



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 2, 2017 – 12:03 PM EDT

PDB ID : 5OVW
Title : Nanobody-bound BtuF, the vitamin B12 binding protein in Escherichia coli
Authors : Mireku, S.A.; Sauer, M.M.; Glockshuber, R.; Locher, K.P.
Deposited on : unknown
Resolution : 2.65 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at 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.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20030345

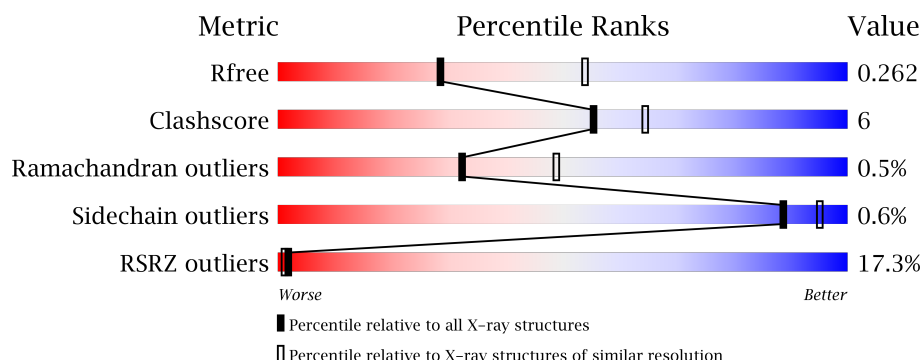
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	3491 (2.70-2.62)
Clashscore	112137	1026 (2.68-2.64)
Ramachandran outliers	110173	1010 (2.68-2.64)
Sidechain outliers	110143	1010 (2.68-2.64)
RSRZ outliers	101464	3511 (2.70-2.62)

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 ≥ 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	A	289	<div> <div>5%</div> <div> <div></div> <div>72%</div> <div>12%</div> <div>15%</div> </div> </div>
1	B	289	<div> <div>11%</div> <div> <div></div> <div>73%</div> <div>11%</div> <div>15%</div> </div> </div>
1	C	289	<div> <div>16%</div> <div> <div></div> <div>73%</div> <div>12%</div> <div>15%</div> </div> </div>
1	D	289	<div> <div>3%</div> <div> <div></div> <div>73%</div> <div>12%</div> <div>15%</div> </div> </div>
1	E	289	<div> <div>7%</div> <div> <div></div> <div>74%</div> <div>11%</div> <div>15%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	289	
2	G	159	
2	H	159	
2	I	159	
2	J	159	
2	K	159	
2	L	159	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17352 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 Vitamin B12-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	245	Total 1907	C 1216	N 332	O 355	S 4	0	0	0
1	B	245	Total 1907	C 1216	N 332	O 355	S 4	0	0	0
1	C	245	Total 1907	C 1216	N 332	O 355	S 4	0	0	0
1	D	245	Total 1907	C 1216	N 332	O 355	S 4	0	0	0
1	E	245	Total 1907	C 1216	N 332	O 355	S 4	0	0	0
1	F	245	Total 1907	C 1216	N 332	O 355	S 4	0	0	0

There are 264 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	initiating methionine	UNP P37028
A	-1	LYS	-	expression tag	UNP P37028
A	0	LYS	-	expression tag	UNP P37028
A	1	THR	-	expression tag	UNP P37028
A	2	ALA	-	expression tag	UNP P37028
A	3	ILE	-	expression tag	UNP P37028
A	4	ALA	-	expression tag	UNP P37028
A	5	ILE	-	expression tag	UNP P37028
A	6	ALA	-	expression tag	UNP P37028
A	7	VAL	-	expression tag	UNP P37028
A	8	ALA	-	expression tag	UNP P37028
A	9	LEU	-	expression tag	UNP P37028
A	10	ALA	-	expression tag	UNP P37028
A	11	GLY	-	expression tag	UNP P37028
A	12	PHE	-	expression tag	UNP P37028
A	13	ALA	-	expression tag	UNP P37028
A	14	THR	-	expression tag	UNP P37028

