



# Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 09:53 AM GMT

PDB ID : 1MCF  
Title : PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEP-TIDE LIGANDS  
Authors : Edmundson, A.B.; Harris, D.L.; Fan, Z.-C.; Guddat, L.W.  
Deposited on : 1993-02-25  
Resolution : 2.70 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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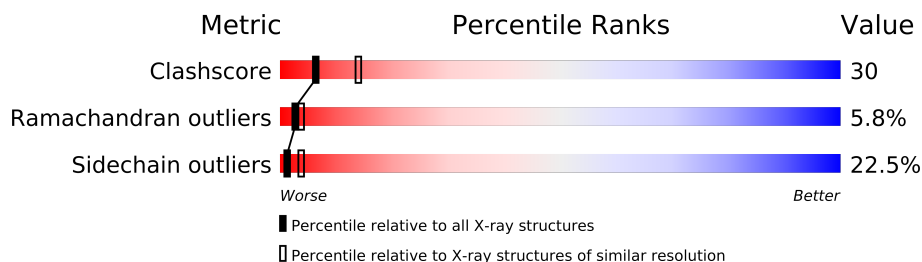
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 21963  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.70 Å.

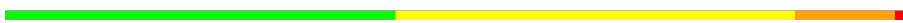
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	216	
1	B	216	
2	P	7	

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 3261 atoms, of which 0 are hydrogen and 0 are deuterium.

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 IMMUNOGLOBULIN LAMBDA DIMER MCG (LIGHT CHAIN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	216	Total	C	N	O	S	0	0	0
			1605	1000	266	334	5			
1	B	216	Total	C	N	O	S	0	0	0
			1605	1000	266	334	5			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	ILE	PHE	CONFLICT	PIR S14675
A	23	THR	SER	CONFLICT	PIR S14675
A	29	VAL	ILE	CONFLICT	PIR S14675
A	31	GLY	ASN	CONFLICT	PIR S14675
A	39	GLN	ARG	CONFLICT	PIR S14675
A	42	ALA	PRO	CONFLICT	PIR S14675
A	48	VAL	LEU	CONFLICT	PIR S14675
A	49	ILE	MET	CONFLICT	PIR S14675
A	54	ASN	THR	CONFLICT	PIR S14675
A	62	ASP	ASN	CONFLICT	PIR S14675
A	94	GLU	ALA	CONFLICT	PIR S14675
A	97	ASP	ASN	CONFLICT	PIR S14675
A	98	ASN	SER	CONFLICT	PIR S14675
A	99	PHE	LEU	CONFLICT	PIR S14675
A	100	VAL	ILE	CONFLICT	PIR S14675
A	103	THR	GLY	CONFLICT	PIR S14675
A	106	LYS	ARG	CONFLICT	PIR S14675
A	107	VAL	LEU	CONFLICT	PIR S14675
A	116	ASN	ALA	CONFLICT	PIR S14675
A	118	THR	SER	CONFLICT	PIR S14675
A	156	GLY	SER	CONFLICT	PIR S14675
A	167	LYS	THR	CONFLICT	PIR S14675
B	20	ILE	PHE	CONFLICT	PIR S14675
B	23	THR	SER	CONFLICT	PIR S14675

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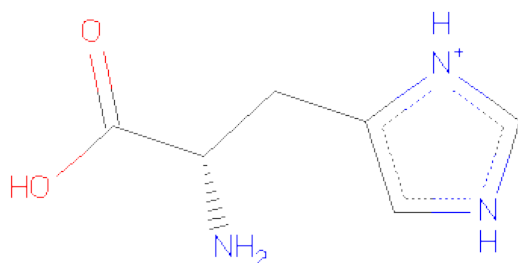
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Chain	Residue	Modelled	Actual	Comment	Reference
B	29	VAL	ILE	CONFLICT	PIR S14675
B	31	GLY	ASN	CONFLICT	PIR S14675
B	39	GLN	ARG	CONFLICT	PIR S14675
B	42	ALA	PRO	CONFLICT	PIR S14675
B	48	VAL	LEU	CONFLICT	PIR S14675
B	49	ILE	MET	CONFLICT	PIR S14675
B	54	ASN	THR	CONFLICT	PIR S14675
B	62	ASP	ASN	CONFLICT	PIR S14675
B	94	GLU	ALA	CONFLICT	PIR S14675
B	97	ASP	ASN	CONFLICT	PIR S14675
B	98	ASN	SER	CONFLICT	PIR S14675
B	99	PHE	LEU	CONFLICT	PIR S14675
B	100	VAL	ILE	CONFLICT	PIR S14675
B	103	THR	GLY	CONFLICT	PIR S14675
B	106	LYS	ARG	CONFLICT	PIR S14675
B	107	VAL	LEU	CONFLICT	PIR S14675
B	116	ASN	ALA	CONFLICT	PIR S14675
B	118	THR	SER	CONFLICT	PIR S14675
B	156	GLY	SER	CONFLICT	PIR S14675
B	167	LYS	THR	CONFLICT	PIR S14675

- Molecule 2 is a protein called PEPTIDE N-ACETYL-L-GLN-D-PHE-L-HIS-D-PRO-B-AL A-B-ALA-OH.

