -h,-k,l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	3 of 85223 reflections (0.004%)	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	9938	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.64 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.4820e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	P	0.76	0/191	0.82	0/252
1	Q	0.73	0/183	0.83	0/241
1	R	0.61	0/183	0.72	0/241
1	S	0.66	0/183	0.68	0/241
1	T	0.73	0/176	0.90	0/231
1	U	0.62	0/191	0.75	0/252
2	A	0.74	2/1430 (0.1%)	0.77	0/1943
2	B	0.78	1/1447 (0.1%)	0.80	1/1966 (0.1%)
2	C	0.61	0/1368	0.77	0/1859
2	D	0.68	1/1375 (0.1%)	0.77	0/1869
2	E	0.70	0/1388	0.79	0/1887
2	F	0.68	0/1375	0.76	0/1869
All	All	0.70	4/9490 (0.0%)	0.78	1/12851 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	74	GLU	CD-OE1	6.37	1.32	1.25
2	B	74	GLU	CD-OE1	5.76	1.31	1.25
2	D	74	GLU	CD-OE1	5.57	1.31	1.25
2	A	74	GLU	CD-OE2	-5.30	1.19	1.25

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	43	ARG	NE-CZ-NH2	-5.10	117.75	120.30

There are no chirality outliers.

There are no planarity outliers.



## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	P	187	0	172	6	0
1	Q	179	0	165	5	0
1	R	179	0	165	1	0
1	S	179	0	165	2	0
1	T	172	0	158	2	0
1	U	187	0	172	4	0
2	A	1391	0	1369	14	0
2	B	1408	0	1384	14	0
2	C	1331	0	1303	14	0
2	D	1338	0	1310	12	0
2	E	1351	0	1322	10	0
2	F	1338	0	1310	6	0
3	B	1	0	0	0	0
3	D	1	0	0	0	0
3	P	1	0	0	0	0
3	S	1	0	0	0	0
3	U	1	0	0	0	0
4	A	8	0	14	0	0
4	B	8	0	14	0	0
4	D	8	0	14	4	0
4	E	16	0	28	3	0
4	F	24	0	42	3	0
5	A	126	0	0	6	0
5	B	117	0	0	5	0
5	C	66	0	0	3	0
5	D	76	0	0	4	0
5	E	107	0	0	9	0
5	F	80	0	0	2	0
5	P	11	0	0	0	0
5	Q	10	0	0	1	0
5	R	11	0	0	0	0
5	S	8	0	0	0	0
5	T	8	0	0	0	0
5	U	9	0	0	0	0
All	All	9938	0	9107	80	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 4.

