



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 11:28 PM UTC

PDB ID : 1BEV / pdb_00001bev
Title : BOVINE ENTEROVIRUS VG-5-27
Authors : Smyth, M.; Tate, J.; Lyons, C.; Hoey, E.; Martin, S.; Stuart, D.
Deposited on : 1996-04-03
Resolution : 3.00 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

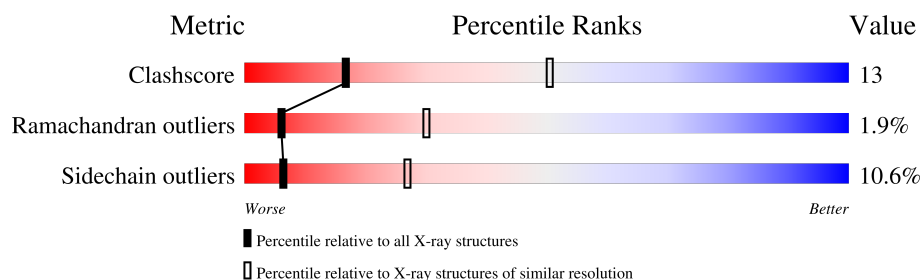
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)

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 of 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	1	281	
2	2	248	
3	3	242	
4	4	68	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6315 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 BOVINE ENTEROVIRUS COAT PROTEINS VP1 TO VP4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	268	Total	C	N	O	S	0	0	0
			2099	1323	361	404	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	15	ALA	VAL	conflict	UNP P12915
1	24	SER	THR	conflict	UNP P12915
1	94	HIS	ASN	conflict	UNP P12915
1	237	TYR	CYS	conflict	UNP P12915

- Molecule 2 is a protein called BOVINE ENTEROVIRUS COAT PROTEINS VP1 TO VP4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	2	244	Total	C	N	O	S	0	0	0
			1890	1201	325	357	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	62	ARG	ALA	conflict	UNP P12915
2	101	LEU	ILE	conflict	UNP P12915

- Molecule 3 is a protein called BOVINE ENTEROVIRUS COAT PROTEINS VP1 TO VP4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	3	242	Total	C	N	O	S	0	0	0
			1871	1195	306	358	12			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	32	PRO	LEU	conflict	UNP P12915
3	154	ILE	VAL	conflict	UNP P12915

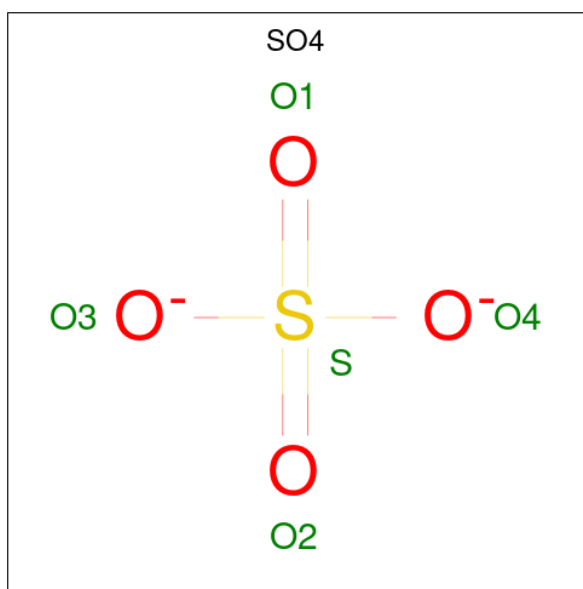
- Molecule 4 is a protein called BOVINE ENTEROVIRUS COAT PROTEINS VP1 TO VP4.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	4	40	Total	C	N	O	0	0	0
			299	185	52	62			

There is a discrepancy between the modelled and reference sequences:

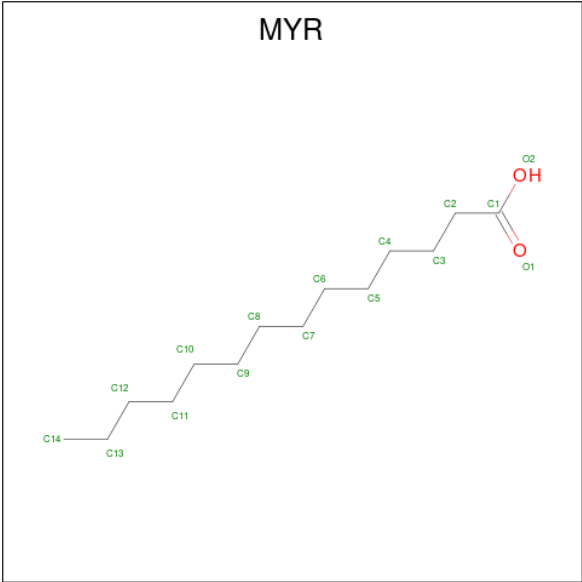
Chain	Residue	Modelled	Actual	Comment	Reference
4	16	GLN	GLY	conflict	UNP P12915

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	1	1	Total	O	S	0	0
			5	4	1		
5	2	1	Total	O	S	0	0
			5	4	1		

- Molecule 6 is MYRISTIC ACID (CCD ID: MYR) (formula: C₁₄H₂₈O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	1	1	Total	C	O	0	0
			16	14	2		

- Molecule 7 is water.

