



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:51 PM GMT

PDB ID : 1MCN  
Title : PRINCIPLES AND PITFALLS IN DESIGNING SITE DIRECTED PEP-  
TIDE LIGANDS  
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Deposited on : 1993-02-25  
Resolution : 2.70 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) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

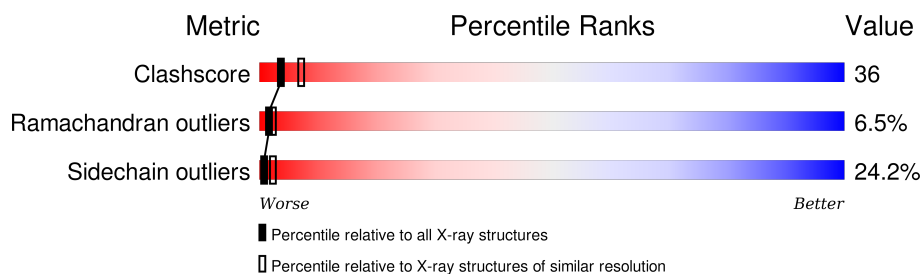
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 Å.

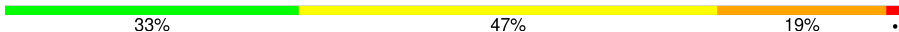


Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	216	 33% 47% 19% .
1	B	216	 35% 46% 17% .
2	P	4	 25% 75%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3231 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 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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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-D-HIS-L-PRO-NH<sub>2</sub>.

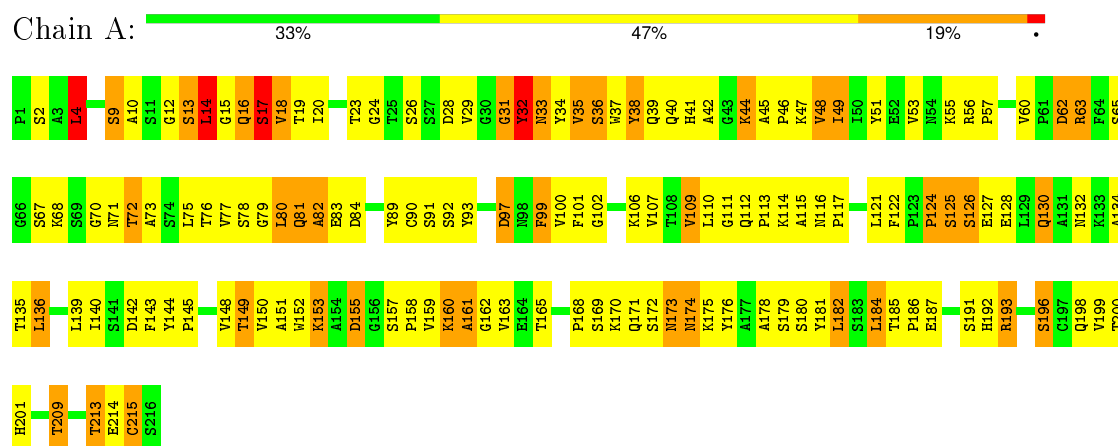
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	P	4	Total	C	N	O	0	0	1
			21	13	5	3			

### 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)



## 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, $\alpha$ , $\beta$ , $\gamma$	72.30 Å 72.30 Å 185.90 Å 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, $R_{free}$	0.183 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3231	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: DHI, ACE, NH2

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	0.86	0/1644	1.39	6/2241 (0.3%)
1	B	0.86	0/1644	1.40	11/2241 (0.5%)
2	P	1.33	0/7	1.38	0/8
All	All	0.86	0/3295	1.40	17/4490 (0.4%)