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Chain	Residue	Modelled	Actual	Comment	Reference
A	15	VAL	-	expression tag	UNP P37028
A	16	ALA	-	expression tag	UNP P37028
A	17	GLN	-	expression tag	UNP P37028
A	18	ALA	-	expression tag	UNP P37028
A	19	ALA	-	expression tag	UNP P37028
A	20	SER	-	expression tag	UNP P37028
A	21	MET	-	expression tag	UNP P37028
A	267	SER	-	expression tag	UNP P37028
A	268	GLY	-	expression tag	UNP P37028
A	269	SER	-	expression tag	UNP P37028
A	270	LEU	-	expression tag	UNP P37028
A	271	GLU	-	expression tag	UNP P37028
A	272	VAL	-	expression tag	UNP P37028
A	273	LEU	-	expression tag	UNP P37028
A	274	PHE	-	expression tag	UNP P37028
A	275	GLN	-	expression tag	UNP P37028
A	276	GLY	-	expression tag	UNP P37028
A	277	PRO	-	expression tag	UNP P37028
A	278	GLY	-	expression tag	UNP P37028
A	279	GLY	-	expression tag	UNP P37028
A	280	SER	-	expression tag	UNP P37028
A	281	HIS	-	expression tag	UNP P37028
A	282	HIS	-	expression tag	UNP P37028
A	283	HIS	-	expression tag	UNP P37028
A	284	HIS	-	expression tag	UNP P37028
A	285	HIS	-	expression tag	UNP P37028
A	286	HIS	-	expression tag	UNP P37028
B	-2	MET	-	initiating methionine	UNP P37028
B	-1	LYS	-	expression tag	UNP P37028
B	0	LYS	-	expression tag	UNP P37028
B	1	THR	-	expression tag	UNP P37028
B	2	ALA	-	expression tag	UNP P37028
B	3	ILE	-	expression tag	UNP P37028
B	4	ALA	-	expression tag	UNP P37028
B	5	ILE	-	expression tag	UNP P37028
B	6	ALA	-	expression tag	UNP P37028
B	7	VAL	-	expression tag	UNP P37028
B	8	ALA	-	expression tag	UNP P37028
B	9	LEU	-	expression tag	UNP P37028
B	10	ALA	-	expression tag	UNP P37028
B	11	GLY	-	expression tag	UNP P37028
B	12	PHE	-	expression tag	UNP P37028

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Chain	Residue	Modelled	Actual	Comment	Reference
B	13	ALA	-	expression tag	UNP P37028
B	14	THR	-	expression tag	UNP P37028
B	15	VAL	-	expression tag	UNP P37028
B	16	ALA	-	expression tag	UNP P37028
B	17	GLN	-	expression tag	UNP P37028
B	18	ALA	-	expression tag	UNP P37028
B	19	ALA	-	expression tag	UNP P37028
B	20	SER	-	expression tag	UNP P37028
B	21	MET	-	expression tag	UNP P37028
B	267	SER	-	expression tag	UNP P37028
B	268	GLY	-	expression tag	UNP P37028
B	269	SER	-	expression tag	UNP P37028
B	270	LEU	-	expression tag	UNP P37028
B	271	GLU	-	expression tag	UNP P37028
B	272	VAL	-	expression tag	UNP P37028
B	273	LEU	-	expression tag	UNP P37028
B	274	PHE	-	expression tag	UNP P37028
B	275	GLN	-	expression tag	UNP P37028
B	276	GLY	-	expression tag	UNP P37028
B	277	PRO	-	expression tag	UNP P37028
B	278	GLY	-	expression tag	UNP P37028
B	279	GLY	-	expression tag	UNP P37028
B	280	SER	-	expression tag	UNP P37028
B	281	HIS	-	expression tag	UNP P37028
B	282	HIS	-	expression tag	UNP P37028
B	283	HIS	-	expression tag	UNP P37028
B	284	HIS	-	expression tag	UNP P37028
B	285	HIS	-	expression tag	UNP P37028
B	286	HIS	-	expression tag	UNP P37028
C	-2	MET	-	initiating methionine	UNP P37028
C	-1	LYS	-	expression tag	UNP P37028
C	0	LYS	-	expression tag	UNP P37028
C	1	THR	-	expression tag	UNP P37028
C	2	ALA	-	expression tag	UNP P37028
C	3	ILE	-	expression tag	UNP P37028
C	4	ALA	-	expression tag	UNP P37028
C	5	ILE	-	expression tag	UNP P37028
C	6	ALA	-	expression tag	UNP P37028
C	7	VAL	-	expression tag	UNP P37028
C	8	ALA	-	expression tag	UNP P37028
C	9	LEU	-	expression tag	UNP P37028
C	10	ALA	-	expression tag	UNP P37028

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Chain	Residue	Modelled	Actual	Comment	Reference
C	11	GLY	-	expression tag	UNP P37028
C	12	PHE	-	expression tag	UNP P37028
C	13	ALA	-	expression tag	UNP P37028
C	14	THR	-	expression tag	UNP P37028
C	15	VAL	-	expression tag	UNP P37028
C	16	ALA	-	expression tag	UNP P37028
C	17	GLN	-	expression tag	UNP P37028
C	18	ALA	-	expression tag	UNP P37028
C	19	ALA	-	expression tag	UNP P37028
C	20	SER	-	expression tag	UNP P37028
C	21	MET	-	expression tag	UNP P37028
C	267	SER	-	expression tag	UNP P37028
C	268	GLY	-	expression tag	UNP P37028
C	269	SER	-	expression tag	UNP P37028
C	270	LEU	-	expression tag	UNP P37028
C	271	GLU	-	expression tag	UNP P37028
C	272	VAL	-	expression tag	UNP P37028
C	273	LEU	-	expression tag	UNP P37028
C	274	PHE	-	expression tag	UNP P37028
C	275	GLN	-	expression tag	UNP P37028
C	276	GLY	-	expression tag	UNP P37028
C	277	PRO	-	expression tag	UNP P37028
C	278	GLY	-	expression tag	UNP P37028
C	279	GLY	-	expression tag	UNP P37028
C	280	SER	-	expression tag	UNP P37028
C	281	HIS	-	expression tag	UNP P37028
C	282	HIS	-	expression tag	UNP P37028
C	283	HIS	-	expression tag	UNP P37028
C	284	HIS	-	expression tag	UNP P37028
C	285	HIS	-	expression tag	UNP P37028
C	286	HIS	-	expression tag	UNP P37028
D	-2	MET	-	initiating methionine	UNP P37028
D	-1	LYS	-	expression tag	UNP P37028
D	0	LYS	-	expression tag	UNP P37028
D	1	THR	-	expression tag	UNP P37028
D	2	ALA	-	expression tag	UNP P37028
D	3	ILE	-	expression tag	UNP P37028
D	4	ALA	-	expression tag	UNP P37028
D	5	ILE	-	expression tag	UNP P37028
D	6	ALA	-	expression tag	UNP P37028
D	7	VAL	-	expression tag	UNP P37028
D	8	ALA	-	expression tag	UNP P37028