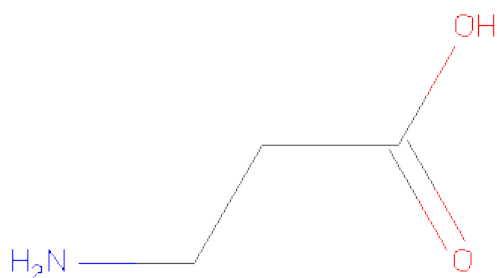
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	P	1	Total	C	N	O	0	0	0
			9	5	2	2			

- Molecule 3 is HISTIDINE (three-letter code: HIS) (formula: C<sub>6</sub>H<sub>10</sub>N<sub>3</sub>O<sub>2</sub>).



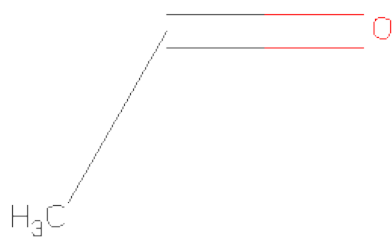
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	P	1	Total	C	N	O	0	0
			10	6	3	1		

- Molecule 4 is BETA-ALANINE (three-letter code: BAL) (formula:  $C_3H_7NO_2$ ).



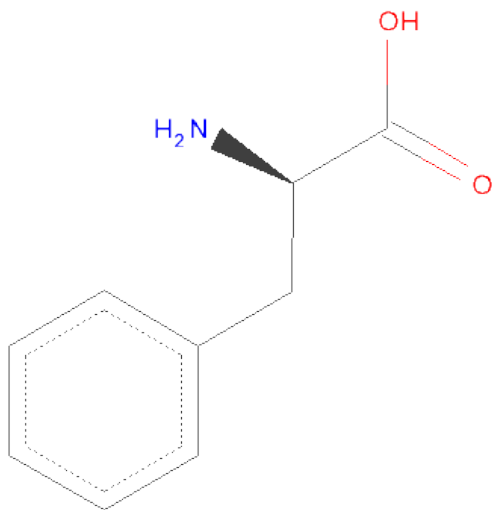
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	P	1	Total	C	N	O	0	0
			5	3	1	1		
4	P	1	Total	C	N	O	0	0
			6	3	1	2		

- Molecule 5 is ACETYL GROUP (three-letter code: ACE) (formula:  $C_2H_4O$ ).



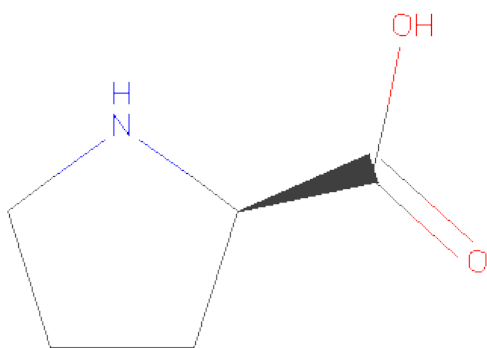
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	P	1	Total	C	O	0	0
			3	2	1		

- Molecule 6 is D-PHENYLALANINE (three-letter code: DPN) (formula: C<sub>9</sub>H<sub>11</sub>NO<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	P	1	Total	C	N	O	0	0
			11	9	1	1		

- Molecule 7 is D-PROLINE (three-letter code: DPR) (formula: C<sub>5</sub>H<sub>9</sub>NO<sub>2</sub>).



