



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 22, 2020 – 09:46 PM EST

PDB ID : 1MCD
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 : Not provided

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/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 : 1.8.0 (224370), CSD as540be (2019)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.8

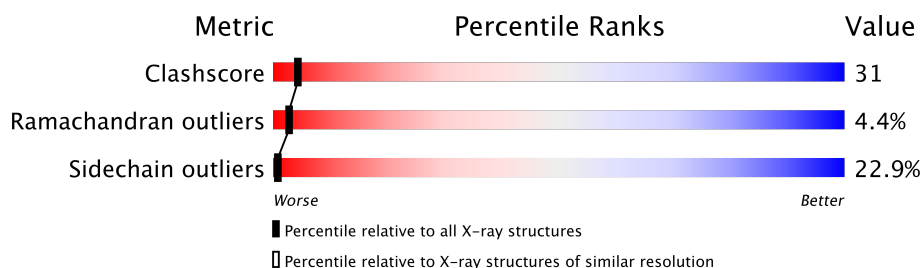
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is unknown.

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	122126	-
Ramachandran outliers	120053	-
Sidechain outliers	120020	-

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	216	<div> <div style="width: 38%; background-color: green;"></div> <div style="width: 50%; background-color: yellow;"></div> <div style="width: 10%; background-color: orange;"></div> <div style="width: 2%; background-color: red;"></div> </div> <div>38% 50% 10% .</div>
1	B	216	<div> <div style="width: 36%; background-color: green;"></div> <div style="width: 51%; background-color: yellow;"></div> <div style="width: 12%; background-color: orange;"></div> <div style="width: 1%; background-color: red;"></div> </div> <div>36% 51% 12% .</div>
2	P	6	<div> <div style="width: 17%; background-color: green;"></div> <div style="width: 83%; background-color: yellow;"></div> </div> <div>17% 83%</div>

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
2	DPR	P	4	-	-	X	-

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3247 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-1 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 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	PRO	-	expression tag	UNP P0DOX8
B	1	PRO	-	expression tag	UNP P0DOX8

- Molecule 2 is a protein called PEPTIDE N-ACETYL-D-PHE-B-ALA-L-HIS-D-PRO-NH₂.

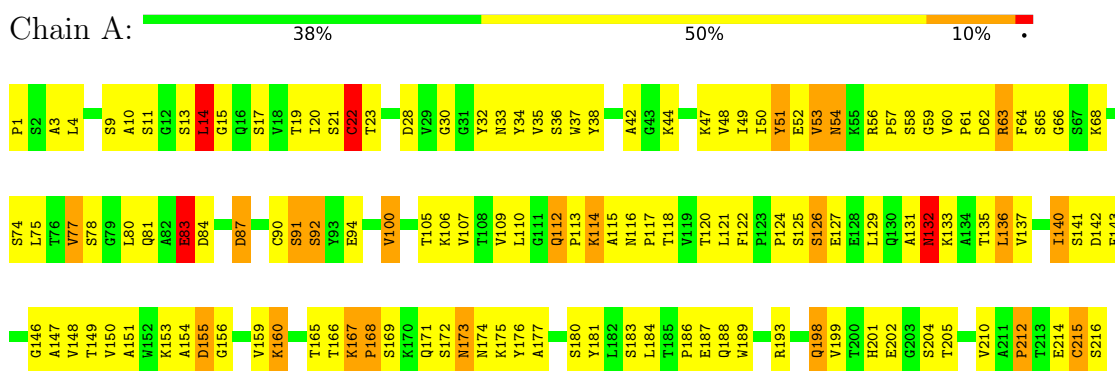
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	P	6	Total	C	N	O	0	0	1
			37	25	7	5			

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 the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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-1 light chain



- Molecule 1: Immunoglobulin lambda-1 light chain



- Molecule 2: PEPTIDE N-ACETYL-D-PHE-B-ALA-L-HIS-D-PRO-NH2



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	72.30Å 72.30Å 185.90Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – (Not available)	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-(Not available))	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ, X-PLOR	Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3247	wwPDB-VP
Average B, all atoms (Å ²)	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, 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	0.83	0/1644	1.38	9/2241 (0.4%)
1	B	0.89	1/1644 (0.1%)	1.42	11/2241 (0.5%)
2	P	0.76	0/10	1.09	0/12
All	All	0.86	1/3298 (0.0%)	1.40	20/4494 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	215	CYS	CB-SG	-5.56	1.72	1.81