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Chain	Residue	Modelled	Actual	Comment	Reference
D	9	LEU	-	expression tag	UNP P37028
D	10	ALA	-	expression tag	UNP P37028
D	11	GLY	-	expression tag	UNP P37028
D	12	PHE	-	expression tag	UNP P37028
D	13	ALA	-	expression tag	UNP P37028
D	14	THR	-	expression tag	UNP P37028
D	15	VAL	-	expression tag	UNP P37028
D	16	ALA	-	expression tag	UNP P37028
D	17	GLN	-	expression tag	UNP P37028
D	18	ALA	-	expression tag	UNP P37028
D	19	ALA	-	expression tag	UNP P37028
D	20	SER	-	expression tag	UNP P37028
D	21	MET	-	expression tag	UNP P37028
D	267	SER	-	expression tag	UNP P37028
D	268	GLY	-	expression tag	UNP P37028
D	269	SER	-	expression tag	UNP P37028
D	270	LEU	-	expression tag	UNP P37028
D	271	GLU	-	expression tag	UNP P37028
D	272	VAL	-	expression tag	UNP P37028
D	273	LEU	-	expression tag	UNP P37028
D	274	PHE	-	expression tag	UNP P37028
D	275	GLN	-	expression tag	UNP P37028
D	276	GLY	-	expression tag	UNP P37028
D	277	PRO	-	expression tag	UNP P37028
D	278	GLY	-	expression tag	UNP P37028
D	279	GLY	-	expression tag	UNP P37028
D	280	SER	-	expression tag	UNP P37028
D	281	HIS	-	expression tag	UNP P37028
D	282	HIS	-	expression tag	UNP P37028
D	283	HIS	-	expression tag	UNP P37028
D	284	HIS	-	expression tag	UNP P37028
D	285	HIS	-	expression tag	UNP P37028
D	286	HIS	-	expression tag	UNP P37028
E	-2	MET	-	initiating methionine	UNP P37028
E	-1	LYS	-	expression tag	UNP P37028
E	0	LYS	-	expression tag	UNP P37028
E	1	THR	-	expression tag	UNP P37028
E	2	ALA	-	expression tag	UNP P37028
E	3	ILE	-	expression tag	UNP P37028
E	4	ALA	-	expression tag	UNP P37028
E	5	ILE	-	expression tag	UNP P37028
E	6	ALA	-	expression tag	UNP P37028

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Chain	Residue	Modelled	Actual	Comment	Reference
E	7	VAL	-	expression tag	UNP P37028
E	8	ALA	-	expression tag	UNP P37028
E	9	LEU	-	expression tag	UNP P37028
E	10	ALA	-	expression tag	UNP P37028
E	11	GLY	-	expression tag	UNP P37028
E	12	PHE	-	expression tag	UNP P37028
E	13	ALA	-	expression tag	UNP P37028
E	14	THR	-	expression tag	UNP P37028
E	15	VAL	-	expression tag	UNP P37028
E	16	ALA	-	expression tag	UNP P37028
E	17	GLN	-	expression tag	UNP P37028
E	18	ALA	-	expression tag	UNP P37028
E	19	ALA	-	expression tag	UNP P37028
E	20	SER	-	expression tag	UNP P37028
E	21	MET	-	expression tag	UNP P37028
E	267	SER	-	expression tag	UNP P37028
E	268	GLY	-	expression tag	UNP P37028
E	269	SER	-	expression tag	UNP P37028
E	270	LEU	-	expression tag	UNP P37028
E	271	GLU	-	expression tag	UNP P37028
E	272	VAL	-	expression tag	UNP P37028
E	273	LEU	-	expression tag	UNP P37028
E	274	PHE	-	expression tag	UNP P37028
E	275	GLN	-	expression tag	UNP P37028
E	276	GLY	-	expression tag	UNP P37028
E	277	PRO	-	expression tag	UNP P37028
E	278	GLY	-	expression tag	UNP P37028
E	279	GLY	-	expression tag	UNP P37028
E	280	SER	-	expression tag	UNP P37028
E	281	HIS	-	expression tag	UNP P37028
E	282	HIS	-	expression tag	UNP P37028
E	283	HIS	-	expression tag	UNP P37028
E	284	HIS	-	expression tag	UNP P37028
E	285	HIS	-	expression tag	UNP P37028
E	286	HIS	-	expression tag	UNP P37028
F	-2	MET	-	initiating methionine	UNP P37028
F	-1	LYS	-	expression tag	UNP P37028
F	0	LYS	-	expression tag	UNP P37028
F	1	THR	-	expression tag	UNP P37028
F	2	ALA	-	expression tag	UNP P37028
F	3	ILE	-	expression tag	UNP P37028
F	4	ALA	-	expression tag	UNP P37028