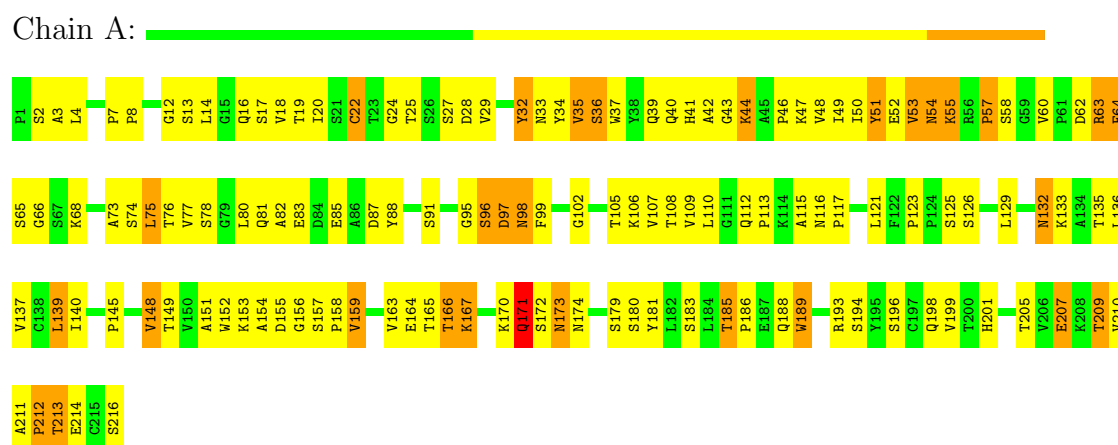
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
7	P	1	7	5	1	1	0	0

### 3 Residue-property plots

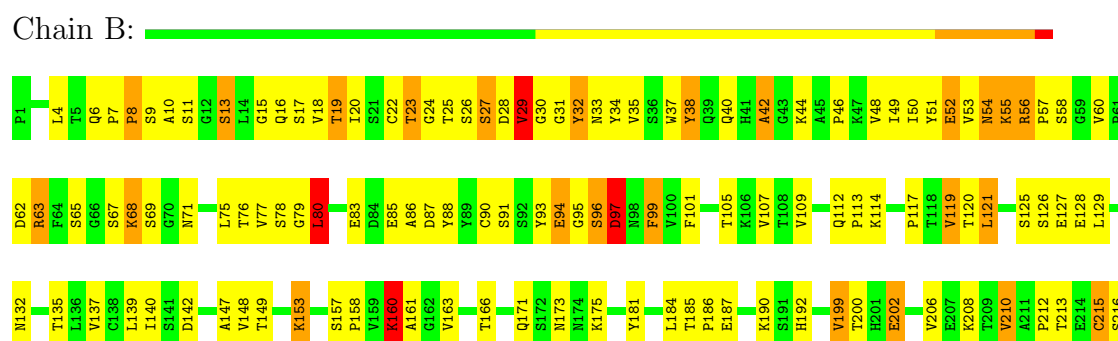
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

- Molecule 1: IMMUNOGLOBULIN LAMBDA DIMER MCG (LIGHT CHAIN)



- Molecule 1: IMMUNOGLOBULIN LAMBDA DIMER MCG (LIGHT CHAIN)



- Molecule 2: PEPTIDE N-ACETYL-L-GLN-D-PHE-L-HIS-D-PRO-B-ALA-B-ALA-OH





## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	72.30Å 72.30Å 185.90Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	6.00 – 2.70	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-2.70)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ, X-PLOR	Depositor
R, $R_{free}$	0.194 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3261	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	0.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DPN, BAL, DPR, ACE

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	0.83	0/1644	1.32	4/2241 (0.2%)
1	B	0.83	0/1644	1.38	11/2241 (0.5%)
2	P	0.53	0/8	1.27	0/9
All	All	0.83	0/3296	1.35	15/4491 (0.3%)

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	97	ASP	CA-CB-CG	7.42	129.72	113.40
1	A	22	CYS	CA-CB-SG	7.01	126.62	114.00
1	A	64	PHE	N-CA-CB	6.46	122.23	110.60
1	B	202	GLU	CA-CB-CG	6.40	127.48	113.40
1	A	64	PHE	O-C-N	5.75	131.91	122.70
1	B	187	GLU	CA-CB-CG	5.49	125.49	113.40
1	B	63	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	B	80	LEU	CB-CA-C	5.46	120.56	110.20
1	B	76	THR	O-C-N	5.44	131.40	122.70
1	A	171	GLN	CA-CB-CG	5.36	125.19	113.40
1	B	87	ASP	CB-CG-OD2	-5.32	113.51	118.30
1	B	80	LEU	CA-CB-CG	5.15	127.14	115.30
1	B	184	LEU	CA-CB-CG	5.12	127.08	115.30
1	B	52	GLU	CA-CB-CG	5.12	124.66	113.40
1	B	19	THR	N-CA-CB	5.02	119.85	110.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1605	0	1540	102	0
1	B	1605	0	1540	86	0
2	P	9	0	8	5	0
3	P	10	0	6	10	0
4	P	11	0	9	9	0
5	P	3	0	3	4	0
6	P	11	0	7	3	0
7	P	7	0	7	5	0
All	All	3261	0	3120	192	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 30.