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	215	CYS	CA-CB-SG	12.37	136.27	114.00
1	B	34	TYR	CA-CB-CG	8.08	128.75	113.40
1	A	22	CYS	CA-CB-SG	7.96	128.33	114.00
1	A	215	CYS	CA-CB-SG	7.81	128.06	114.00
1	A	214	GLU	CA-CB-CG	6.99	128.78	113.40
1	A	51	TYR	CA-CB-CG	6.85	126.42	113.40
1	B	193	ARG	NE-CZ-NH1	6.83	123.71	120.30
1	B	99	PHE	CA-CB-CG	6.83	130.28	113.90
1	A	202	GLU	CA-CB-CG	6.19	127.02	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	31	GLY	N-CA-C	-5.92	98.31	113.10
1	B	189	TRP	CA-CB-CG	5.86	124.84	113.70
1	B	32	TYR	CA-CB-CG	-5.84	102.30	113.40
1	A	83	GLU	CA-CB-CG	5.62	125.77	113.40
1	B	97	ASP	CB-CG-OD1	5.56	123.31	118.30
1	B	30	GLY	N-CA-C	-5.48	99.40	113.10
1	B	181	TYR	CA-CB-CG	5.48	123.81	113.40
1	A	215	CYS	N-CA-CB	5.25	120.05	110.60
1	B	22	CYS	CA-CB-SG	5.10	123.19	114.00
1	A	54	ASN	N-CA-CB	5.07	119.72	110.60
1	A	168	PRO	N-CA-C	5.02	125.16	112.10

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	PRO	Peptide
1	A	167	LYS	Peptide

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	98	0
1	B	1605	0	1540	100	0
2	P	37	0	29	9	0
All	All	3247	0	3109	197	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 31.