All (80) 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)
2:A:84:VAL:HG21	2:A:96:GLY:HA2	1.51	0.91
2:E:43:ARG:HD2	5:E:362:HOH:O	1.73	0.88
2:A:21:ASN:HB2	5:A:318:HOH:O	1.86	0.76
2:D:70:MET:CE	5:D:341:HOH:O	2.35	0.74
4:D:202:MPD:H53	4:D:202:MPD:HM1	1.69	0.73
2:A:74:GLU:HG2	5:A:370:HOH:O	1.92	0.68
1:U:24:LYS:O	1:U:25:THR:HG23	1.93	0.68
2:A:74:GLU:OE2	5:A:370:HOH:O	2.10	0.68
2:B:18:LEU:HD21	2:B:88:GLN:HG2	1.75	0.67
2:A:84:VAL:HG21	2:A:96:GLY:CA	2.22	0.66
2:A:84:VAL:CG2	2:A:96:GLY:HA2	2.25	0.64
1:U:25:THR:HB	2:E:55:ILE:HD13	1.81	0.64
4:E:201:MPD:H51	5:E:407:HOH:O	1.98	0.61
2:B:93:THR:HG21	2:B:98:LYS:HE3	1.83	0.60
2:C:46:LYS:HE3	4:F:203:MPD:HM1	1.84	0.60
1:Q:25:THR:HG23	2:C:55:ILE:HD11	1.85	0.58
2:A:55:ILE:HD12	2:A:55:ILE:N	2.20	0.57
2:A:70:MET:CE	5:A:380:HOH:O	2.52	0.57
2:E:127:TRP:CD1	2:E:128:GLN:HG3	2.40	0.56
2:B:93:THR:HG21	2:B:98:LYS:CE	2.37	0.55
2:D:74:GLU:HG2	5:E:301:HOH:O	2.06	0.54
2:E:20:GLN:HG2	5:E:384:HOH:O	2.07	0.54
2:B:84:VAL:HG21	2:B:96:GLY:HA2	1.90	0.53
2:C:70:MET:CE	5:C:241:HOH:O	2.56	0.53
2:A:98:LYS:HA	2:A:98:LYS:HE2	1.90	0.53
1:P:3:HIS:CE1	5:B:333:HOH:O	2.62	0.53
2:E:70:MET:HE3	5:E:400:HOH:O	2.10	0.52
2:F:74:GLU:OE2	5:F:351:HOH:O	2.19	0.52
2:D:70:MET:HE3	5:D:341:HOH:O	2.03	0.52
2:B:178:GLY:C	5:B:323:HOH:O	2.48	0.51
2:B:18:LEU:CD2	2:B:88:GLN:HG2	2.41	0.51
2:F:71:PRO:HG3	2:F:172:ILE:HD11	1.93	0.51
1:P:3:HIS:HE1	5:B:333:HOH:O	1.93	0.50
2:C:71:PRO:HG3	2:C:172:ILE:HD11	1.94	0.50
4:D:202:MPD:C5	4:D:202:MPD:HM1	2.41	0.49
2:D:62:LYS:NZ	5:D:311:HOH:O	2.46	0.49
1:P:25:THR:HB	2:B:55:ILE:HD13	1.93	0.49
1:T:24:LYS:HG3	1:T:25:THR:HG23	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:25:THR:HB	2:B:55:ILE:CD1	2.43	0.48
1:U:25:THR:CB	2:E:55:ILE:HD13	2.43	0.48
2:B:127:TRP:CD1	2:B:128:GLN:HG3	2.49	0.48
2:C:62:LYS:HA	2:C:62:LYS:HE2	1.94	0.48
2:C:70:MET:HE1	5:C:241:HOH:O	2.14	0.47
2:D:174:GLN:HB2	4:D:202:MPD:H11	1.97	0.47
1:S:15:HIS:HB2	4:F:203:MPD:HM3	1.96	0.47
2:A:70:MET:HE3	5:A:380:HOH:O	2.14	0.47
2:C:6:ASP:N	5:C:232:HOH:O	2.48	0.47
1:T:3:HIS:CD2	2:D:65:ASN:HB3	2.50	0.46
1:Q:16:ARG:NH1	2:B:42:LEU:HD12	2.30	0.46
1:Q:25:THR:HB	5:Q:101:HOH:O	2.15	0.46
1:P:16:ARG:HD3	2:A:42:LEU:HD12	1.98	0.46
2:B:74:GLU:OE2	5:B:311:HOH:O	2.21	0.46
2:C:174:GLN:HB2	4:F:201:MPD:H52	1.97	0.46
2:D:81:GLN:HG2	5:D:313:HOH:O	2.15	0.45
1:Q:25:THR:HG23	2:C:55:ILE:CD1	2.47	0.45
2:E:81:GLN:HG2	5:E:313:HOH:O	2.17	0.45
4:E:201:MPD:C5	5:E:407:HOH:O	2.58	0.45
2:F:157:LYS:NZ	2:F:163:GLU:OE1	2.50	0.44
1:Q:3:HIS:CD2	2:C:65:ASN:HB3	2.52	0.44
2:A:71:PRO:HG3	2:A:172:ILE:HD11	2.00	0.44
2:F:74:GLU:HG2	5:F:351:HOH:O	2.18	0.43
2:C:31:TRP:CE3	2:C:138:TYR:HB3	2.53	0.43
2:F:127:TRP:NE1	2:F:128:GLN:HG3	2.33	0.43
2:C:62:LYS:HA	2:C:62:LYS:CE	2.48	0.42
2:E:31:TRP:CE3	2:E:138:TYR:HB3	2.54	0.42
2:A:128:GLN:HG3	5:B:323:HOH:O	2.20	0.42
2:E:84:VAL:CG2	2:E:93:THR:OG1	2.67	0.42
1:S:10:CYS:HA	2:D:134:TRP:CH2	2.55	0.41
2:B:46:LYS:HE3	4:E:201:MPD:CM	2.49	0.41
2:D:31:TRP:CE3	2:D:138:TYR:HB3	2.54	0.41
2:E:70:MET:CE	5:E:400:HOH:O	2.65	0.41
2:D:74:GLU:OE2	5:E:301:HOH:O	2.22	0.41
2:D:18:LEU:HD13	2:D:109:ARG:HG3	2.02	0.41
1:R:10:CYS:HA	2:C:134:TRP:CH2	2.55	0.41
2:D:72:LEU:O	4:D:202:MPD:HM1	2.20	0.40
2:A:98:LYS:HE3	5:A:314:HOH:O	2.20	0.40
1:U:10:CYS:HA	2:F:134:TRP:CH2	2.56	0.40
1:P:1:ASP:N	2:B:59:GLU:HG2	2.36	0.40
2:C:161:LEU:HA	2:C:162:PRO:HD3	1.99	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:71:PRO:HG3	2:B:172:ILE:HD11	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	P	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
1	Q	22/25 (88%)	21 (96%)	1 (4%)	0	100	100
1	R	22/25 (88%)	21 (96%)	1 (4%)	0	100	100
1	S	22/25 (88%)	21 (96%)	1 (4%)	0	100	100
1	T	21/25 (84%)	20 (95%)	1 (5%)	0	100	100
1	U	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
2	A	170/188 (90%)	166 (98%)	4 (2%)	0	100	100
2	B	173/188 (92%)	167 (96%)	6 (4%)	0	100	100
2	C	159/188 (85%)	154 (97%)	5 (3%)	0	100	100
2	D	160/188 (85%)	156 (98%)	4 (2%)	0	100	100
2	E	162/188 (86%)	158 (98%)	4 (2%)	0	100	100
2	F	160/188 (85%)	155 (97%)	5 (3%)	0	100	100
All	All	1117/1278 (87%)	1083 (97%)	34 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