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	22	CYS	CA-CB-SG	8.11	128.60	114.00
1	B	4	LEU	CA-CB-CG	6.47	130.17	115.30
1	B	187	GLU	CA-CB-CG	6.08	126.79	113.40
1	B	128	GLU	CA-CB-CG	6.05	126.71	113.40
1	A	4	LEU	CA-CB-CG	6.00	129.10	115.30
1	A	130	GLN	CA-CB-CG	5.89	126.37	113.40
1	B	181	TYR	CA-CB-CG	5.89	124.60	113.40
1	B	136	LEU	CA-CB-CG	5.80	128.65	115.30
1	A	155	ASP	CB-CA-C	5.80	122.00	110.40
1	B	63	ARG	NE-CZ-NH1	5.68	123.14	120.30
1	B	204	SER	N-CA-CB	5.68	119.02	110.50
1	B	22	CYS	CB-CA-C	5.65	121.70	110.40
1	A	14	LEU	CA-CB-CG	5.47	127.88	115.30
1	B	94	GLU	CA-CB-CG	5.45	125.38	113.40
1	A	31	GLY	N-CA-C	-5.24	100.00	113.10
1	B	33	ASN	CB-CA-C	5.17	120.73	110.40
1	A	136	LEU	CA-CB-CG	5.05	126.92	115.30

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	A	1605	0	1540	119	0
1	B	1605	0	1540	117	0
2	P	21	0	17	3	0
All	All	3231	0	3097	226	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 36.