All (197) 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:28:ASP:O	1:B:32:TYR:HB2	1.69	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:4:LEU:HD23	1:B:22:CYS:SG	2.14	0.88
1:A:131:ALA:O	1:A:132:ASN:HB2	1.74	0.87
1:A:117:PRO:HB3	1:A:143:PHE:HB3	1.57	0.87
1:B:10:ALA:O	1:B:107:VAL:HA	1.85	0.76
1:B:214:GLU:O	1:B:215:CYS:HB3	1.84	0.76
1:A:173:ASN:ND2	1:A:175:LYS:HB2	2.00	0.76
1:B:52:GLU:HG2	1:B:55:LYS:NZ	2.02	0.74
1:A:165:THR:HG22	1:A:167:LYS:HD3	1.69	0.73
1:A:171:GLN:HE21	1:A:177:ALA:HB2	1.52	0.73
1:A:63:ARG:O	1:A:77:VAL:HA	1.88	0.73
1:A:59:GLY:O	1:A:60:VAL:HG23	1.89	0.71
1:B:40:GLN:O	1:B:86:ALA:HB1	1.90	0.71
1:A:126:SER:O	1:A:129:LEU:HB2	1.91	0.71
1:A:126:SER:HA	1:A:129:LEU:HD12	1.72	0.71
1:B:37:TRP:HB2	1:B:50:ILE:HB	1.73	0.70
1:B:124:PRO:HD3	1:B:136:LEU:HG	1.71	0.69
1:A:48:VAL:O	1:A:57:PRO:HG2	1.93	0.68
1:B:45:ALA:HB1	1:B:46:PRO:CD	2.24	0.68
1:A:171:GLN:HB2	1:A:175:LYS:O	1.95	0.67
1:A:35:VAL:HA	1:A:91:SER:O	1.94	0.67
1:B:153:LYS:HZ2	1:B:198:GLN:HB2	1.57	0.67
2:P:3:HIS:HB3	2:P:4:DPR:HD2	1.78	0.66
1:B:173:ASN:ND2	1:B:175:LYS:HG3	2.11	0.66
1:B:16:GLN:O	1:B:80:LEU:HB2	1.96	0.65
1:A:150:VAL:HG11	1:A:180:SER:OG	1.95	0.65
1:B:143:PHE:CE2	1:B:148:VAL:HB	2.31	0.65
1:A:65:SER:O	1:A:75:LEU:HD12	1.97	0.65
1:B:32:TYR:OH	1:B:93:TYR:N	2.30	0.65
1:B:149:THR:O	1:B:199:VAL:HA	1.97	0.65
1:A:198:GLN:NE2	1:A:205:THR:HG21	2.12	0.64
1:B:185:THR:OG1	1:B:188:GLN:HB2	1.97	0.64
1:A:166:THR:HG21	1:B:166:THR:HG21	1.80	0.63
1:B:155:ASP:OD1	1:B:193:ARG:HD2	1.98	0.63
1:A:166:THR:HG21	1:B:166:THR:CG2	2.28	0.63
1:B:35:VAL:HA	1:B:91:SER:O	1.98	0.63
1:A:142:ASP:H	1:A:171:GLN:HE22	1.48	0.62
1:B:36:SER:OG	2:P:1:DPN:HD2	2.00	0.62
1:B:153:LYS:NZ	1:B:196:SER:HB2	2.15	0.61
1:B:52:GLU:HG2	1:B:55:LYS:HZ2	1.63	0.61
1:A:154:ALA:HB2	1:A:159:VAL:CG2	2.30	0.61
1:B:32:TYR:OH	1:B:34:TYR:HB2	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:9:SER:HB2	1:B:147:ALA:HB3	1.82	0.60
1:B:173:ASN:ND2	1:B:175:LYS:HZ3	1.99	0.60
1:A:165:THR:HG23	1:A:180:SER:HB3	1.84	0.60
1:B:173:ASN:HD22	1:B:175:LYS:HZ3	1.50	0.59
1:A:155:ASP:OD2	1:A:193:ARG:HB2	2.02	0.59
1:B:149:THR:HB	1:B:200:THR:OG1	2.02	0.59
1:A:87:ASP:OD1	1:A:106:LYS:HG2	2.01	0.59
2:P:3:HIS:HB3	2:P:4:DPR:CD	2.32	0.59
1:B:41:HIS:HB2	1:B:44:LYS:CG	2.33	0.59
1:A:63:ARG:HB3	1:A:78:SER:H	1.66	0.58
1:B:41:HIS:HB2	1:B:44:LYS:HG2	1.85	0.58
1:A:14:LEU:HD22	1:A:110:LEU:O	2.03	0.58
1:A:121:LEU:HD23	1:A:210:VAL:HG13	1.85	0.58
1:A:54:ASN:OD1	1:A:65:SER:HA	2.04	0.58
1:B:56:ARG:HG3	1:B:60:VAL:HB	1.85	0.57
1:A:184:LEU:HA	1:A:188:GLN:OE1	2.05	0.56
1:B:214:GLU:O	1:B:215:CYS:CB	2.53	0.56
1:A:87:ASP:HA	1:A:105:THR:O	2.05	0.56
1:B:67:SER:HB3	1:B:74:SER:HB2	1.86	0.56
1:B:41:HIS:ND1	1:B:86:ALA:HB2	2.21	0.56
1:B:69:SER:O	1:B:71:ASN:N	2.39	0.55
1:B:17:SER:HB3	1:B:78:SER:HA	1.88	0.55
1:A:56:ARG:HD3	1:A:64:PHE:O	2.06	0.55
1:A:147:ALA:O	1:A:201:HIS:HD2	1.91	0.54