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Chain	Residue	Modelled	Actual	Comment	Reference
F	5	ILE	-	expression tag	UNP P37028
F	6	ALA	-	expression tag	UNP P37028
F	7	VAL	-	expression tag	UNP P37028
F	8	ALA	-	expression tag	UNP P37028
F	9	LEU	-	expression tag	UNP P37028
F	10	ALA	-	expression tag	UNP P37028
F	11	GLY	-	expression tag	UNP P37028
F	12	PHE	-	expression tag	UNP P37028
F	13	ALA	-	expression tag	UNP P37028
F	14	THR	-	expression tag	UNP P37028
F	15	VAL	-	expression tag	UNP P37028
F	16	ALA	-	expression tag	UNP P37028
F	17	GLN	-	expression tag	UNP P37028
F	18	ALA	-	expression tag	UNP P37028
F	19	ALA	-	expression tag	UNP P37028
F	20	SER	-	expression tag	UNP P37028
F	21	MET	-	expression tag	UNP P37028
F	267	SER	-	expression tag	UNP P37028
F	268	GLY	-	expression tag	UNP P37028
F	269	SER	-	expression tag	UNP P37028
F	270	LEU	-	expression tag	UNP P37028
F	271	GLU	-	expression tag	UNP P37028
F	272	VAL	-	expression tag	UNP P37028
F	273	LEU	-	expression tag	UNP P37028
F	274	PHE	-	expression tag	UNP P37028
F	275	GLN	-	expression tag	UNP P37028
F	276	GLY	-	expression tag	UNP P37028
F	277	PRO	-	expression tag	UNP P37028
F	278	GLY	-	expression tag	UNP P37028
F	279	GLY	-	expression tag	UNP P37028
F	280	SER	-	expression tag	UNP P37028
F	281	HIS	-	expression tag	UNP P37028
F	282	HIS	-	expression tag	UNP P37028
F	283	HIS	-	expression tag	UNP P37028
F	284	HIS	-	expression tag	UNP P37028
F	285	HIS	-	expression tag	UNP P37028
F	286	HIS	-	expression tag	UNP P37028

- Molecule 2 is a protein called Nanobody.

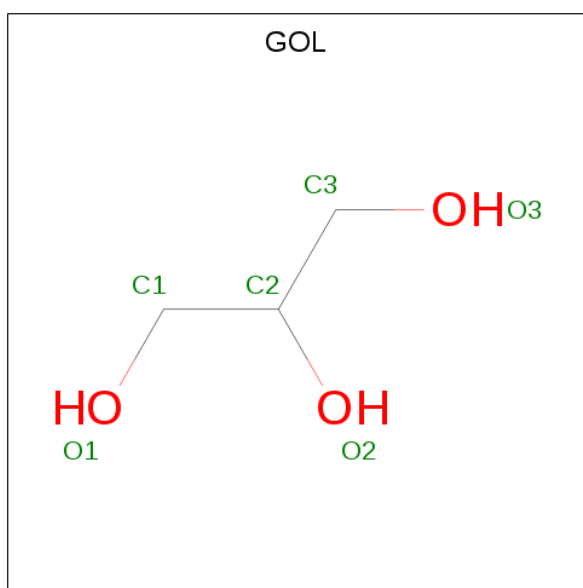
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	126	Total	C	N	O	S	0	0	0
			936	578	165	187	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	126	Total	C	N	O	S	0	0	0
			936	578	165	187	6			
2	I	126	Total	C	N	O	S	0	0	0
			936	578	165	187	6			
2	J	126	Total	C	N	O	S	0	0	0
			936	578	165	187	6			
2	K	126	Total	C	N	O	S	0	0	0
			936	578	165	187	6			
2	L	126	Total	C	N	O	S	0	0	0
			936	578	165	187	6			

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		
3	E	1	Total	C	O	0	0
			6	3	3		
3	F	1	Total	C	O	0	0
			6	3	3		
3	H	1	Total	C	O	0	0
			6	3	3		