All (192) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:P:9:BAL:HA1	7:P:12:DPR:HA	1.22	1.16
1:B:215:CYS:SG	1:B:216:SER:N	2.46	0.89
4:P:9:BAL:HA1	7:P:12:DPR:CA	2.06	0.85
1:B:126:SER:HB3	1:B:215:CYS:SG	2.20	0.82
1:A:54:ASN:HB2	1:A:66:GLY:O	1.80	0.81
1:A:35:VAL:HA	1:A:91:SER:O	1.83	0.77
4:P:9:BAL:CA	7:P:12:DPR:HA	2.10	0.75
1:B:9:SER:HB3	1:B:147:ALA:HB3	1.67	0.75
1:A:123:PRO:HA	1:A:136:LEU:HD23	1.71	0.71
1:B:121:LEU:HD13	1:B:210:VAL:HB	1.73	0.71
1:B:29:VAL:HG13	1:B:30:GLY:N	2.06	0.71
2:P:1:GLN:HB3	3:P:7:HIS:HB2	1.72	0.69
1:A:51:TYR:HB2	3:P:7:HIS:CE1	2.27	0.69
1:A:55:LYS:O	1:A:57:PRO:HD3	1.93	0.68
1:B:37:TRP:HB2	1:B:50:ILE:HB	1.75	0.68
1:A:68:LYS:HZ3	1:A:68:LYS:HB3	1.59	0.68
1:B:94:GLU:O	1:B:96:SER:N	2.22	0.67
1:B:101:PHE:HE1	5:P:10:ACE:H3	1.60	0.66
1:A:53:VAL:HG11	1:A:68:LYS:HZ2	1.60	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:10:ALA:O	1:B:107:VAL:HA	1.95	0.66
1:A:41:HIS:O	1:A:44:LYS:HB2	1.95	0.66
1:A:85:GLU:HG3	1:A:108:THR:HA	1.78	0.65
1:A:152:TRP:HE1	1:A:180:SER:HG	1.42	0.64
3:P:7:HIS:C	4:P:8:BAL:N	2.51	0.64
3:P:7:HIS:O	4:P:8:BAL:N	2.31	0.64
1:A:51:TYR:CD1	1:A:55:LYS:HB3	2.33	0.64
1:B:160:LYS:HE2	1:B:161:ALA:H	1.63	0.63
1:A:105:THR:HG22	1:A:107:VAL:HG23	1.81	0.63
4:P:9:BAL:H	7:P:12:DPR:C	2.10	0.63
1:B:4:LEU:HD13	1:B:90:CYS:SG	2.40	0.62
1:B:51:TYR:O	1:B:55:LYS:HB2	2.01	0.61
1:A:132:ASN:HD22	1:A:186:PRO:HG2	1.65	0.61
1:A:82:ALA:HB1	1:A:112:GLN:OE1	2.01	0.61
1:A:48:VAL:HG21	1:B:99:PHE:CD1	2.35	0.60
1:A:62:ASP:CG	1:A:63:ARG:H	2.05	0.60
1:A:17:SER:HA	1:A:80:LEU:HG	1.83	0.60
1:B:173:ASN:HD22	1:B:175:LYS:NZ	1.99	0.60
1:B:126:SER:HA	1:B:129:LEU:HD12	1.82	0.60
1:A:155:ASP:O	1:A:157:SER:N	2.35	0.60
1:B:119:VAL:HA	1:B:139:LEU:O	2.03	0.59
1:A:68:LYS:HA	1:A:73:ALA:HA	1.85	0.59
1:A:4:LEU:O	1:A:102:GLY:HA2	2.04	0.57
1:A:148:VAL:HG22	1:A:201:HIS:HB2	1.86	0.57
2:P:1:GLN:HB3	3:P:7:HIS:CB	2.35	0.57
1:B:173:ASN:HD21	1:B:175:LYS:HB2	1.69	0.57
1:A:123:PRO:HA	1:A:136:LEU:CD2	2.35	0.57
1:B:25:THR:O	1:B:27:SER:N	2.38	0.57
1:A:48:VAL:HG11	5:P:10:ACE:H2	1.86	0.56
1:A:36:SER:HB3	1:A:51:TYR:HA	1.87	0.56