1:A:80:LEU:HD22	1:A:109:VAL:HG21	1.89	0.54
1:B:171:GLN:HB2	1:B:173:ASN:OD1	2.08	0.54
1:B:32:TYR:HH	1:B:93:TYR:HB3	1.73	0.54
1:B:38:TYR:HE1	1:B:91:SER:HB2	1.73	0.54
1:A:153:LYS:HD2	1:A:156:GLY:O	2.08	0.54
1:A:159:VAL:C	1:A:160:LYS:HD2	2.28	0.54
1:A:10:ALA:HB3	1:A:107:VAL:HG22	1.90	0.54
1:A:122:PHE:HB2	1:A:137:VAL:HG13	1.89	0.54
1:B:122:PHE:O	1:B:136:LEU:HD23	2.08	0.54
1:B:45:ALA:HB1	1:B:46:PRO:HD3	1.90	0.54
1:B:4:LEU:HA	1:B:24:GLY:HA2	1.90	0.54
1:B:186:PRO:O	1:B:190:LYS:HG2	2.09	0.53
1:B:64:PHE:CE1	1:B:77:VAL:HG22	2.44	0.53
1:B:41:HIS:O	1:B:43:GLY:N	2.42	0.53
1:A:117:PRO:HB2	1:A:140:ILE:HG23	1.90	0.53
1:B:108:THR:HG21	1:B:145:PRO:HB3	1.91	0.53
1:B:185:THR:OG1	1:B:187:GLU:HG3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:52:GLU:HB3	1:B:55:LYS:HD3	1.90	0.53
1:B:171:GLN:OE1	1:B:177:ALA:HB2	2.09	0.52
1:A:165:THR:CG2	1:A:167:LYS:HD3	2.40	0.52
1:A:136:LEU:HD11	1:A:184:LEU:HD11	1.92	0.52
2:P:4:DPR:HD3	2:P:5:NH2:N	2.25	0.51
1:B:1:PRO:O	1:B:3:ALA:N	2.43	0.51
1:B:198:GLN:HB2	1:B:207:GLU:HG3	1.91	0.51
1:A:38:TYR:HA	1:A:47:LYS:O	2.11	0.51
1:B:52:GLU:HG2	1:B:55:LYS:HZ3	1.72	0.51
1:A:140:ILE:HG13	1:A:199:VAL:HG21	1.92	0.51
1:A:19:THR:CG2	1:A:74:SER:HB3	2.41	0.51
1:A:150:VAL:HA	1:A:198:GLN:O	2.11	0.51
1:A:94:GLU:HG2	1:A:100:VAL:HG22	1.93	0.50
1:A:49:ILE:O	1:A:57:PRO:HD2	2.11	0.50
1:A:171:GLN:HG2	1:B:164:GLU:HG3	1.94	0.50
1:B:134:ALA:HB3	1:B:184:LEU:O	2.11	0.50
1:A:53:VAL:HG13	1:A:68:LYS:HB2	1.94	0.50
1:B:173:ASN:ND2	1:B:175:LYS:NZ	2.60	0.50
1:B:63:ARG:NH2	1:B:84:ASP:OD1	2.44	0.50
1:A:181:TYR:CD2	1:B:139:LEU:HD11	2.47	0.49
1:B:196:SER:OG	1:B:209:THR:HG22	2.11	0.49
2:P:1:DPN:C	2:P:1:DPN:CD1	2.91	0.49
1:A:81:GLN:OE1	1:A:84:ASP:OD2	2.31	0.49
1:A:4:LEU:HD23	1:A:22:CYS:SG	2.53	0.49
1:B:8:PRO:HG3	1:B:149:THR:HB	1.95	0.48
1:A:36:SER:O	1:A:90:CYS:HA	2.13	0.48
1:A:15:GLY:H	1:A:80:LEU:HB2	1.78	0.48
1:B:164:GLU:O	1:B:180:SER:HA	2.13	0.48
1:B:17:SER:HA	1:B:77:VAL:O	2.14	0.48
1:A:131:ALA:O	1:A:132:ASN:CB	2.53	0.48
1:A:114:LYS:NZ	1:A:114:LYS:HB2	2.29	0.48
1:A:149:THR:O	1:A:199:VAL:HA	2.13	0.48
1:A:114:LYS:HB2	1:A:114:LYS:HZ3	1.79	0.48
1:B:34:TYR:CD2	1:B:93:TYR:HD2	2.31	0.48
1:A:151:ALA:HB3	1:A:198:GLN:HB3	1.96	0.48
1:B:153:LYS:HZ2	1:B:198:GLN:CB	2.27	0.47
1:A:124:PRO:HD3	1:A:136:LEU:HD22	1.97	0.47
1:A:87:ASP:CG	1:A:106:LYS:HG2	2.33	0.47
1:B:54:ASN:C	1:B:54:ASN:HD22	2.17	0.47
1:A:169:SER:O	1:A:176:TYR:HA	2.14	0.47
1:B:153:LYS:HZ1	1:B:196:SER:HB2	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:PRO:O	1:A:189:TRP:HB3	2.15	0.47
2:P:3:HIS:CB	2:P:4:DPR:HD2	2.44	0.47
1:B:12:GLY:O	1:B:109:VAL:HA	2.15	0.46
1:B:39:GLN:HG3	1:B:39:GLN:O	2.15	0.46
1:A:167:LYS:HB3	1:A:168:PRO:CD	2.45	0.46
1:A:14:LEU:HD13	1:A:109:VAL:CG1	2.46	0.46
1:A:28:ASP:HB3	1:A:94:GLU:HB3	1.96	0.46
1:B:125:SER:OG	1:B:128:GLU:HG3	2.15	0.46
1:B:173:ASN:HD22	1:B:175:LYS:NZ	2.14	0.46