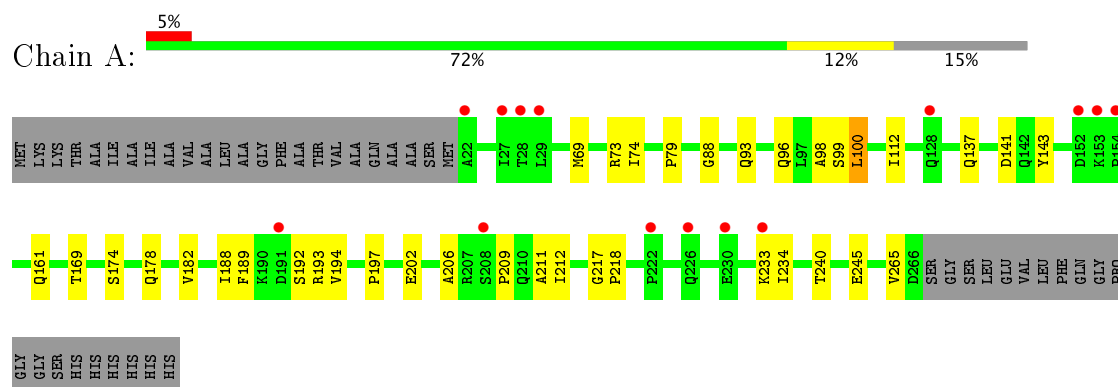
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	42	Total 42	O 42	0	0
4	B	37	Total 37	O 37	0	0
4	C	10	Total 10	O 10	0	0
4	D	66	Total 66	O 66	0	0
4	E	25	Total 25	O 25	0	0
4	F	17	Total 17	O 17	0	0
4	G	4	Total 4	O 4	0	0
4	H	14	Total 14	O 14	0	0
4	I	2	Total 2	O 2	0	0
4	J	27	Total 27	O 27	0	0
4	K	13	Total 13	O 13	0	0
4	L	7	Total 7	O 7	0	0

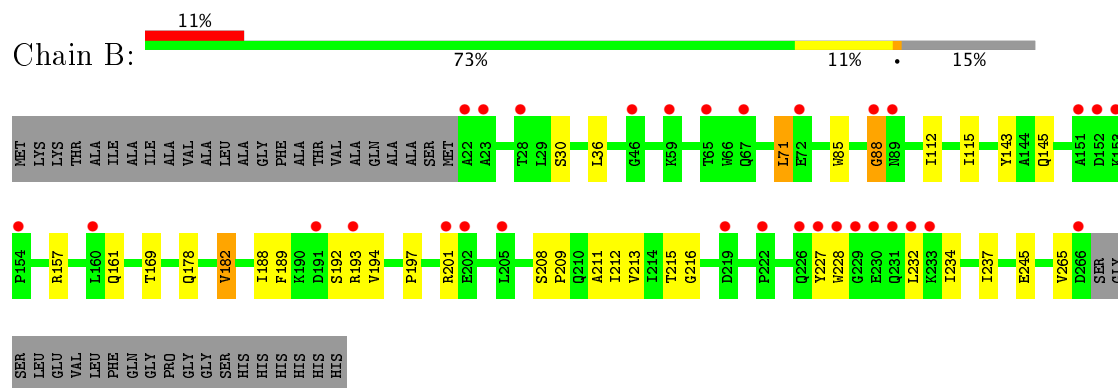
3 Residue-property plots [i](#)

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

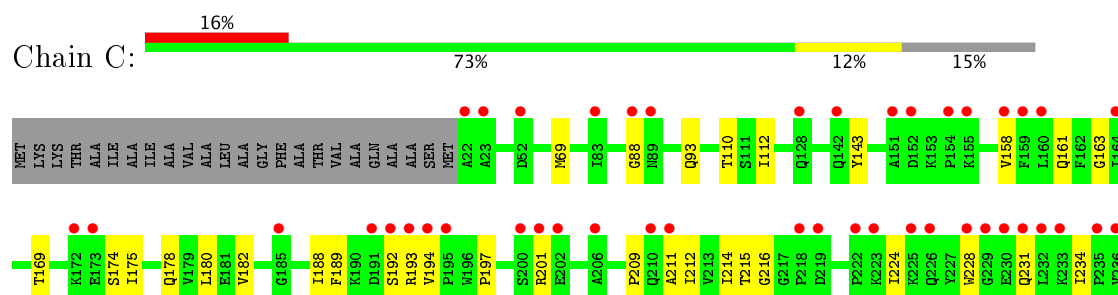
• Molecule 1: Vitamin B12-binding protein



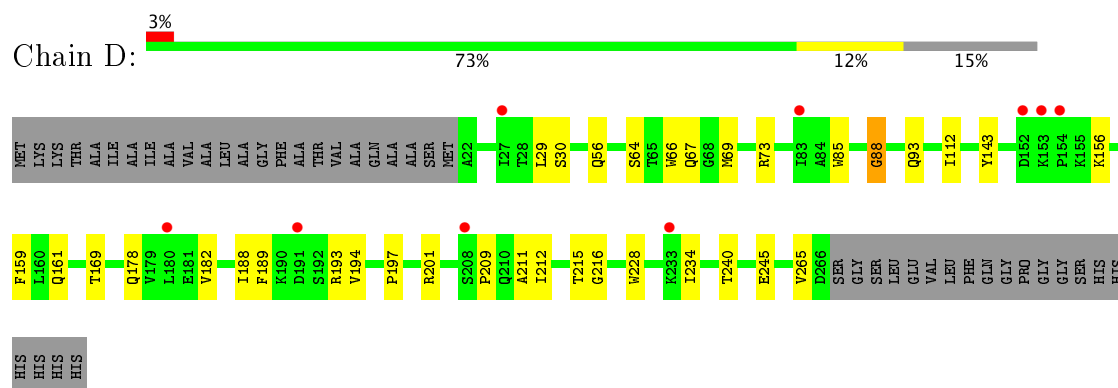
• Molecule 1: Vitamin B12-binding protein