1:B:56:ARG:HG3	1:B:60:VAL:CG1	2.35	0.56
1:B:29:VAL:HG13	1:B:30:GLY:H	1.70	0.56
1:B:48:VAL:HG11	6:P:11:DPN:CZ	2.36	0.56
1:A:63:ARG:CB	1:A:78:SER:HB2	2.35	0.56
1:A:77:VAL:CG2	1:A:80:LEU:HD21	2.37	0.55
1:B:48:VAL:HG11	6:P:11:DPN:HZ	1.89	0.55
1:B:28:ASP:O	1:B:29:VAL:HG12	2.07	0.55
1:A:63:ARG:HG3	1:A:78:SER:O	2.07	0.55
1:A:4:LEU:HD23	1:A:22:CYS:SG	2.47	0.55
1:B:192:HIS:O	1:B:212:PRO:HG2	2.07	0.55
1:B:101:PHE:CE1	5:P:10:ACE:H3	2.42	0.55
1:A:53:VAL:HG11	1:A:68:LYS:NZ	2.22	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:17:SER:HA	1:B:77:VAL:O	2.08	0.54
1:A:132:ASN:C	1:A:133:LYS:HD2	2.27	0.54
1:B:6:GLN:HB3	1:B:105:THR:OG1	2.07	0.54
1:A:95:GLY:O	1:A:96:SER:C	2.45	0.54
1:A:46:PRO:HG2	1:B:101:PHE:CE2	2.42	0.53
4:P:9:BAL:N	7:P:12:DPR:C	2.71	0.53
1:A:121:LEU:HD21	1:A:210:VAL:HG12	1.91	0.53
1:B:117:PRO:HB2	1:B:140:ILE:HG23	1.91	0.53
1:A:27:SER:O	1:A:32:TYR:HE1	1.92	0.53
1:A:99:PHE:CE1	4:P:8:BAL:HB2	2.44	0.52
1:B:125:SER:O	1:B:128:GLU:HB2	2.09	0.52
1:B:16:GLN:O	1:B:80:LEU:HB3	2.09	0.52
1:A:116:ASN:HA	1:A:201:HIS:CD2	2.45	0.52
1:A:51:TYR:CE1	1:A:55:LYS:HB3	2.45	0.52
1:A:185:THR:O	1:A:188:GLN:HB2	2.10	0.52
1:B:53:VAL:HG21	1:B:68:LYS:HG2	1.91	0.51
1:A:196:SER:HB3	1:A:209:THR:HG23	1.92	0.51
1:A:62:ASP:CG	1:A:63:ARG:N	2.64	0.51
1:A:133:LYS:HD2	1:A:133:LYS:N	2.26	0.51
1:B:11:SER:OG	1:B:114:LYS:HE2	2.11	0.51
1:A:2:SER:O	1:A:3:ALA:HB3	2.11	0.51
1:B:15:GLY:C	1:B:79:GLY:HA2	2.32	0.50
1:A:65:SER:O	1:A:75:LEU:HA	2.11	0.50
1:A:52:GLU:HG3	3:P:7:HIS:CE1	2.47	0.50
1:A:48:VAL:CG2	1:B:99:PHE:HD1	2.22	0.50
1:A:125:SER:O	1:A:129:LEU:HD12	2.11	0.50
1:B:57:PRO:HD2	1:B:60:VAL:HG21	1.92	0.50
1:B:163:VAL:HA	1:B:181:TYR:O	2.12	0.50
1:B:4:LEU:HD23	1:B:24:GLY:HA2	1.95	0.49
1:A:139:LEU:HD11	1:B:181:TYR:CD2	2.47	0.49
1:A:48:VAL:HG21	1:B:99:PHE:HD1	1.75	0.49
1:B:38:TYR:OH	5:P:10:ACE:H1	2.12	0.49
1:A:189:TRP:CH2	1:A:212:PRO:HA	2.47	0.49
1:B:38:TYR:O	1:B:88:TYR:HA	2.13	0.49
1:A:64:PHE:CE1	1:A:77:VAL:HG12	2.48	0.49
1:A:171:GLN:O	1:A:173:ASN:N	2.44	0.49
1:A:164:GLU:HB2	1:A:181:TYR:CZ	2.48	0.49
1:B:173:ASN:HD22	1:B:175:LYS:HZ2	1.59	0.48