1:B:85:GLU:O	1:B:86:ALA:HB2	2.16	0.46
1:A:33:ASN:HA	1:A:68:LYS:NZ	2.30	0.46
1:A:60:VAL:HA	1:A:61:PRO:HD3	1.72	0.46
1:B:65:SER:O	1:B:75:LEU:HA	2.16	0.46
1:A:66:GLY:HA2	1:A:74:SER:O	2.16	0.46
1:B:32:TYR:OH	1:B:93:TYR:HB3	2.16	0.45
1:A:126:SER:CA	1:A:129:LEU:HD12	2.44	0.45
1:A:114:LYS:O	1:A:114:LYS:HG3	2.16	0.45
1:A:49:ILE:HD11	1:A:75:LEU:HD21	1.98	0.45
1:A:91:SER:HA	1:A:100:VAL:O	2.17	0.45
2:P:2:BAL:O	2:P:3:HIS:CG	2.70	0.45
1:A:56:ARG:NH1	1:A:64:PHE:O	2.46	0.45
1:B:36:SER:CB	2:P:1:DPN:HD2	2.46	0.45
1:A:189:TRP:CZ2	1:A:212:PRO:HG3	2.53	0.44
1:B:124:PRO:HG2	1:B:189:TRP:NE1	2.32	0.44
1:A:14:LEU:HD13	1:A:109:VAL:HG11	1.99	0.44
1:B:170:LYS:HD2	1:B:176:TYR:CZ	2.53	0.44
1:B:211:ALA:HA	1:B:212:PRO:HD3	1.86	0.44
1:B:32:TYR:HE2	1:B:92:SER:HG	1.66	0.44
1:A:112:GLN:NE2	1:A:174:ASN:HD21	2.15	0.44
1:A:20:ILE:HD12	1:A:20:ILE:N	2.33	0.44
1:B:8:PRO:HG3	1:B:149:THR:CB	2.48	0.44
1:B:28:ASP:OD2	1:B:94:GLU:HB2	2.18	0.44
1:A:116:ASN:HA	1:A:117:PRO:HD3	1.93	0.43
1:A:37:TRP:CE2	1:A:75:LEU:HB2	2.53	0.43
1:A:117:PRO:HB2	1:A:140:ILE:CG2	2.49	0.43
1:B:34:TYR:OH	2:P:3:HIS:CE1	2.71	0.43
1:A:3:ALA:HA	1:A:100:VAL:CG1	2.48	0.43
1:A:112:GLN:CD	1:A:174:ASN:HD21	2.21	0.43
1:A:57:PRO:HB3	1:B:97:ASP:OD1	2.19	0.43
1:B:3:ALA:HB3	1:B:100:VAL:HG11	2.00	0.43
1:B:128:GLU:O	1:B:131:ALA:HB3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:160:LYS:HD3	1:B:161:ALA:N	2.33	0.43
1:B:28:ASP:HB3	1:B:94:GLU:HA	2.01	0.43
1:A:115:ALA:CB	1:A:175:LYS:HZ3	2.32	0.42
1:A:112:GLN:HA	1:A:113:PRO:HD3	1.76	0.42
1:A:115:ALA:HB2	1:A:175:LYS:NZ	2.34	0.42
1:A:19:THR:HG22	1:A:74:SER:HB3	2.00	0.42
1:A:122:PHE:HB2	1:A:137:VAL:CG1	2.50	0.42
1:A:80:LEU:HD22	1:A:109:VAL:CG2	2.49	0.42
1:B:38:TYR:O	1:B:88:TYR:HA	2.19	0.42
1:A:146:GLY:O	1:A:168:PRO:HG2	2.20	0.42
1:A:171:GLN:C	1:A:173:ASN:H	2.23	0.42
1:A:54:ASN:C	1:A:54:ASN:ND2	2.73	0.42
1:A:137:VAL:HG21	1:B:137:VAL:HG11	2.02	0.42
1:A:115:ALA:CB	1:A:175:LYS:NZ	2.83	0.42
1:B:25:THR:HB	1:B:26:SER:H	1.61	0.41
1:A:49:ILE:HA	1:A:60:VAL:HG21	2.01	0.41
1:A:57:PRO:HB2	1:A:60:VAL:HG23	2.01	0.41
1:B:45:ALA:HB1	1:B:46:PRO:HD2	2.02	0.41
1:B:33:ASN:O	1:B:53:VAL:HG23	2.20	0.41
1:A:215:CYS:SG	1:B:216:SER:N	2.94	0.41
1:A:34:TYR:O	1:A:92:SER:HA	2.21	0.41
1:B:91:SER:HA	1:B:100:VAL:O	2.20	0.41
1:B:22:CYS:HB3	1:B:73:ALA:HB3	2.02	0.41
1:B:94:GLU:HB3	1:B:98:ASN:OD1	2.21	0.41
1:B:82:ALA:C	1:B:84:ASP:H	2.24	0.41
1:B:7:PRO:HA	1:B:8:PRO:HD2	1.85	0.41
1:A:83:GLU:O	1:A:83:GLU:HG3	2.22	0.40
1:B:122:PHE:HA	1:B:123:PRO:HD3	1.87	0.40
1:A:4:LEU:HD13	1:A:100:VAL:HB	2.03	0.40
1:B:213:THR:O	1:B:214:GLU:HB2	2.21	0.40
1:B:41:HIS:CD2	1:B:44:LYS:HE3	2.57	0.40
1:B:57:PRO:O	1:B:60:VAL:HG23	2.21	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%)	176 (82%)	27 (13%)	11 (5%)	2	2
1	B	214/216 (99%)	183 (86%)	23 (11%)	8 (4%)	4	4
2	P	1/6 (17%)	1 (100%)	0	0	100	100
All	All	429/438 (98%)	360 (84%)	50 (12%)	19 (4%)	3	3