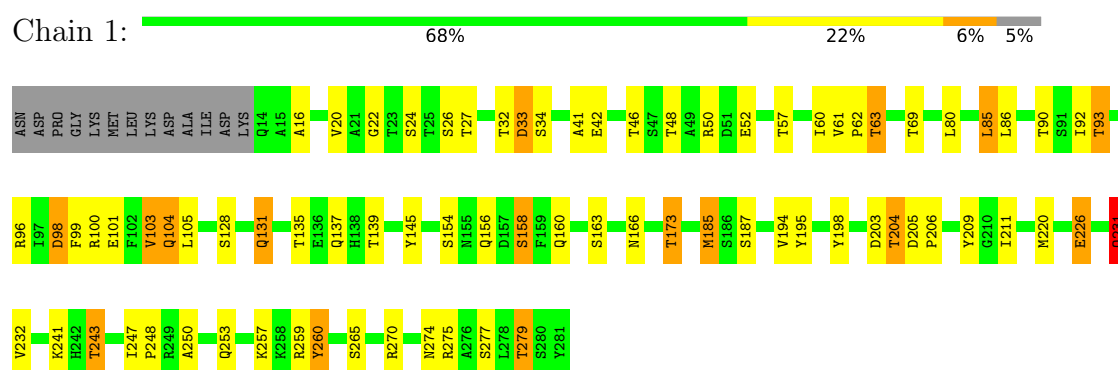
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	1	49	Total	O	0	0
			49	49		
7	2	51	Total	O	0	0
			51	51		
7	3	30	Total	O	0	0
			30	30		

3 Residue-property plots

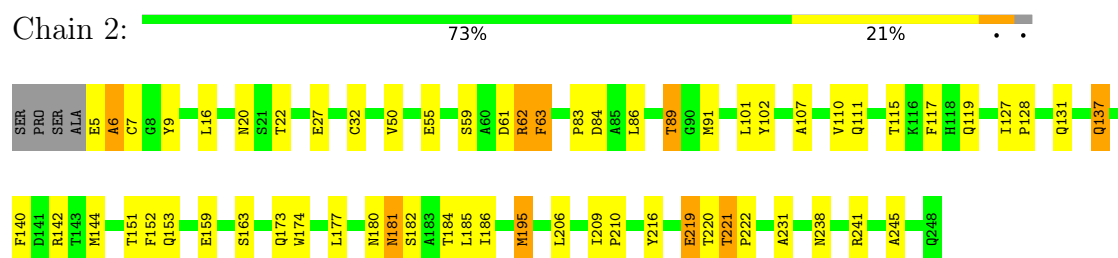
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

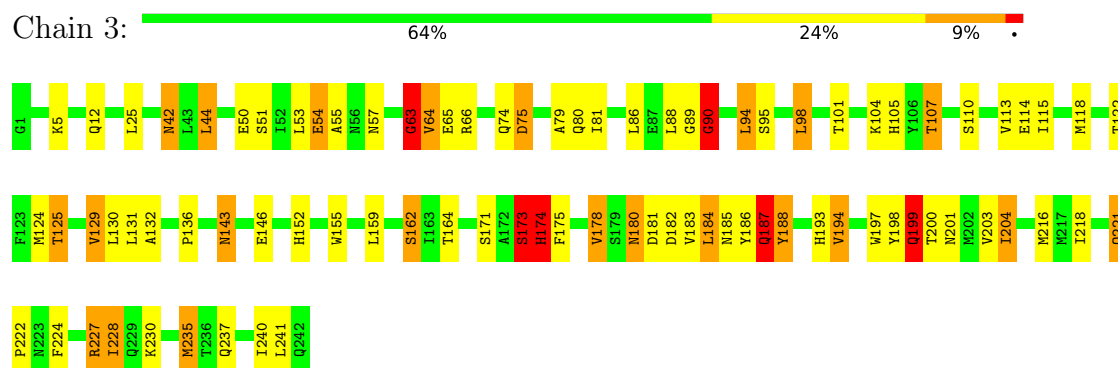
• Molecule 1: BOVINE ENTEROVIRUS COAT PROTEINS VP1 TO VP4