1:B:96:SER:O	1:B:97:ASP:HB3	2.13	0.48
1:B:38:TYR:HE1	1:B:91:SER:HB2	1.78	0.48
1:A:19:THR:HG23	1:A:76:THR:OG1	2.12	0.48
1:A:63:ARG:HB2	1:A:78:SER:HB2	1.96	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:145:PRO:O	1:A:201:HIS:HE1	1.97	0.47
1:B:112:GLN:HB2	1:B:113:PRO:CD	2.44	0.47
2:P:1:GLN:NE2	2:P:1:GLN:HA	2.28	0.47
1:B:6:GLN:HG2	1:B:22:CYS:SG	2.54	0.47
1:A:153:LYS:C	1:A:159:VAL:HG12	2.35	0.47
1:A:132:ASN:ND2	1:A:186:PRO:HG2	2.31	0.46
1:B:40:GLN:OE1	1:B:46:PRO:HG3	2.15	0.46
1:B:23:THR:HA	1:B:71:ASN:O	2.15	0.46
1:A:151:ALA:HB3	1:A:198:GLN:HB3	1.98	0.46
1:B:28:ASP:O	1:B:31:GLY:HA3	2.15	0.46
1:A:115:ALA:O	1:A:201:HIS:NE2	2.48	0.46
1:A:116:ASN:HD22	1:A:201:HIS:HD2	1.64	0.46
1:B:85:GLU:HG3	1:B:109:VAL:HG23	1.98	0.46
1:A:95:GLY:O	1:A:97:ASP:N	2.48	0.46
1:A:112:GLN:HA	1:A:113:PRO:HD3	1.80	0.46
1:A:137:VAL:HG11	1:B:137:VAL:HG11	1.98	0.46
1:B:49:ILE:O	1:B:50:ILE:HG12	2.15	0.45
1:A:2:SER:O	1:A:3:ALA:CB	2.64	0.45
1:A:34:TYR:HD1	3:P:7:HIS:CG	2.35	0.45
1:B:13:SER:O	1:B:16:GLN:HB2	2.17	0.45
1:A:37:TRP:HD1	1:A:50:ILE:HG21	1.79	0.45
1:B:42:ALA:O	1:B:44:LYS:NZ	2.49	0.45
1:A:37:TRP:H	1:A:50:ILE:HG22	1.81	0.45
1:B:54:ASN:C	1:B:54:ASN:HD22	2.20	0.45
1:B:56:ARG:HG3	1:B:60:VAL:HG12	1.99	0.45
1:A:77:VAL:HG23	1:A:80:LEU:HD21	1.99	0.45
1:A:155:ASP:OD1	1:A:193:ARG:HB3	2.17	0.45
1:A:20:ILE:O	1:A:74:SER:HA	2.17	0.45
1:A:77:VAL:HG23	1:A:77:VAL:O	2.17	0.44
1:B:171:GLN:HB2	1:B:173:ASN:OD1	2.17	0.44
1:B:119:VAL:HG22	1:B:208:LYS:HG2	1.99	0.44
1:A:51:TYR:HB2	3:P:7:HIS:HE1	1.79	0.44
2:P:1:GLN:O	6:P:11:DPN:CD1	2.65	0.44
1:A:85:GLU:HA	1:A:107:VAL:O	2.18	0.44
1:B:8:PRO:HG3	1:B:200:THR:HG22	2.00	0.44
1:A:211:ALA:O	1:A:213:THR:N	2.50	0.44
1:A:34:TYR:HD1	3:P:7:HIS:ND1	2.16	0.44
1:A:17:SER:OG	1:A:18:VAL:N	2.51	0.44
1:B:40:GLN:O	1:B:86:ALA:HB1	2.18	0.44
1:A:181:TYR:CD2	1:B:139:LEU:HD11	2.53	0.44
1:B:160:LYS:HD3	1:B:160:LYS:H	1.83	0.44
1:B:157:SER:HA	1:B:158:PRO:HD2	1.83	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:97:ASP:OD1	4:P:8:BAL:O	2.36	0.43
1:A:40:GLN:NE2	1:A:44:LYS:O	2.50	0.43