All (226) 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:B:35:VAL:HG12	1:B:53:VAL:HG12	1.39	1.04
1:B:94:GLU:HB3	1:B:98:ASN:HB2	1.43	0.98
1:A:10:ALA:HB3	1:A:107:VAL:HG22	1.48	0.94
1:B:9:SER:HB2	1:B:147:ALA:HB3	1.49	0.93
1:A:57:PRO:HD2	1:A:60:VAL:HG21	1.57	0.86
1:A:99:PHE:HZ	2:P:1:DHI:HD2	1.44	0.82
1:A:114:LYS:HG2	1:A:145:PRO:HD3	1.61	0.82
1:A:148:VAL:HG12	1:A:201:HIS:HB2	1.62	0.81
1:A:18:VAL:HG12	1:A:77:VAL:HB	1.63	0.80
1:B:194:SER:HB2	1:B:209:THR:HG23	1.63	0.80
1:A:81:GLN:O	1:A:83:GLU:N	2.15	0.79
1:A:63:ARG:NH1	1:A:63:ARG:HA	1.98	0.79
1:B:29:VAL:HA	1:B:32:TYR:HB2	1.63	0.79
1:A:171:GLN:HB2	1:A:173:ASN:OD1	1.83	0.78
1:A:68:LYS:HA	1:A:73:ALA:HA	1.66	0.77
1:A:15:GLY:O	1:A:79:GLY:HA2	1.86	0.76
1:A:18:VAL:HB	1:A:80:LEU:HD11	1.69	0.75
1:A:63:ARG:HH11	1:A:63:ARG:HA	1.52	0.75
1:A:40:GLN:HG3	1:A:44:LYS:O	1.87	0.74
1:B:20:ILE:HD11	1:B:107:VAL:HG21	1.70	0.72
1:B:37:TRP:CE2	1:B:75:LEU:HB2	2.24	0.72
1:A:99:PHE:CZ	2:P:1:DHI:HD2	2.25	0.72
1:B:121:LEU:HD12	1:B:137:VAL:O	1.91	0.71
1:B:182:LEU:HD23	1:B:184:LEU:HD11	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:112:GLN:HB3	1:B:113:PRO:HD2	1.73	0.70
1:A:57:PRO:HA	1:B:97:ASP:HB2	1.73	0.69
1:A:160:LYS:O	1:A:163:VAL:HG23	1.92	0.69
1:A:112:GLN:OE1	1:A:174:ASN:HB2	1.92	0.69
1:A:110:LEU:HD12	1:A:111:GLY:H	1.59	0.68
1:A:127:GLU:HA	1:A:130:GLN:HG2	1.77	0.67
1:A:48:VAL:HG21	1:B:99:PHE:CD2	2.29	0.67
1:A:68:LYS:HG3	1:A:73:ALA:HB2	1.77	0.67
1:B:150:VAL:HG22	1:B:199:VAL:HG12	1.77	0.67
1:A:63:ARG:HG3	1:A:78:SER:HB3	1.77	0.67
1:B:116:ASN:HD22	1:B:201:HIS:HD2	1.43	0.66
1:B:16:GLN:O	1:B:80:LEU:HB2	1.95	0.66
1:B:10:ALA:HB3	1:B:107:VAL:HG22	1.79	0.64
1:B:119:VAL:HG21	1:B:206:VAL:HB	1.79	0.64
1:B:127:GLU:HG2	1:B:130:GLN:NE2	2.13	0.64
1:A:29:VAL:HG12	1:A:71:ASN:HA	1.80	0.64
1:A:48:VAL:O	1:A:57:PRO:HG2	1.98	0.64
1:A:140:ILE:HD13	1:A:178:ALA:O	1.98	0.64
1:B:10:ALA:O	1:B:107:VAL:HA	1.99	0.63
1:B:54:ASN:HD22	1:B:55:LYS:N	1.95	0.63
1:B:54:ASN:ND2	1:B:55:LYS:HG3	2.13	0.63
1:B:12:GLY:O	1:B:109:VAL:HA	1.98	0.62
1:B:140:ILE:HD12	1:B:199:VAL:HG21	1.80	0.62
1:B:40:GLN:O	1:B:86:ALA:HB1	1.98	0.62
1:B:112:GLN:HB3	1:B:113:PRO:CD	2.30	0.62
1:B:116:ASN:ND2	1:B:201:HIS:HD2	1.97	0.62
1:B:18:VAL:HB	1:B:80:LEU:HD11	1.82	0.61
1:A:196:SER:HB2	1:A:209:THR:HG23	1.81	0.61
1:B:214:GLU:O	1:B:216:SER:N	2.33	0.61
1:A:37:TRP:HA	1:A:89:TYR:O	2.00	0.60
1:A:49:ILE:HG12	1:A:60:VAL:HG13	1.83	0.60
1:B:37:TRP:CE3	1:B:75:LEU:HD12	2.37	0.60