• Molecule 2: BOVINE ENTEROVIRUS COAT PROTEINS VP1 TO VP4



• Molecule 3: BOVINE ENTEROVIRUS COAT PROTEINS VP1 TO VP4



• Molecule 4: BOVINE ENTEROVIRUS COAT PROTEINS VP1 TO VP4

Chain 4: 40% 13% 6% 41%

GLY	ALA	GLN	LEU	SER	ARG	ASN	THR	ALA	ALA	GLY	SER	HIS	THR	THR	GLN	THR	TYR	ALA	THR	GLY	GLY	S23	T24	I25	K26	Y27	N28	N29	I30	A37	K43	Q44	D45	F46	T47	Q48	D59	V60	I61	K62	GLU	THR	ALA	VAL	PRO	LEU	LYS
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	388.20Å 392.60Å 360.70Å 90.00° 112.70° 90.00°	Depositor
Resolution (Å)	25.00 – 3.00	Depositor
% Data completeness (in resolution range)	42.5 (25.00-3.00)	Depositor
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.225 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6315	wwPDB-VP
Average B, all atoms (Å ²)	20.0	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: SO4, 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	1	0.63	0/2158	1.12	14/2939 (0.5%)
2	2	0.62	2/1944 (0.1%)	1.10	14/2664 (0.5%)
3	3	0.62	1/1919 (0.1%)	1.18	22/2618 (0.8%)
4	4	0.76	0/305	1.09	3/416 (0.7%)
All	All	0.63	3/6326 (0.0%)	1.13	53/8637 (0.6%)

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
2	2	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	195	MET	SD-CE	-5.76	1.65	1.79
2	2	61	ASP	CA-CB	5.54	1.59	1.52
3	3	124	MET	SD-CE	-5.49	1.65	1.79

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	173	SER	N-CA-C	14.05	128.54	111.40
1	1	103	VAL	N-CA-C	11.00	121.83	110.72
2	2	245	ALA	N-CA-C	8.57	123.86	113.23
2	2	55	GLU	CA-C-N	8.39	129.20	119.47
2	2	55	GLU	C-N-CA	8.39	129.20	119.47
1	1	185	MET	N-CA-C	8.39	123.51	113.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	25	LEU	CA-C-N	7.89	127.96	119.28
3	3	25	LEU	C-N-CA	7.89	127.96	119.28
1	1	187	SER	N-CA-C	-7.64	103.41	112.89
2	2	7	CYS	N-CA-C	7.31	121.61	112.03
3	3	65	GLU	N-CA-C	-7.23	103.93	112.89
3	3	54	GLU	N-CA-C	-7.12	100.78	110.68
3	3	162	SER	N-CA-C	6.96	120.37	110.14
1	1	260	TYR	N-CA-C	6.86	121.73	112.88
2	2	177	LEU	N-CA-C	6.76	120.40	111.75
3	3	55	ALA	N-CA-C	6.60	119.47	111.82
2	2	180	ASN	N-CA-C	6.60	119.74	109.52
3	3	188	TYR	N-CA-C	-6.46	104.31	111.36
2	2	50	VAL	N-CA-C	6.46	121.08	112.04
3	3	187	GLN	N-CA-C	-6.37	105.61	113.19
2	2	181	ASN	N-CA-CB	-6.34	100.55	110.44
1	1	99	PHE	N-CA-C	-6.24	102.95	111.56
3	3	75	ASP	N-CA-C	-6.23	104.15	112.94
2	2	144	MET	CA-C-N	6.22	127.03	120.12
2	2	144	MET	C-N-CA	6.22	127.03	120.12
3	3	199	GLN	N-CA-C	-6.20	103.83	112.45
1	1	250	ALA	CA-C-N	-6.12	113.98	120.03
1	1	250	ALA	C-N-CA	-6.12	113.98	120.03
2	2	137	GLN	CA-C-N	6.05	126.02	119.78
2	2	137	GLN	C-N-CA	6.05	126.02	119.78
1	1	231	GLN	N-CA-C	6.03	123.63	110.80
4	4	60	VAL	N-CA-C	6.02	117.05	108.93
3	3	180	ASN	N-CA-C	-5.89	104.75	112.41
3	3	136	PRO	N-CA-C	5.74	119.54	111.33
3	3	95	SER	N-CA-C	5.70	119.49	112.54
3	3	152	HIS	N-CA-C	5.68	117.43	108.96
1	1	243	THR	N-CA-C	5.62	119.08	110.20
1	1	98	ASP	CB-CA-C	-5.55	98.30	110.67
3	3	63	GLY	N-CA-C	5.40	125.98	113.18
1	1	166	ASN	CA-C-N	-5.34	114.48	120.14
1	1	166	ASN	C-N-CA	-5.34	114.48	120.14
1	1	156	GLN	N-CA-C	-5.29	105.68	111.82
4	4	30	ILE	N-CA-C	5.29	120.34	109.34
3	3	88	LEU	N-CA-C	-5.24	106.57	113.17
1	1	104	GLN	N-CA-C	5.21	116.64	111.07
2	2	63	PHE	N-CA-C	5.17	117.98	109.76
3	3	79	ALA	N-CA-C	5.06	117.63	110.50
2	2	153	GLN	N-CA-C	-5.03	107.27	113.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	221	GLN	CA-C-N	5.03	126.13	119.84
3	3	221	GLN	C-N-CA	5.03	126.13	119.84
3	3	90	GLY	N-CA-C	5.01	125.06	113.18
3	3	204	ILE	N-CA-C	5.01	113.40	107.84
4	4	27	TYR	N-CA-C	5.00	117.84	110.59