1:A:37:TRP:N	1:A:50:ILE:HG22	2.34	0.43
1:B:153:LYS:HA	1:B:157:SER:O	2.19	0.43
1:B:29:VAL:HG23	1:B:71:ASN:OD1	2.18	0.43
1:B:55:LYS:O	1:B:56:ARG:HB3	2.17	0.43
1:A:18:VAL:H	1:A:77:VAL:HG23	1.83	0.43
1:A:20:ILE:HD12	1:A:75:LEU:HD23	2.00	0.43
1:A:214:GLU:HB3	1:A:216:SER:OG	2.18	0.43
1:B:119:VAL:HG13	1:B:206:VAL:HG11	2.01	0.43
1:B:68:LYS:HD2	1:B:69:SER:N	2.34	0.43
1:A:24:GLY:HA3	1:A:29:VAL:CG2	2.48	0.43
1:A:88:TYR:CE1	1:A:107:VAL:HB	2.54	0.43
1:A:12:GLY:HA3	1:A:80:LEU:CD1	2.48	0.43
1:B:173:ASN:ND2	1:B:175:LYS:NZ	2.65	0.43
1:B:119:VAL:HG22	1:B:208:LYS:CG	2.48	0.43
1:B:112:GLN:HB2	1:B:113:PRO:HD2	2.01	0.43
1:A:7:PRO:HA	1:A:8:PRO:HD3	1.82	0.43
1:A:196:SER:HB2	1:A:207:GLU:OE1	2.19	0.43
1:A:117:PRO:CB	1:A:140:ILE:HG22	2.49	0.43
1:B:29:VAL:O	1:B:32:TYR:N	2.52	0.42
1:A:48:VAL:CG2	1:B:99:PHE:CD1	2.99	0.42
1:A:140:ILE:HG23	1:A:199:VAL:HG11	2.02	0.42
1:B:93:TYR:OH	1:B:96:SER:HB3	2.20	0.42
1:A:153:LYS:HA	1:A:158:PRO:HA	2.01	0.42
1:B:149:THR:O	1:B:199:VAL:HA	2.20	0.42
1:B:29:VAL:CG1	1:B:30:GLY:N	2.74	0.42
1:B:15:GLY:O	1:B:79:GLY:HA2	2.19	0.42
1:B:20:ILE:HG12	1:B:105:THR:HG21	2.01	0.42
1:A:49:ILE:HG22	1:A:60:VAL:HG13	2.02	0.42
1:A:116:ASN:HB3	1:A:117:PRO:HD2	2.02	0.41
1:A:213:THR:O	1:A:213:THR:CG2	2.68	0.41
1:A:126:SER:HB3	1:A:216:SER:HB3	2.02	0.41
1:A:54:ASN:ND2	1:A:55:LYS:N	2.69	0.41
1:B:186:PRO:O	1:B:190:LYS:HB2	2.20	0.41
1:B:51:TYR:CE1	1:B:55:LYS:HB3	2.55	0.41
1:B:35:VAL:HB	1:B:53:VAL:CG2	2.51	0.41
1:B:52:GLU:O	1:B:53:VAL:HB	2.21	0.41
1:B:185:THR:HA	1:B:186:PRO:HD3	1.91	0.41
1:B:18:VAL:CG1	1:B:19:THR:N	2.84	0.41
1:A:82:ALA:HA	1:A:109:VAL:HG21	2.02	0.41
1:A:95:GLY:O	1:A:98:ASN:N	2.53	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:51:TYR:CZ	1:B:55:LYS:HD2	2.56	0.40
1:A:166:THR:HG23	1:A:167:LYS:O	2.21	0.40
1:A:18:VAL:HG13	1:A:77:VAL:CG2	2.50	0.40
2:P:1:GLN:HB3	3:P:7:HIS:CG	2.56	0.40
1:A:24:GLY:HA3	1:A:29:VAL:HG21	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	214/216 (99%)	175 (82%)	27 (13%)	12 (6%)	3	4
1	B	214/216 (99%)	177 (83%)	24 (11%)	13 (6%)	2	3
All	All	428/432 (99%)	352 (82%)	51 (12%)	25 (6%)	3	4