1:B:34:TYR:HD2	1:B:93:TYR:HB3	1.68	0.59
1:B:38:TYR:HE1	1:B:91:SER:HG	1.50	0.59
1:B:150:VAL:HG11	1:B:180:SER:OG	2.02	0.59
1:B:116:ASN:HD22	1:B:201:HIS:CD2	2.21	0.58
1:B:86:ALA:HB3	1:B:88:TYR:HE1	1.67	0.58
1:A:51:TYR:CZ	1:A:55:LYS:HB3	2.38	0.58
1:A:36:SER:O	1:A:90:CYS:HA	2.04	0.58
1:B:6:GLN:NE2	1:B:105:THR:H	2.02	0.58
1:A:82:ALA:HA	1:A:109:VAL:HG11	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:TYR:HB2	1:A:174:ASN:O	2.04	0.57
1:A:142:ASP:HA	1:A:175:LYS:HB3	1.85	0.57
1:A:215:CYS:SG	1:B:215:CYS:C	2.83	0.57
1:A:150:VAL:HG11	1:A:180:SER:OG	2.05	0.57
1:A:45:ALA:HA	1:B:89:TYR:HE2	1.69	0.57
1:B:143:PHE:CE2	1:B:148:VAL:HG13	2.41	0.56
1:B:39:GLN:HG3	1:B:88:TYR:CE1	2.40	0.56
2:P:1:DHI:O	2:P:3:NH2:N	2.38	0.56
1:A:169:SER:O	1:A:176:TYR:HA	2.05	0.56
1:B:198:GLN:NE2	1:B:205:THR:HG23	2.21	0.55
1:B:140:ILE:HD11	1:B:148:VAL:HG11	1.88	0.55
1:B:93:TYR:HE1	1:B:96:SER:HA	1.70	0.55
1:B:94:GLU:HB3	1:B:98:ASN:CB	2.27	0.55
1:A:168:PRO:HB2	1:A:176:TYR:HB3	1.87	0.55
1:A:185:THR:HB	1:A:186:PRO:HD2	1.89	0.55
1:A:15:GLY:O	1:A:17:SER:N	2.40	0.55
1:A:33:ASN:ND2	1:A:68:LYS:NZ	2.54	0.54
1:A:65:SER:OG	1:A:76:THR:HB	2.08	0.54
1:B:159:VAL:HG11	1:B:182:LEU:HD11	1.90	0.54
1:B:184:LEU:HD12	1:B:184:LEU:N	2.23	0.54
1:B:49:ILE:HG12	1:B:64:PHE:CD2	2.43	0.54
1:A:33:ASN:HD22	1:A:68:LYS:HZ2	1.55	0.54
1:A:28:ASP:OD1	1:A:29:VAL:HG23	2.08	0.54
1:B:54:ASN:C	1:B:54:ASN:HD22	2.12	0.53
1:A:4:LEU:HD23	1:A:101:PHE:O	2.09	0.53
1:B:6:GLN:HG2	1:B:105:THR:OG1	2.08	0.53
1:B:154:ALA:HB2	1:B:195:TYR:CE1	2.44	0.53
1:A:39:GLN:O	1:A:46:PRO:HA	2.08	0.53
1:A:196:SER:CB	1:A:209:THR:HG23	2.38	0.53
1:B:145:PRO:O	1:B:201:HIS:HE1	1.92	0.52
1:B:86:ALA:HB3	1:B:88:TYR:CE1	2.42	0.52
1:B:171:GLN:HE22	1:B:177:ALA:HB2	1.73	0.52
1:B:115:ALA:HB1	1:B:142:ASP:O	2.10	0.52
1:A:91:SER:HB2	1:A:101:PHE:CD2	2.44	0.52
1:A:56:ARG:NH2	1:A:62:ASP:HA	2.25	0.52
1:B:110:LEU:HD12	1:B:110:LEU:O	2.10	0.52
1:B:20:ILE:HG22	1:B:37:TRP:CH2	2.45	0.51
1:B:185:THR:O	1:B:188:GLN:HB2	2.11	0.51
1:B:38:TYR:CD2	1:B:48:VAL:HG22	2.45	0.51
1:B:27:SER:O	1:B:28:ASP:HB2	2.09	0.51
1:A:134:ALA:O	1:A:184:LEU:HD12	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:PRO:HB3	1:A:143:PHE:HB3	1.92	0.51
1:A:173:ASN:C	1:A:175:LYS:H	2.13	0.51
1:A:18:VAL:HG12	1:A:77:VAL:CB	2.39	0.50
1:A:215:CYS:SG	1:B:215:CYS:O	2.69	0.50
1:A:20:ILE:HD13	1:A:75:LEU:HB3	1.93	0.50
1:B:112:GLN:OE1	1:B:144:TYR:CE1	2.65	0.50
1:B:38:TYR:CE2	1:B:48:VAL:HG22	2.47	0.50
1:A:152:TRP:HB2	1:A:159:VAL:HG13	1.93	0.49