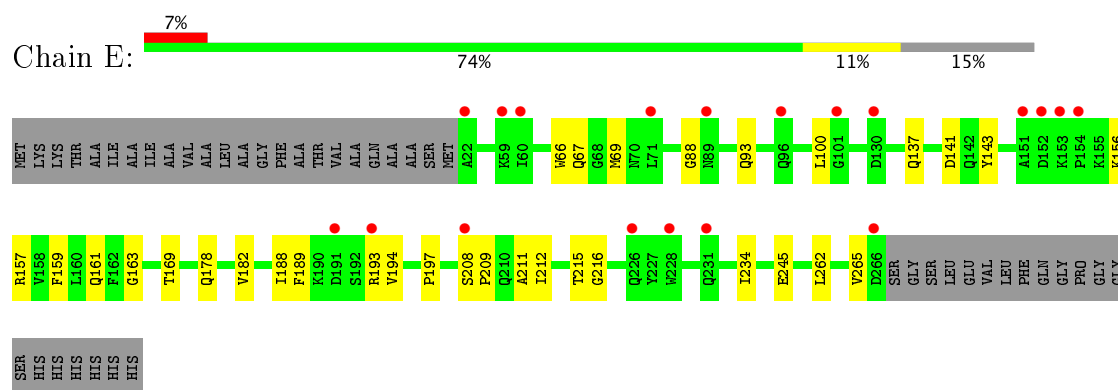
• Molecule 1: Vitamin B12-binding protein



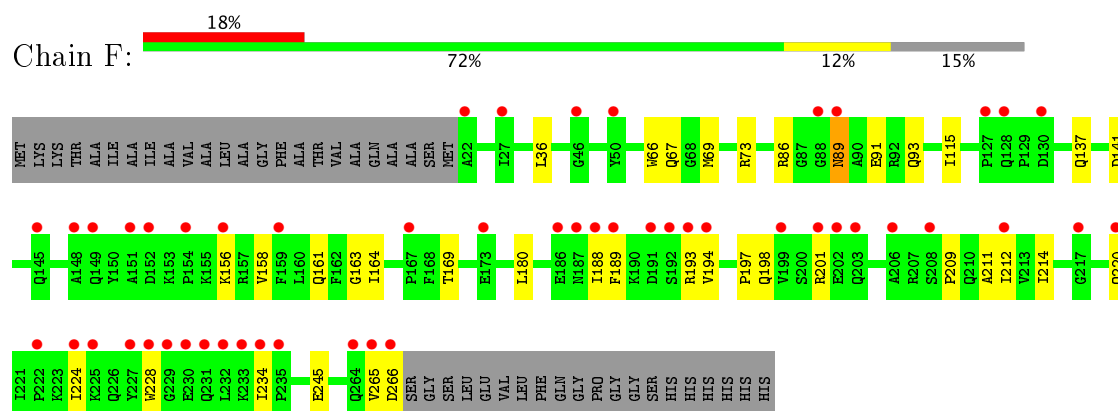
- Molecule 1: Vitamin B12-binding protein



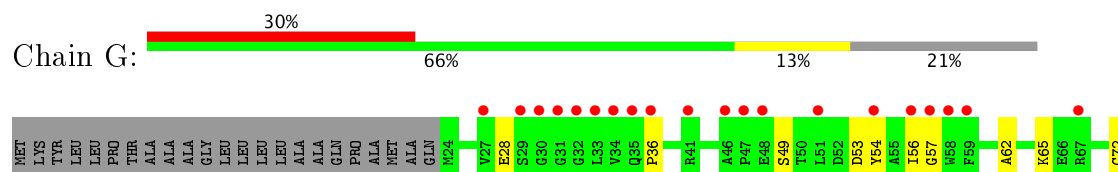
- Molecule 1: Vitamin B12-binding protein

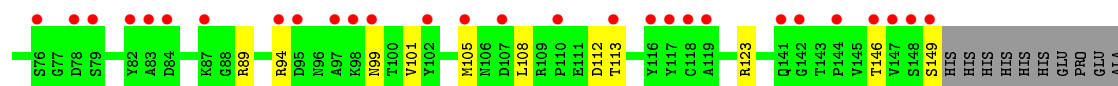


- Molecule 1: Vitamin B12-binding protein

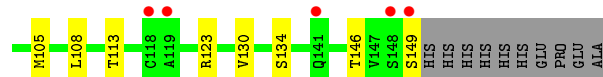
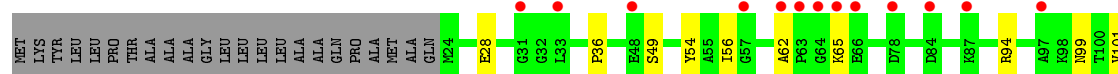


- Molecule 2: Nanobody

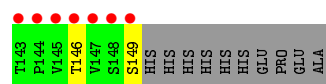
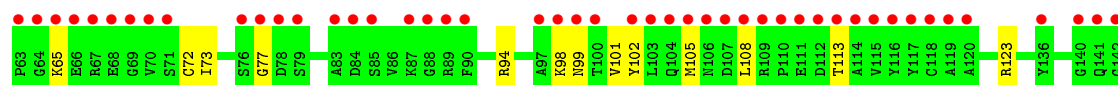
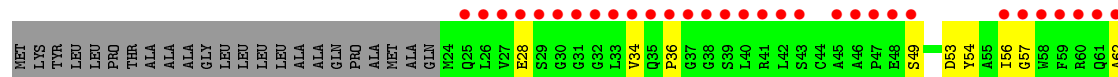