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	SER
1	A	97	ASP
1	A	172	SER
1	A	173	ASN
1	B	26	SER
1	B	95	GLY
1	B	96	SER
1	A	16	GLN
1	A	53	VAL
1	A	154	ALA
1	A	156	GLY
1	A	212	PRO
1	B	27	SER
1	B	29	VAL
1	B	42	ALA

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Mol	Chain	Res	Type
1	B	160	LYS
1	A	42	ALA
1	B	94	GLU
1	B	97	ASP
1	B	202	GLU
1	B	56	ARG
1	B	83	GLU
1	B	55	LYS
1	A	43	GLY
1	A	57	PRO

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	181/181 (100%)	136 (75%)	45 (25%)	1	2
1	B	181/181 (100%)	145 (80%)	36 (20%)	2	5
2	P	1/4 (25%)	1 (100%)	0	100	100
All	All	363/366 (99%)	282 (78%)	81 (22%)	1	4

All (81) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	SER
1	A	14	LEU
1	A	25	THR
1	A	28	ASP
1	A	32	TYR
1	A	33	ASN
1	A	35	VAL
1	A	36	SER
1	A	39	GLN
1	A	44	LYS
1	A	47	LYS
1	A	51	TYR
1	A	54	ASN

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Mol	Chain	Res	Type
1	A	55	LYS
1	A	58	SER
1	A	63	ARG
1	A	75	LEU
1	A	81	GLN
1	A	83	GLU
1	A	87	ASP
1	A	98	ASN
1	A	106	LYS
1	A	110	LEU
1	A	132	ASN
1	A	135	THR
1	A	139	LEU
1	A	148	VAL
1	A	149	THR
1	A	159	VAL
1	A	163	VAL
1	A	165	THR
1	A	166	THR
1	A	167	LYS
1	A	170	LYS
1	A	171	GLN
1	A	174	ASN
1	A	179	SER
1	A	183	SER
1	A	185	THR
1	A	189	TRP
1	A	194	SER
1	A	205	THR
1	A	207	GLU
1	A	209	THR
1	A	213	THR
1	B	7	PRO
1	B	8	PRO
1	B	13	SER
1	B	23	THR
1	B	29	VAL
1	B	32	TYR
1	B	33	ASN
1	B	34	TYR
1	B	38	TYR
1	B	54	ASN

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Mol	Chain	Res	Type
1	B	58	SER
1	B	62	ASP
1	B	63	ARG
1	B	65	SER
1	B	67	SER
1	B	68	LYS
1	B	75	LEU
1	B	78	SER
1	B	80	LEU
1	B	97	ASP
1	B	99	PHE
1	B	119	VAL
1	B	120	THR
1	B	121	LEU
1	B	127	GLU
1	B	132	ASN
1	B	135	THR
1	B	142	ASP
1	B	148	VAL
1	B	153	LYS
1	B	160	LYS
1	B	166	THR
1	B	199	VAL
1	B	210	VAL
1	B	213	THR
1	B	215	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	ASN
1	A	40	GLN
1	A	41	HIS
1	A	98	ASN
1	A	116	ASN
1	A	132	ASN
1	A	198	GLN
1	B	40	GLN
1	B	54	ASN
1	B	98	ASN
1	B	130	GLN
1	B	132	ASN

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Mol	Chain	Res	Type
1	B	173	ASN
2	P	1	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

6 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$
5	ACE	P	10	2	2,2,2	0.48	0	1,1,1	0.13	0
6	DPN	P	11	-	11,11,12	5.52	3 (27%)	11,13,15	5.06	3 (27%)
7	DPR	P	12	-	7,7,8	8.44	3 (42%)	6,8,10	1.09	1 (16%)
3	HIS	P	7	-	10,10,11	5.43	2 (20%)	10,12,14	1.20	1 (10%)
4	BAL	P	8	4	4,4,5	8.16	2 (50%)	1,3,5	5.05	1 (100%)
4	BAL	P	9	4	5,5,5	0.84	0	5,5,5	1.97	2 (40%)

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
5	ACE	P	10	2	-	0/0/0/0	0/0/0/0
6	DPN	P	11	-	-	0/4/6/8	0/1/1/1
7	DPR	P	12	-	-	0/0/9/11	0/1/1/1
3	HIS	P	7	-	-	0/4/6/8	0/1/1/1
4	BAL	P	8	4	-	0/1/2/3	0/0/0/0
4	BAL	P	9	4	-	0/3/3/3	0/0/0/0

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	P	12	DPR	O-C	21.36	1.26	1.11
6	P	11	DPN	O-C	16.98	1.23	1.11
3	P	7	HIS	O-C	16.88	1.23	1.11
4	P	8	BAL	O-C	16.14	1.22	1.11
7	P	12	DPR	CB-CA	-5.88	1.46	1.53
6	P	11	DPN	CA-C	5.12	1.58	1.48
6	P	11	DPN	CB-CA	-3.86	1.43	1.53
3	P	7	HIS	CA-C	2.49	1.52	1.48
4	P	8	BAL	CA-C	2.37	1.54	1.47
7	P	12	DPR	CA-C	2.30	1.52	1.48

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	P	11	DPN	C-CA-N	-14.57	99.28	113.83
6	P	11	DPN	CG-CB-CA	7.21	131.43	114.42
4	P	8	BAL	CA-CB-N	5.05	124.98	112.31
3	P	7	HIS	C-CA-N	-3.53	110.31	113.83
6	P	11	DPN	CB-CA-N	3.22	127.03	112.03
4	P	9	BAL	CA-CB-N	3.21	120.37	112.31
4	P	9	BAL	CB-CA-C	2.56	118.58	113.48
7	P	12	DPR	CG-CD-N	-2.17	100.34	105.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.