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

resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	P	23/23 (100%)	22 (96%)	1 (4%)	35	34
1	Q	22/23 (96%)	21 (96%)	1 (4%)	34	32
1	R	22/23 (96%)	20 (91%)	2 (9%)	12	7
1	S	22/23 (96%)	20 (91%)	2 (9%)	12	7
1	T	21/23 (91%)	20 (95%)	1 (5%)	31	29
1	U	23/23 (100%)	20 (87%)	3 (13%)	5	2
2	A	155/169 (92%)	152 (98%)	3 (2%)	65	70
2	B	157/169 (93%)	153 (98%)	4 (2%)	55	59
2	C	149/169 (88%)	147 (99%)	2 (1%)	76	82
2	D	150/169 (89%)	144 (96%)	6 (4%)	38	38
2	E	152/169 (90%)	149 (98%)	3 (2%)	63	68
2	F	150/169 (89%)	145 (97%)	5 (3%)	45	47
All	All	1046/1152 (91%)	1013 (97%)	33 (3%)	46	48

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	15	HIS
1	Q	15	HIS
1	R	3	HIS
1	R	15	HIS
1	S	15	HIS
1	S	25	THR
1	T	15	HIS
1	U	2	THR
1	U	15	HIS
1	U	25	THR
2	A	6	ASP
2	A	28	HIS
2	A	98	LYS
2	B	14	SER
2	B	28	HIS
2	B	88	GLN
2	B	128	GLN
2	C	87	SER

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Mol	Chain	Res	Type
2	C	112	SER
2	D	21	ASN
2	D	28	HIS
2	D	57	GLU
2	D	107	LEU
2	D	112	SER
2	D	163	GLU
2	E	5	SER
2	E	21	ASN
2	E	128	GLN
2	F	7	LEU
2	F	20	GLN
2	F	28	HIS
2	F	77	GLU
2	F	128	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 5 are monoatomic - leaving 8 for Mogul analysis.

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	$\# Z  > 2$
4	MPD	A	201	-	6,7,7	0.36	0	7,10,10	0.45	0
4	MPD	B	202	-	6,7,7	0.50	0	7,10,10	1.24	0
4	MPD	D	202	-	6,7,7	0.46	0	7,10,10	0.51	0
4	MPD	E	201	-	6,7,7	0.26	0	7,10,10	0.62	0
4	MPD	E	202	-	6,7,7	0.42	0	7,10,10	0.67	0
4	MPD	F	201	-	6,7,7	0.31	0	7,10,10	0.77	0
4	MPD	F	202	-	6,7,7	0.37	0	7,10,10	0.63	0
4	MPD	F	203	-	6,7,7	0.32	0	7,10,10	0.65	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
4	MPD	A	201	-	-	0/5/5/5	0/0/0/0
4	MPD	B	202	-	-	0/5/5/5	0/0/0/0
4	MPD	D	202	-	-	0/5/5/5	0/0/0/0
4	MPD	E	201	-	-	0/5/5/5	0/0/0/0
4	MPD	E	202	-	-	0/5/5/5	0/0/0/0
4	MPD	F	201	-	-	0/5/5/5	0/0/0/0
4	MPD	F	202	-	-	0/5/5/5	0/0/0/0
4	MPD	F	203	-	-	0/5/5/5	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.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	202	MPD	4	0
4	E	201	MPD	3	0
4	F	201	MPD	1	0
4	F	203	MPD	2	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	P	25/25 (100%)	0.20	3 (12%) 6 8	17, 21, 77, 107	0
1	Q	24/25 (96%)	0.48	4 (16%) 2 3	17, 24, 77, 90	0
1	R	24/25 (96%)	0.23	4 (16%) 2 3	25, 32, 74, 78	0
1	S	24/25 (96%)	0.36	4 (16%) 2 3	25, 31, 75, 86	0
1	T	23/25 (92%)	0.98	3 (13%) 5 6	21, 29, 73, 94	0
1	U	25/25 (100%)	0.74	5 (20%) 1 2	22, 27, 88, 92	0
2	A	172/188 (91%)	-0.18	9 (5%) 31 39	17, 30, 58, 88	0
2	B	175/188 (93%)	-0.05	12 (6%) 20 27	14, 30, 74, 137	0
2	C	163/188 (86%)	0.07	9 (5%) 29 37	19, 47, 72, 82	0
2	D	164/188 (87%)	-0.03	5 (3%) 54 62	21, 43, 67, 80	0
2	E	166/188 (88%)	0.00	8 (4%) 34 43	16, 35, 67, 90	0
2	F	164/188 (87%)	-0.23	5 (3%) 54 62	21, 38, 56, 72	1 (0%)
All	All	1149/1278 (89%)	0.00	71 (6%) 24 32	14, 36, 72, 137	1 (0%)