1:B:6:GLN:HB3	1:B:104:GLY:H	1.77	0.49
1:A:35:VAL:HA	1:A:91:SER:O	2.12	0.49
1:A:165:THR:HG23	1:A:180:SER:HB3	1.94	0.49
1:B:41:HIS:O	1:B:43:GLY:N	2.46	0.49
1:A:121:LEU:HD12	1:A:122:PHE:H	1.77	0.49
1:A:162:GLY:O	1:A:182:LEU:HA	2.12	0.49
1:B:56:ARG:HB3	1:B:60:VAL:HG12	1.94	0.49
1:B:56:ARG:HB3	1:B:60:VAL:CG1	2.43	0.49
1:B:150:VAL:HG22	1:B:199:VAL:CG1	2.43	0.49
1:B:64:PHE:HZ	1:B:88:TYR:HH	1.59	0.48
1:A:186:PRO:HG2	1:A:187:GLU:OE2	2.13	0.48
1:A:38:TYR:HB3	1:A:46:PRO:HB3	1.95	0.48
1:B:49:ILE:HD12	1:B:60:VAL:HG22	1.95	0.48
1:A:68:LYS:HE2	1:A:70:GLY:O	2.14	0.48
1:A:9:SER:HA	1:A:106:LYS:O	2.13	0.48
1:B:51:TYR:HD2	1:B:57:PRO:HG3	1.78	0.48
1:B:114:LYS:HD3	1:B:145:PRO:HD3	1.97	0.47
1:A:139:LEU:HD12	1:A:179:SER:OG	2.14	0.47
1:B:40:GLN:HB3	1:B:46:PRO:HA	1.97	0.47
1:A:116:ASN:ND2	1:A:201:HIS:HD2	2.12	0.47
1:A:155:ASP:OD1	1:A:193:ARG:HB3	2.15	0.47
1:B:143:PHE:HE1	1:B:177:ALA:HA	1.80	0.47
1:A:77:VAL:HG12	1:A:80:LEU:HD13	1.96	0.47
1:B:127:GLU:O	1:B:130:GLN:N	2.48	0.47
1:A:122:PHE:HB3	1:B:122:PHE:HD2	1.80	0.47
1:A:33:ASN:ND2	1:A:68:LYS:HZ2	2.11	0.46
1:A:116:ASN:HD22	1:A:201:HIS:HD2	1.62	0.46
1:A:12:GLY:HA2	1:A:16:GLN:NE2	2.31	0.46
1:B:194:SER:HB2	1:B:209:THR:CG2	2.40	0.46
1:A:23:THR:OG1	1:A:72:THR:HG23	2.15	0.46
1:B:30:GLY:C	1:B:32:TYR:H	2.19	0.46
1:B:37:TRP:CD2	1:B:75:LEU:HB2	2.51	0.46
1:B:185:THR:OG1	1:B:188:GLN:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:PRO:O	1:B:147:ALA:HB1	2.16	0.45
1:B:140:ILE:CD1	1:B:199:VAL:HG21	2.45	0.45
1:A:170:LYS:HG2	1:A:176:TYR:CE2	2.52	0.45
1:B:124:PRO:HD2	1:B:189:TRP:CZ2	2.52	0.45
1:B:189:TRP:CZ2	1:B:212:PRO:HA	2.51	0.45
1:B:119:VAL:CG2	1:B:206:VAL:HB	2.47	0.45
1:B:70:GLY:O	1:B:71:ASN:HB2	2.17	0.45
1:A:159:VAL:HA	1:A:160:LYS:HE3	1.99	0.45
1:B:34:TYR:CD2	1:B:93:TYR:HB3	2.48	0.45
1:A:163:VAL:HA	1:A:181:TYR:O	2.17	0.44
1:A:171:GLN:HB3	1:B:164:GLU:HG2	2.00	0.44
1:B:6:GLN:HG3	1:B:21:SER:O	2.18	0.44
1:B:81:GLN:O	1:B:84:ASP:HB2	2.17	0.44
1:B:143:PHE:HD1	1:B:143:PHE:H	1.65	0.44
1:A:80:LEU:HD22	1:A:80:LEU:H	1.83	0.44
1:A:26:SER:O	1:A:31:GLY:N	2.46	0.44
1:A:16:GLN:O	1:A:17:SER:HB2	2.17	0.44
1:B:18:VAL:HG12	1:B:77:VAL:HB	2.00	0.44
1:B:39:GLN:O	1:B:46:PRO:HA	2.18	0.43
1:B:188:GLN:O	1:B:192:HIS:ND1	2.45	0.43
1:A:31:GLY:C	1:A:32:TYR:CD1	2.91	0.43
1:A:124:PRO:O	1:A:125:SER:CB	2.65	0.43
1:A:115:ALA:HB2	1:A:175:LYS:HE2	1.99	0.43
1:A:33:ASN:HD22	1:A:68:LYS:NZ	2.14	0.43
1:A:153:LYS:HA	1:A:157:SER:O	2.18	0.43
