



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:26 PM GMT

PDB ID : 1AR7
Title : P1/MAHONEY POLIOVIRUS, DOUBLE MUTANT P1095S + H2142Y
Authors : Wien, M.W.; Curry, S.; Filman, D.J.; Hogle, J.M.
Deposited on : 1997-08-11
Resolution : 2.90 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
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 (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

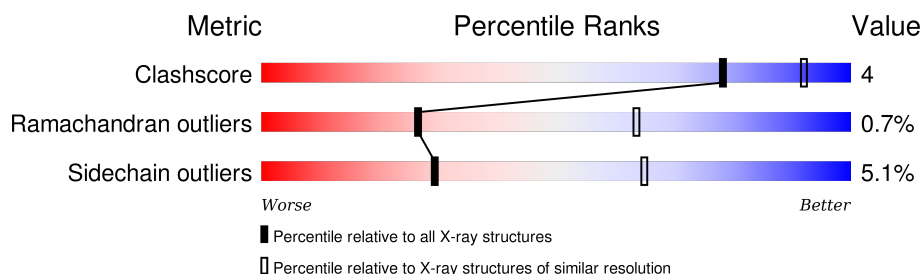
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	0	5	<div> <div>80%</div> <div>20%</div> </div>
2	1	302	<div> <div>78%</div> <div>13%</div> <div>• 6%</div> </div>
3	2	272	<div> <div>83%</div> <div>13%</div> <div>• •</div> </div>
4	3	238	<div> <div>87%</div> <div>10%</div> <div>• •</div> </div>
5	4	68	<div> <div>66%</div> <div>21%</div> <div>• 12%</div> </div>

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7212 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 P1/MAHONEY POLIOVIRUS.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	0	5	Total	C	N	O	0	0	0
			29	15	5	9			

- Molecule 2 is a protein called P1/MAHONEY POLIOVIRUS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1	283	Total	C	N	O	S	0	0	0
			2221	1414	378	424	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	95	SER	PRO	ENGINEERED	UNP P03300

- Molecule 3 is a protein called P1/MAHONEY POLIOVIRUS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	2	268	Total	C	N	O	S	0	0	0
			2087	1320	356	397	14			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	142	TYR	HIS	ENGINEERED	UNP P03300

- Molecule 4 is a protein called P1/MAHONEY POLIOVIRUS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	3	235	Total	C	N	O	S	0	0	0
			1834	1169	299	349	17			

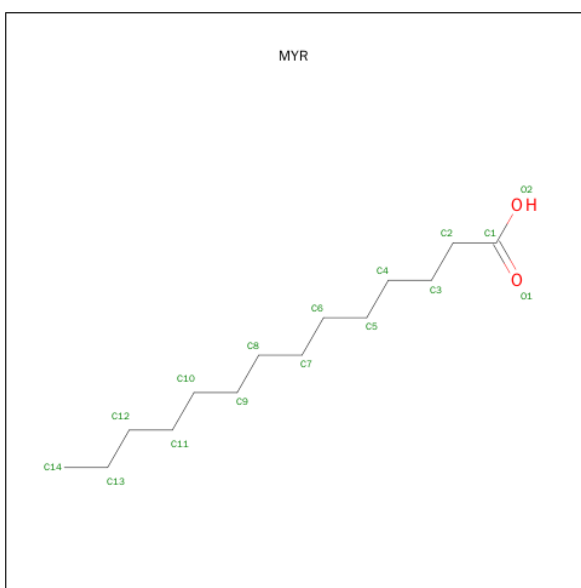
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	123	SER	PHE	CONFLICT	UNP P03300

- Molecule 5 is a protein called P1/MAHONEY POLIOVIRUS.

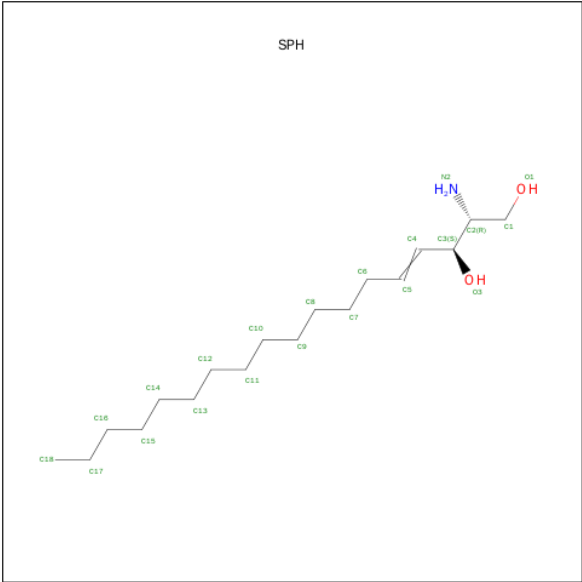
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	4	60	Total	C	N	O	S	0	0	0
			462	286	78	97	1			