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	101	PRO	10.2
1	T	4	PHE	9.3
2	B	100	GLY	8.5
1	Q	4	PHE	8.4
1	U	4	PHE	7.3
2	A	97	ILE	7.2
1	U	2	THR	6.9
1	S	4	PHE	6.0
2	B	99	SER	6.0
1	R	4	PHE	5.9
2	B	4	THR	5.9

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Mol	Chain	Res	Type	RSRZ
2	A	101	PRO	5.8
2	B	102	GLY	5.7
2	F	104	THR	5.7
2	B	96	GLY	5.3
1	U	1	ASP	5.2
1	P	4	PHE	5.1
2	A	96	GLY	5.1
2	A	103	ARG	5.0
1	P	2	THR	5.0
2	B	103	ARG	4.9
1	Q	2	THR	4.8
2	B	5	SER	4.8
2	E	4	THR	4.8
2	D	104	THR	4.6
2	C	60	GLU	4.4
2	E	104	THR	4.1
2	A	98	LYS	4.0
2	F	7	LEU	3.9
2	E	60	GLU	3.9
2	B	97	ILE	3.9
2	B	98	LYS	3.8
1	R	2	THR	3.7
2	C	6	ASP	3.7
2	A	99	SER	3.7
1	S	25	THR	3.7
2	E	7	LEU	3.6
2	F	6	ASP	3.6
2	A	100	GLY	3.6
1	S	3	HIS	3.5
1	U	3	HIS	3.5
1	U	25	THR	3.5
2	D	129	ASN	3.3
1	T	3	HIS	3.3
2	C	129	ASN	3.3
2	B	6	ASP	3.1
2	E	5	SER	3.0
2	D	6	ASP	3.0
2	C	12	PRO	3.0
2	D	87	SER	3.0
2	C	14	SER	2.9
2	F	129	ASN	2.9
2	B	178	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
2	A	102	GLY	2.8
1	Q	3	HIS	2.8
2	C	7	LEU	2.8
1	R	3	HIS	2.8
2	E	129	ASN	2.8
2	E	6	ASP	2.8
2	F	60	GLU	2.8
1	S	2	THR	2.7
1	P	1	ASP	2.7
1	R	25	THR	2.6
2	A	95	GLY	2.6
2	C	28	HIS	2.5
2	D	95	GLY	2.4
1	T	25	THR	2.3
2	E	25	ASN	2.2
2	C	13	LEU	2.2
1	Q	6	ILE	2.2
2	C	121	VAL	2.2

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	MPD	F	203	8/8	0.71	0.37	10.48	62,67,69,71	0
4	MPD	A	201	8/8	0.69	0.30	6.40	56,57,62,69	0
4	MPD	B	202	8/8	0.83	0.19	4.12	41,45,50,64	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	MPD	E	201	8/8	0.90	0.19	3.59	48,54,56,57	0
4	MPD	F	201	8/8	0.87	0.18	2.99	55,59,66,68	0
4	MPD	D	202	8/8	0.76	0.21	2.81	47,58,61,63	0
3	CL	B	201	1/1	0.95	0.06	-1.50	76,76,76,76	0
4	MPD	F	202	8/8	0.70	0.31	-	58,72,76,82	0
3	CL	P	101	1/1	0.97	0.12	-	61,61,61,61	0
3	CL	S	101	1/1	0.92	0.07	-	70,70,70,70	0
4	MPD	E	202	8/8	0.69	0.29	-	72,76,81,94	0
3	CL	D	201	1/1	0.91	0.11	-	80,80,80,80	0
3	CL	U	101	1/1	0.95	0.07	-	62,62,62,62	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.