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	62	ASP
1	A	155	ASP
1	B	25	THR
1	B	42	ALA
1	B	70	GLY
1	A	53	VAL
1	A	132	ASN
1	B	2	SER
1	B	214	GLU
1	B	215	CYS
1	A	14	LEU
1	A	172	SER
1	A	42	ALA
1	A	187	GLU
1	A	83	GLU
1	A	212	PRO
1	B	30	GLY
1	B	146	GLY
1	A	30	GLY

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	1
1	B	181/181 (100%)	139 (77%)	42 (23%)	1	1
2	P	1/1 (100%)	1 (100%)	0	100	100
All	All	363/363 (100%)	280 (77%)	83 (23%)	1	1

All (83) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	SER
1	A	11	SER
1	A	13	SER
1	A	14	LEU
1	A	17	SER
1	A	21	SER
1	A	22	CYS
1	A	23	THR
1	A	32	TYR
1	A	44	LYS
1	A	50	ILE
1	A	51	TYR
1	A	52	GLU
1	A	58	SER
1	A	63	ARG
1	A	77	VAL
1	A	83	GLU
1	A	87	ASP
1	A	91	SER
1	A	92	SER
1	A	100	VAL
1	A	112	GLN
1	A	114	LYS
1	A	118	THR
1	A	120	THR
1	A	125	SER
1	A	126	SER
1	A	127	GLU
1	A	132	ASN
1	A	133	LYS
1	A	135	THR
1	A	136	LEU
1	A	140	ILE
1	A	141	SER

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Mol	Chain	Res	Type
1	A	148	VAL
1	A	160	LYS
1	A	173	ASN
1	A	183	SER
1	A	198	GLN
1	A	204	SER
1	A	216	SER
1	B	13	SER
1	B	14	LEU
1	B	18	VAL
1	B	21	SER
1	B	23	THR
1	B	26	SER
1	B	27	SER
1	B	28	ASP
1	B	29	VAL
1	B	39	GLN
1	B	44	LYS
1	B	47	LYS
1	B	54	ASN
1	B	58	SER
1	B	65	SER
1	B	67	SER
1	B	72	THR
1	B	76	THR
1	B	90	CYS
1	B	91	SER
1	B	92	SER
1	B	97	ASP
1	B	103	THR
1	B	121	LEU
1	B	136	LEU
1	B	138	CYS
1	B	142	ASP
1	B	143	PHE
1	B	153	LYS
1	B	159	VAL
1	B	160	LYS
1	B	166	THR
1	B	167	LYS
1	B	184	LEU
1	B	187	GLU

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Mol	Chain	Res	Type
1	B	188	GLN
1	B	193	ARG
1	B	196	SER
1	B	199	VAL
1	B	210	VAL
1	B	214	GLU
1	B	215	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	112	GLN
1	A	171	GLN
1	A	173	ASN
1	A	174	ASN
1	B	39	GLN
1	B	54	ASN
1	B	116	ASN
1	B	132	ASN
2	P	3	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

3 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
2	BAL	P	2	2	4,4,5	2.04	1 (25%)	3,3,5	4.08	1 (33%)

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	BAL	P	2	2	-	0/1/2/3	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	2	BAL	CA-C	4.05	1.60	1.49

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	2	BAL	CB-CA-C	-6.73	101.33	111.27

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	P	2	BAL	1	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 ⓘ

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 is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.