- Molecule 6 is MYRISTIC ACID (three-letter code: MYR) (formula: C₁₄H₂₈O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	4	1	Total	C	O	0	0
			15	14	1		

- Molecule 7 is SPHINGOSINE (three-letter code: SPH) (formula: C₁₈H₃₇NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	1	1	Total	C	N	O	0	0
			21	18	1	2		

- Molecule 8 is water.


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	0	1	Total	O	0	0
			1	1		
8	1	180	Total	O	0	0
			180	180		
8	2	174	Total	O	0	0
			174	174		
8	3	142	Total	O	0	0
			142	142		
8	4	46	Total	O	0	0
			46	46		

3 Residue-property plots [i](#)

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


Note EDS was not executed.

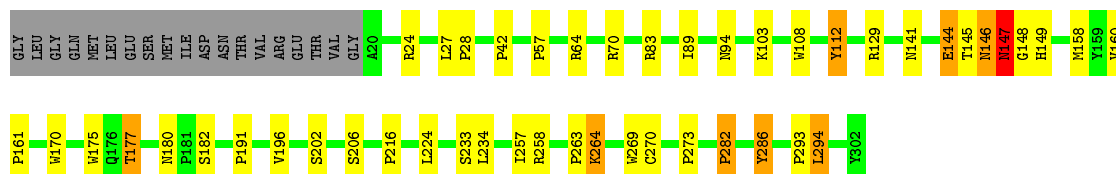
• Molecule 1: P1/MAHONEY POLIOVIRUS

Chain 0:  80% 20%




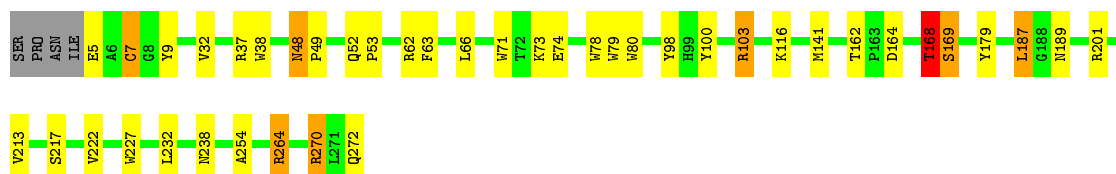
• Molecule 2: P1/MAHONEY POLIOVirus

Chain 1:  78% 13% 6%




• Molecule 3: P1/MAHONEY POLIOVIRUS

Chain 2:  83% 13% ..



• Molecule 4: P1/MAHONEY POLIOVIRUS

Chain 3:  87% 10% ..



• Molecule 5: P1/MAHONEY POLIOVIRUS

Chain 4:  66% 21% 12%



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	319.95Å 355.10Å 377.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	11.00 – 2.90	Depositor
% Data completeness (in resolution range)	81.0 (11.00-2.90)	Depositor
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.0	Depositor
R, R_{free}	0.234 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7212	wwPDB-VP
Average B, all atoms (Å ²)	13.0	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: SPH, MYR

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	0	0.97	0/28	1.48	0/36
2	1	0.87	0/2283	1.46	25/3120 (0.8%)
3	2	0.80	0/2144	1.47	29/2931 (1.0%)
4	3	0.82	0/1881	1.33	18/2562 (0.7%)
5	4	0.88	0/469	1.46	5/632 (0.8%)
All	All	0.84	0/6805	1.43	77/9281 (0.8%)

There are no bond length outliers.