1:A:77:VAL:CG1	1:A:80:LEU:HD13	2.49	0.43
1:A:65:SER:O	1:A:75:LEU:HD23	2.18	0.43
1:B:38:TYR:HE1	1:B:91:SER:OG	2.01	0.43
1:A:170:LYS:H	1:B:167:LYS:HZ1	1.66	0.42
1:A:20:ILE:HD12	1:A:20:ILE:N	2.34	0.42
1:A:19:THR:HA	1:A:75:LEU:O	2.18	0.42
1:A:160:LYS:O	1:A:161:ALA:C	2.57	0.42
1:A:126:SER:O	1:A:130:GLN:HG2	2.19	0.42
1:A:28:ASP:OD1	1:A:29:VAL:N	2.52	0.42
1:B:51:TYR:CD2	1:B:57:PRO:HG3	2.54	0.42
1:B:94:GLU:HG2	1:B:95:GLY:H	1.83	0.42
1:B:14:LEU:HA	1:B:80:LEU:O	2.19	0.42
1:B:120:THR:OG1	1:B:122:PHE:HE1	2.02	0.42
1:B:20:ILE:O	1:B:74:SER:HA	2.20	0.42
1:B:1:PRO:HD2	1:B:94:GLU:OE2	2.20	0.42
1:A:35:VAL:HG11	1:A:73:ALA:HB1	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:63:ARG:CG	1:A:78:SER:HB3	2.46	0.42
1:B:127:GLU:O	1:B:130:GLN:HB2	2.20	0.42
1:B:49:ILE:CD1	1:B:60:VAL:HG22	2.50	0.42
1:A:41:HIS:O	1:A:42:ALA:C	2.57	0.42
1:A:48:VAL:HG21	1:B:99:PHE:CG	2.54	0.42
1:B:211:ALA:HA	1:B:212:PRO:HD2	1.87	0.42
1:A:34:TYR:O	1:A:92:SER:HA	2.20	0.42
1:A:191:SER:O	1:A:192:HIS:ND1	2.53	0.42
1:A:47:LYS:HD2	1:A:49:ILE:CD1	2.50	0.41
1:B:2:SER:O	1:B:100:VAL:HG23	2.20	0.41
1:A:45:ALA:HA	1:B:89:TYR:CE2	2.52	0.41
1:A:169:SER:OG	1:B:167:LYS:N	2.52	0.41
1:A:157:SER:HA	1:A:158:PRO:HD3	1.76	0.41
1:A:4:LEU:HB2	1:A:102:GLY:HA2	2.02	0.41
1:A:90:CYS:O	1:A:91:SER:HB2	2.19	0.41
1:B:20:ILE:HG22	1:B:37:TRP:HH2	1.83	0.41
1:B:41:HIS:CE1	1:B:86:ALA:HB2	2.55	0.41
1:A:149:THR:O	1:A:199:VAL:HA	2.20	0.41
1:A:160:LYS:NZ	1:A:160:LYS:H	2.18	0.41
1:B:119:VAL:HG22	1:B:199:VAL:HG22	2.02	0.41
1:A:38:TYR:CD1	1:A:38:TYR:N	2.88	0.41
1:A:4:LEU:HD13	1:A:24:GLY:HA3	2.01	0.41
1:B:37:TRP:HB2	1:B:50:ILE:HB	2.01	0.41
1:B:170:LYS:HG2	1:B:176:TYR:CE1	2.56	0.41
1:B:9:SER:HB2	1:B:147:ALA:CB	2.35	0.41
1:B:198:GLN:HE22	1:B:205:THR:CG2	2.34	0.41
1:A:17:SER:HA	1:A:80:LEU:HD22	2.03	0.41
1:A:47:LYS:HD2	1:A:49:ILE:HD12	2.03	0.40
1:A:17:SER:H	1:A:80:LEU:CD2	2.33	0.40
1:A:112:GLN:HA	1:A:113:PRO:HD3	1.92	0.40
1:B:93:TYR:CE1	1:B:96:SER:HA	2.52	0.40
1:A:151:ALA:HB3	1:A:198:GLN:HB3	2.02	0.40
1:B:155:ASP:HA	1:B:193:ARG:NH2	2.37	0.40
1:A:12:GLY:HA2	1:A:16:GLN:HE22	1.85	0.40
1:A:13:SER:O	1:A:16:GLN:HB3	2.21	0.40
1:B:37:TRP:CD2	1:B:75:LEU:HD12	2.57	0.40
1:A:93:TYR:CE1	1:A:97:ASP:HA	2.56	0.40
1:A:13:SER:O	1:A:14:LEU:C	2.60	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%)	167 (78%)	33 (15%)	14 (6%)	1	2
1	B	214/216 (99%)	173 (81%)	28 (13%)	13 (6%)	2	3
2	P	1/4 (25%)	0	0	1 (100%)	0	0
All	All	429/436 (98%)	340 (79%)	61 (14%)	28 (6%)	1	2