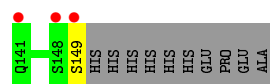
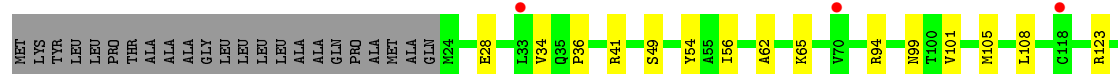
- Molecule 2: Nanobody



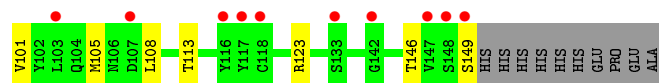
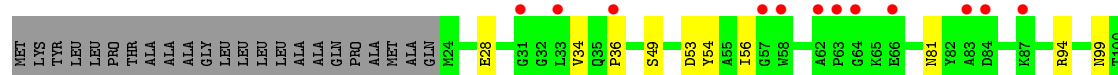
- Molecule 2: Nanobody



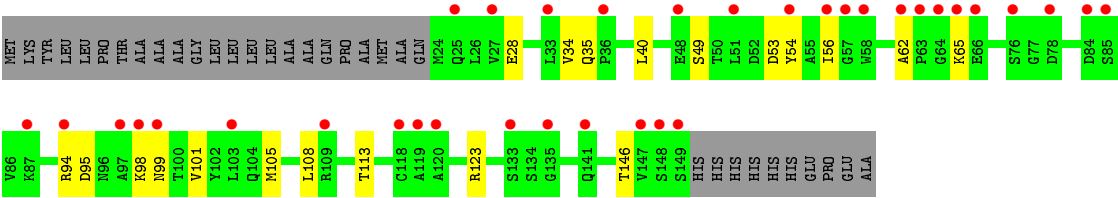
- Molecule 2: Nanobody



- Molecule 2: Nanobody



- Molecule 2: Nanobody



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.80Å 141.00Å 216.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.65 20.00 – 2.65	Depositor EDS
% Data completeness (in resolution range)	85.3 (20.00-2.65) 85.3 (20.00-2.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.95 (at 2.67Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.223 , 0.259 0.226 , 0.262	Depositor DCC
R_{free} test set	3240 reflections (5.07%)	DCC
Wilson B-factor (Å ²)	47.6	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 74.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	17352	wwPDB-VP
Average B, all atoms (Å ²)	101.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.07% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.25	0/1951	0.43	0/2661
1	B	0.25	0/1951	0.42	0/2661
1	C	0.26	0/1951	0.42	0/2661
1	D	0.26	0/1951	0.42	0/2661
1	E	0.25	0/1951	0.42	0/2661
1	F	0.26	0/1951	0.41	0/2661
2	G	0.25	0/955	0.44	0/1295
2	H	0.26	0/955	0.44	0/1295
2	I	0.24	0/955	0.43	0/1295
2	J	0.27	0/955	0.45	0/1295
2	K	0.25	0/955	0.44	0/1295
2	L	0.25	0/955	0.45	0/1295
All	All	0.26	0/17436	0.43	0/23736

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	A	1907	0	1924	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1907	0	1924	26	0
1	C	1907	0	1924	25	0
1	D	1907	0	1924	23	0
1	E	1907	0	1924	19	0
1	F	1907	0	1924	25	0
2	G	936	0	888	12	0
2	H	936	0	888	10	0
2	I	936	0	888	13	0
2	J	936	0	888	11	0
2	K	936	0	888	11	0
2	L	936	0	888	12	0
3	B	6	0	8	1	0
3	D	6	0	8	0	0
3	E	6	0	8	0	0
3	F	6	0	8	1	0
3	H	6	0	8	0	0
4	A	42	0	0	0	0
4	B	37	0	0	0	0
4	C	10	0	0	0	0
4	D	66	0	0	1	0
4	E	25	0	0	0	0
4	F	17	0	0	0	0
4	G	4	0	0	0	0
4	H	14	0	0	0	0
4	I	2	0	0	0	0
4	J	27	0	0	2	0
4	K	13	0	0	0	0
4	L	7	0	0	0	0
All	All	17352	0	16912	200	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 6.