All (77) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1	83	ARG	NE-CZ-NH1	10.21	125.41	120.30
3	2	264	ARG	NE-CZ-NH2	-9.43	115.58	120.30
3	2	38	TRP	CD1-CG-CD2	9.14	113.61	106.30
3	2	227	TRP	CD1-CG-CD2	8.54	113.13	106.30
3	2	78	TRP	CD1-CG-CD2	8.49	113.09	106.30
2	1	269	TRP	CD1-CG-CD2	8.45	113.06	106.30
3	2	38	TRP	CE2-CD2-CG	-8.45	100.54	107.30
2	1	170	TRP	CD1-CG-CD2	8.25	112.90	106.30
2	1	83	ARG	NE-CZ-NH2	-8.18	116.21	120.30
2	1	269	TRP	CE2-CD2-CG	-8.16	100.77	107.30
3	2	80	TRP	CD1-CG-CD2	8.14	112.81	106.30
3	2	264	ARG	NE-CZ-NH1	8.11	124.35	120.30
4	3	71	ARG	NE-CZ-NH1	8.03	124.32	120.30
4	3	223	ARG	NE-CZ-NH2	-8.00	116.30	120.30
3	2	80	TRP	CE2-CD2-CG	-7.97	100.92	107.30
4	3	170	TRP	CE2-CD2-CG	-7.96	100.93	107.30
2	1	175	TRP	CD1-CG-CD2	7.95	112.66	106.30
3	2	79	TRP	CD1-CG-CD2	7.85	112.58	106.30
4	3	156	TRP	CE2-CD2-CG	-7.82	101.04	107.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	3	170	TRP	CD1-CG-CD2	7.82	112.55	106.30
3	2	78	TRP	CE2-CD2-CG	-7.73	101.11	107.30
2	1	175	TRP	CE2-CD2-CG	-7.73	101.12	107.30
2	1	108	TRP	CE2-CD2-CG	-7.44	101.35	107.30
4	3	110	TRP	CD1-CG-CD2	7.42	112.24	106.30
3	2	79	TRP	CE2-CD2-CG	-7.38	101.40	107.30
3	2	103	ARG	NE-CZ-NH2	-7.34	116.63	120.30
3	2	227	TRP	CE2-CD2-CG	-7.29	101.47	107.30
2	1	170	TRP	CE2-CD2-CG	-7.26	101.49	107.30
3	2	201	ARG	NE-CZ-NH1	7.25	123.92	120.30
2	1	108	TRP	CD1-CG-CD2	7.18	112.05	106.30
3	2	100	TYR	CB-CG-CD2	-7.16	116.70	121.00
3	2	71	TRP	CE2-CD2-CG	-7.14	101.59	107.30
4	3	156	TRP	CD1-CG-CD2	7.12	112.00	106.30
5	4	27	TYR	CB-CG-CD2	-7.07	116.76	121.00
3	2	71	TRP	CD1-CG-CD2	6.94	111.85	106.30
2	1	112	TYR	CB-CG-CD2	-6.68	116.99	121.00
2	1	70	ARG	NE-CZ-NH2	-6.60	117.00	120.30
4	3	110	TRP	CE2-CD2-CG	-6.49	102.11	107.30
5	4	34	ARG	NE-CZ-NH1	6.46	123.53	120.30
2	1	64	ARG	NE-CZ-NH1	6.29	123.45	120.30
3	2	168	THR	CA-CB-CG2	6.12	120.97	112.40
4	3	170	TRP	CG-CD2-CE3	6.08	139.37	133.90
4	3	156	TRP	CG-CD2-CE3	6.05	139.35	133.90
2	1	144	GLU	CA-C-N	-6.00	104.01	117.20
4	3	13	TYR	CB-CG-CD2	-6.00	117.40	121.00
5	4	61	LEU	CA-CB-CG	5.95	128.97	115.30
3	2	222	VAL	CG1-CB-CG2	-5.84	101.55	110.90
3	2	168	THR	CA-CB-OG1	-5.82	96.77	109.00
2	1	146	ASN	CA-C-N	-5.78	104.49	117.20
2	1	129	ARG	NE-CZ-NH1	5.68	123.14	120.30
4	3	149	MET	CG-SD-CE	-5.58	91.27	100.20
3	2	164	ASP	CB-CG-OD1	5.57	123.32	118.30
4	3	145	ARG	NE-CZ-NH2	-5.54	117.53	120.30
3	2	38	TRP	CG-CD2-CE3	5.53	138.88	133.90
3	2	62	ARG	NE-CZ-NH2	-5.53	117.54	120.30
5	4	34	ARG	NE-CZ-NH2	-5.50	117.55	120.30
2	1	269	TRP	CB-CG-CD1	-5.50	119.85	127.00
2	1	269	TRP	CG-CD2-CE3	5.50	138.85	133.90
2	1	264	LYS	CB-CA-C	-5.50	99.40	110.40
3	2	98	TYR	CB-CG-CD1	-5.49	117.70	121.00
3	2	270	ARG	NE-CZ-NH1	5.49	123.05	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	2	79	TRP	CB-CG-CD1	-5.43	119.94	127.00
2	1	175	TRP	CG-CD2-CE3	5.40	138.76	133.90
2	1	286	TYR	CB-CG-CD2	-5.34	117.79	121.00
2	1	108	TRP	CG-CD2-CE3	5.32	138.68	133.90
3	2	270	ARG	NE-CZ-NH2	-5.30	117.65	120.30
4	3	170	TRP	CB-CG-CD1	-5.28	120.14	127.00
4	3	65	MET	CG-SD-CE	-5.22	91.84	100.20
2	1	147	ASN	OD1-CG-ND2	-5.19	109.95	121.90
2	1	293	PRO	N-CA-CB	5.17	109.51	103.30
3	2	227	TRP	CG-CD1-NE1	-5.14	104.96	110.10
4	3	110	TRP	CG-CD1-NE1	-5.13	104.97	110.10
3	2	78	TRP	CG-CD1-NE1	-5.11	104.99	110.10
2	1	24	ARG	NE-CZ-NH2	-5.08	117.76	120.30
5	4	14	GLU	N-CA-C	5.06	124.67	111.00
4	3	232	GLU	CA-CB-CG	5.03	124.47	113.40
4	3	124	MET	CG-SD-CE	5.02	108.23	100.20