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	16	GLN
1	A	80	LEU
1	A	82	ALA
1	A	125	SER
1	A	161	ALA
1	B	26	SER
1	B	28	ASP
1	B	29	VAL
1	B	53	VAL
1	B	71	ASN
1	A	2	SER
1	A	32	TYR
1	A	62	ASP
1	A	213	THR
1	B	7	PRO
1	B	42	ALA
1	B	54	ASN
1	A	14	LEU
1	A	132	ASN
1	A	173	ASN
1	A	215	CYS
1	B	45	ALA
2	P	2	PRO
1	A	17	SER

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Mol	Chain	Res	Type
1	B	110	LEU
1	B	94	GLU
1	B	8	PRO
1	B	172	SER

### 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%)	140 (77%)	41 (23%)	1	3
1	B	181/181 (100%)	134 (74%)	47 (26%)	0	2
2	P	1/1 (100%)	1 (100%)	0	100	100
All	All	363/363 (100%)	275 (76%)	88 (24%)	1	2

All (88) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	9	SER
1	A	13	SER
1	A	17	SER
1	A	18	VAL
1	A	32	TYR
1	A	33	ASN
1	A	35	VAL
1	A	36	SER
1	A	38	TYR
1	A	44	LYS
1	A	48	VAL
1	A	49	ILE
1	A	53	VAL
1	A	63	ARG
1	A	67	SER
1	A	72	THR
1	A	81	GLN

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Mol	Chain	Res	Type
1	A	84	ASP
1	A	97	ASP
1	A	99	PHE
1	A	100	VAL
1	A	109	VAL
1	A	124	PRO
1	A	126	SER
1	A	128	GLU
1	A	135	THR
1	A	136	LEU
1	A	149	THR
1	A	153	LYS
1	A	160	LYS
1	A	172	SER
1	A	174	ASN
1	A	182	LEU
1	A	184	LEU
1	A	193	ARG
1	A	196	SER
1	A	200	THR
1	A	209	THR
1	A	213	THR
1	A	214	GLU
1	B	1	PRO
1	B	2	SER
1	B	13	SER
1	B	14	LEU
1	B	21	SER
1	B	22	CYS
1	B	25	THR
1	B	26	SER
1	B	27	SER
1	B	29	VAL
1	B	54	ASN
1	B	60	VAL
1	B	62	ASP
1	B	65	SER
1	B	67	SER
1	B	69	SER
1	B	74	SER
1	B	75	LEU
1	B	78	SER

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Mol	Chain	Res	Type
1	B	80	LEU
1	B	83	GLU
1	B	89	TYR
1	B	92	SER
1	B	99	PHE
1	B	100	VAL
1	B	103	THR
1	B	116	ASN
1	B	120	THR
1	B	122	PHE
1	B	127	GLU
1	B	136	LEU
1	B	140	ILE
1	B	142	ASP
1	B	143	PHE
1	B	153	LYS
1	B	164	GLU
1	B	171	GLN
1	B	175	LYS
1	B	180	SER
1	B	181	TYR
1	B	182	LEU
1	B	184	LEU
1	B	190	LYS
1	B	198	GLN
1	B	204	SER
1	B	205	THR
1	B	216	SER

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

Mol	Chain	Res	Type
1	A	33	ASN
1	A	98	ASN
1	A	116	ASN
1	A	174	ASN
1	B	16	GLN
1	B	33	ASN
1	B	54	ASN
1	B	116	ASN
1	B	130	GLN
1	B	171	GLN

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Mol	Chain	Res	Type
1	B	174	ASN
1	B	198	GLN
1	B	201	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	DHI	P	1	2	5,10,11	1.12	0	3,12,14	1.72	2 (66%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	DHI	P	1	2	-	0/4/6/8	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	1	DHI	O-C-CA	-2.02	120.23	125.49
2	P	1	DHI	CD2-NE2-CE1	2.16	109.11	105.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	P	1	DHI	3	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

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

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

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

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

### 6.3 Carbohydrates [i](#)

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

### 6.4 Ligands [i](#)

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

### 6.5 Other polymers [i](#)

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