The worst 5 of 200 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:156:LYS:NZ	1:E:265:VAL:O	2.06	0.88
2:J:41:ARG:NH1	4:J:201:HOH:O	2.12	0.77
1:F:156:LYS:HZ1	1:F:266:ASP:CG	1.89	0.76
1:C:201:ARG:NH1	1:C:231:GLN:OE1	2.24	0.70
2:L:54:TYR:O	2:L:94:ARG:NH2	2.27	0.68

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	243/289 (84%)	228 (94%)	12 (5%)	3 (1%)	15	24
1	B	243/289 (84%)	228 (94%)	13 (5%)	2 (1%)	22	34
1	C	243/289 (84%)	229 (94%)	12 (5%)	2 (1%)	22	34
1	D	243/289 (84%)	230 (95%)	11 (4%)	2 (1%)	22	34
1	E	243/289 (84%)	230 (95%)	11 (4%)	2 (1%)	22	34
1	F	243/289 (84%)	228 (94%)	14 (6%)	1 (0%)	38	54
2	G	124/159 (78%)	120 (97%)	4 (3%)	0	100	100
2	H	124/159 (78%)	120 (97%)	4 (3%)	0	100	100
2	I	124/159 (78%)	120 (97%)	4 (3%)	0	100	100
2	J	124/159 (78%)	120 (97%)	4 (3%)	0	100	100
2	K	124/159 (78%)	120 (97%)	4 (3%)	0	100	100
2	L	124/159 (78%)	120 (97%)	4 (3%)	0	100	100
All	All	2202/2688 (82%)	2093 (95%)	97 (4%)	12 (0%)	32	49

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	99	SER
1	A	193	ARG
1	B	193	ARG
1	C	193	ARG
1	E	193	ARG

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	205/235 (87%)	202 (98%)	3 (2%)	70	85
1	B	205/235 (87%)	202 (98%)	3 (2%)	70	85
1	C	205/235 (87%)	205 (100%)	0	100	100
1	D	205/235 (87%)	204 (100%)	1 (0%)	91	96
1	E	205/235 (87%)	204 (100%)	1 (0%)	91	96
1	F	205/235 (87%)	204 (100%)	1 (0%)	91	96
2	G	100/124 (81%)	100 (100%)	0	100	100
2	H	100/124 (81%)	100 (100%)	0	100	100
2	I	100/124 (81%)	99 (99%)	1 (1%)	80	90
2	J	100/124 (81%)	100 (100%)	0	100	100
2	K	100/124 (81%)	99 (99%)	1 (1%)	80	90
2	L	100/124 (81%)	100 (100%)	0	100	100
All	All	1830/2154 (85%)	1819 (99%)	11 (1%)	89	95

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	145	GLN
1	B	182	VAL
1	F	89	ASN
1	B	71	LEU
1	E	100	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	177	ASN
1	F	198	GLN
1	C	178	GLN
1	B	178	GLN

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Mol	Chain	Res	Type
1	D	137	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

5 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	GOL	B	301	-	5,5,5	0.36	0	5,5,5	0.31	0
3	GOL	D	301	-	5,5,5	0.33	0	5,5,5	0.27	0
3	GOL	E	301	-	5,5,5	0.31	0	5,5,5	0.27	0
3	GOL	F	301	-	5,5,5	0.35	0	5,5,5	0.32	0
3	GOL	H	201	-	5,5,5	0.34	0	5,5,5	0.28	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
3	GOL	B	301	-	-	0/4/4/4	0/0/0/0
3	GOL	D	301	-	-	0/4/4/4	0/0/0/0
3	GOL	E	301	-	-	0/4/4/4	0/0/0/0
3	GOL	F	301	-	-	0/4/4/4	0/0/0/0
3	GOL	H	201	-	-	0/4/4/4	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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	301	GOL	1	0
3	F	301	GOL	1	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	245/289 (84%)	0.40	14 (5%) 24 22	55, 77, 118, 156	0
1	B	245/289 (84%)	0.61	31 (12%) 4 3	50, 83, 139, 185	0
1	C	245/289 (84%)	1.00	47 (19%) 1 1	65, 102, 168, 201	0
1	D	245/289 (84%)	0.26	9 (3%) 42 40	49, 74, 116, 166	0
1	E	245/289 (84%)	0.60	19 (7%) 14 11	56, 88, 136, 170	0
1	F	245/289 (84%)	1.15	51 (20%) 1 1	59, 101, 163, 212	0
2	G	126/159 (79%)	2.13	48 (38%) 0 0	94, 146, 180, 216	0
2	H	126/159 (79%)	0.84	18 (14%) 3 2	61, 95, 138, 159	0
2	I	126/159 (79%)	3.05	85 (67%) 0 0	78, 158, 221, 252	0
2	J	126/159 (79%)	0.53	6 (4%) 31 29	53, 86, 132, 165	0
2	K	126/159 (79%)	1.01	22 (17%) 2 1	69, 103, 148, 182	0
2	L	126/159 (79%)	1.52	35 (27%) 1 0	79, 114, 163, 186	0
All	All	2226/2688 (82%)	0.96	385 (17%) 2 1	49, 95, 167, 252	0

The worst 5 of 385 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	230	GLU	9.7
1	C	154	PRO	8.5
2	G	32	GLY	8.3
2	I	140	GLY	8.1
1	F	152	ASP	8.1

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, 95th 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(\AA^2)	Q<0.9
3	GOL	E	301	6/6	0.81	0.27	1.39	73,76,82,85	0
3	GOL	H	201	6/6	0.87	0.21	1.37	70,77,82,92	0
3	GOL	B	301	6/6	0.84	0.27	1.19	93,100,103,108	0
3	GOL	F	301	6/6	0.60	0.30	0.71	124,126,129,130	0
3	GOL	D	301	6/6	0.96	0.16	-0.18	66,68,70,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.