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	0	29	0	24	0	0
2	1	2221	0	2171	23	0
3	2	2087	0	2002	19	0
4	3	1834	0	1816	14	0
5	4	462	0	446	7	0
6	4	15	0	27	0	0
7	1	21	0	37	3	0
8	0	1	0	0	0	0
8	1	180	0	0	3	0
8	2	174	0	0	0	0
8	3	142	0	0	1	0
8	4	46	0	0	0	0
All	All	7212	0	6523	47	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (47) 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)
3:2:5:GLU:HG2	3:2:9:TYR:HD2	1.43	0.82
2:1:158:MET:SD	2:1:177:THR:HG23	2.23	0.79
2:1:177:THR:HG22	2:1:180:ASN:HB2	1.64	0.78
3:2:5:GLU:HG2	3:2:9:TYR:CD2	2.27	0.69
4:3:167:VAL:O	4:3:169:PRO:HD3	2.03	0.59
2:1:177:THR:HG21	2:1:182:SER:OG	2.04	0.57
3:2:37:ARG:HG3	4:3:37:PRO:HB3	1.91	0.53
4:3:87:LEU:HD11	4:3:114:LEU:HD12	1.93	0.51
5:4:55:GLU:HG2	5:4:61:LEU:HD23	1.93	0.51
2:1:273:PRO:HB3	3:2:189:ASN:HB2	1.94	0.50
2:1:206:SER:O	7:1:0:SPH:H11	2.12	0.49
3:2:187:LEU:HD22	4:3:65:MET:CE	2.42	0.49
2:1:191:PRO:HG2	4:3:13:TYR:HB2	1.95	0.48
2:1:141:ASN:HA	8:1:471:HOH:O	2.12	0.48
2:1:42:PRO:HA	5:4:63:LYS:O	2.14	0.48
2:1:27:LEU:HB3	2:1:28:PRO:HD2	1.98	0.46
2:1:94:ASN:HA	2:1:103:LYS:HE3	1.98	0.46
2:1:146:ASN:OD1	2:1:147:ASN:HB3	2.15	0.46
2:1:264:LYS:NZ	5:4:37:ALA:O	2.48	0.46
2:1:216:PRO:HB2	3:2:270:ARG:HB3	1.99	0.45
3:2:213:VAL:HG22	4:3:37:PRO:HG2	1.99	0.45
2:1:112:TYR:CE2	7:1:0:SPH:H2	2.52	0.44
3:2:103:ARG:HD2	3:2:217:SER:O	2.17	0.44
3:2:187:LEU:HD13	3:2:232:LEU:HD22	2.00	0.44
5:4:10:VAL:HG21	5:4:25:ILE:HD12	2.00	0.44
2:1:282:PRO:HG2	3:2:141:MET:HE1	1.99	0.44
2:1:57:PRO:HB3	4:3:169:PRO:HB3	1.99	0.43
2:1:89:ILE:HG12	2:1:258:ARG:HG2	1.99	0.43
3:2:116:LYS:HE3	4:3:124:MET:SD	2.58	0.43
2:1:294:LEU:HD22	4:3:57:LEU:HD21	2.01	0.43
4:3:234:LYS:HD3	4:3:234:LYS:HA	1.80	0.43
5:4:57:ILE:HD11	5:4:61:LEU:HB3	2.00	0.43
2:1:257:ILE:HD12	2:1:257:ILE:N	2.35	0.42
3:2:168:THR:HG22	3:2:169:SER:OG	2.20	0.42
7:1:0:SPH:H4	8:1:397:HOH:O	2.18	0.41
3:2:179:TYR:HA	4:3:65:MET:HE3	2.03	0.41
4:3:64:THR:O	4:3:67:MET:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:3:323:HOH:O	5:4:46:PHE:HB2	2.21	0.41
2:1:160:VAL:HA	2:1:161:PRO:HD3	1.81	0.41
2:1:294:LEU:HD13	4:3:67:MET:SD	2.61	0.41
2:1:202:SER:HB2	8:1:425:HOH:O	2.20	0.41
3:2:5:GLU:HG3	3:2:7:CYS:H	1.86	0.41
3:2:63:PHE:CD1	3:2:254:ALA:HB2	2.55	0.41
3:2:187:LEU:HD22	4:3:65:MET:HE2	2.02	0.40
2:1:273:PRO:HB3	3:2:189:ASN:CB	2.51	0.40
3:2:48:ASN:HB3	3:2:49:PRO:HD3	2.03	0.40
3:2:32:VAL:HG13	5:4:56:PRO:HB2	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	0	3/5 (60%)	3 (100%)	0	0	100	100
2	1	281/302 (93%)	262 (93%)	15 (5%)	4 (1%)	14	44
3	2	266/272 (98%)	252 (95%)	13 (5%)	1 (0%)	39	74
4	3	233/238 (98%)	223 (96%)	10 (4%)	0	100	100
5	4	56/68 (82%)	52 (93%)	3 (5%)	1 (2%)	11	37
All	All	839/885 (95%)	792 (94%)	41 (5%)	6 (1%)	26	63

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	1	147	ASN
2	1	148	GLY
2	1	234	LEU
5	4	60	VAL

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Mol	Chain	Res	Type
3	2	48	ASN
2	1	270	CYS

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	0	4/4 (100%)	3 (75%)	1 (25%)	1	2
2	1	245/261 (94%)	233 (95%)	12 (5%)	31	67
3	2	228/232 (98%)	215 (94%)	13 (6%)	25	59
4	3	210/212 (99%)	201 (96%)	9 (4%)	35	71
5	4	52/57 (91%)	49 (94%)	3 (6%)	25	58
All	All	739/766 (96%)	701 (95%)	38 (5%)	29	65

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	10	THR
2	1	144	GLU
2	1	145	THR
2	1	147	ASN
2	1	149	HIS
2	1	177	THR
2	1	196	VAL
2	1	224	LEU
2	1	233	SER
2	1	263	PRO
2	1	282	PRO
2	1	286	TYR
2	1	294	LEU
3	2	7	CYS
3	2	52	GLN
3	2	53	PRO
3	2	66	LEU

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Mol	Chain	Res	Type
3	2	73	LYS
3	2	74	GLU
3	2	162	THR
3	2	168	THR
3	2	169	SER
3	2	187	LEU
3	2	238	ASN
3	2	264	ARG
3	2	272	GLN
4	3	33	PRO
4	3	85	LEU
4	3	93	PRO
4	3	137	PRO
4	3	146	LYS
4	3	149	MET
4	3	208	MET
4	3	218	ASN
4	3	224	LEU
5	4	49	ASP
5	4	50	PRO
5	4	61	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
2	1	65	HIS
2	1	69	HIS
3	2	226	ASN
4	3	218	ASN
5	4	13	HIS
5	4	31	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 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	$\# Z > 2$
7	SPH	1	0	-	19,20,20	0.40	0	16,21,21	1.18	1 (6%)
6	MYR	4	1	5	14,14,15	0.43	0	12,13,15	0.83	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
7	SPH	1	0	-	-	0/21/21/21	0/0/0/0
6	MYR	4	1	5	-	0/11/12/13	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	1	0	SPH	O3-C3-C4	-3.17	101.88	110.78

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
7	1	0	SPH	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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.