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	2	216	TYR	Sidechain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	2099	0	1997	61	0
2	2	1890	0	1816	40	0
3	3	1871	0	1833	73	0
4	4	299	0	261	5	0
5	1	5	0	0	0	0
5	2	5	0	0	0	0
6	1	16	0	27	3	0
7	1	49	0	0	3	0
7	2	51	0	0	6	0
7	3	30	0	0	3	0
All	All	6315	0	5934	155	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 13.

All (155) 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)
3:3:63:GLY:O	3:3:64:VAL:HG12	1.32	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:220:THR:O	2:2:221:THR:HG22	1.44	1.18
3:3:173:SER:O	3:3:174:HIS:HB2	1.52	1.07
2:2:182:SER:OG	7:2:956:HOH:O	1.81	0.97
1:1:52:GLU:HG3	1:1:57:THR:HG21	1.48	0.92
1:1:98:ASP:HB2	1:1:259:ARG:HH21	1.35	0.91
1:1:274:ASN:ND2	3:3:66:ARG:HH21	1.69	0.91
3:3:63:GLY:O	3:3:64:VAL:CG1	2.20	0.89
2:2:220:THR:O	2:2:221:THR:CG2	2.20	0.88
3:3:235:MET:HA	3:3:235:MET:HE2	1.56	0.85
2:2:27:GLU:HB2	2:2:181:ASN:HB2	1.58	0.84
3:3:74:GLN:H	3:3:201:ASN:HD21	1.26	0.83
3:3:107:THR:HG23	3:3:228:ILE:O	1.79	0.83
3:3:181:ASP:OD1	3:3:183:VAL:HG12	1.79	0.82
2:2:59:SER:HB2	2:2:91:MET:HG2	1.62	0.81
1:1:253:GLN:HE22	3:3:101:THR:HG21	1.47	0.79
1:1:274:ASN:HD21	3:3:66:ARG:HH21	1.31	0.77
3:3:125:THR:HB	3:3:204:ILE:HG22	1.66	0.76
1:1:158:SER:HB3	1:1:160:GLN:OE1	1.85	0.75
3:3:54:GLU:OE2	3:3:66:ARG:NH1	2.20	0.73
1:1:274:ASN:ND2	3:3:66:ARG:NH2	2.37	0.72
1:1:42:GLU:CD	3:3:118:MET:HE2	2.15	0.70
1:1:104:GLN:HG2	7:3:253:HOH:O	1.91	0.70
3:3:5:LYS:HE3	7:3:259:HOH:O	1.93	0.68
7:2:996:HOH:O	3:3:125:THR:HG21	1.94	0.68
3:3:5:LYS:O	3:3:5:LYS:HE2	1.94	0.67
3:3:122:THR:OG1	3:3:125:THR:HG22	1.94	0.67
1:1:98:ASP:HB2	1:1:259:ARG:NH2	2.07	0.66
1:1:41:ALA:HB3	3:3:118:MET:HE3	1.78	0.65
1:1:185:MET:HE2	6:1:900:MYR:H111	1.78	0.65
1:1:26:SER:HB2	1:1:57:THR:H	1.61	0.65
1:1:137:GLN:O	1:1:173:THR:HG21	1.98	0.64
3:3:42:ASN:HD22	3:3:44:LEU:H	1.45	0.64
1:1:33:ASP:OD1	1:1:34:SER:N	2.31	0.64
3:3:199:GLN:HE21	3:3:199:GLN:HA	1.60	0.63
3:3:200:THR:HG22	3:3:201:ASN:N	2.12	0.63
3:3:235:MET:HA	3:3:235:MET:CE	2.27	0.63
2:2:89:THR:HG22	7:2:962:HOH:O	1.99	0.62
1:1:195:TYR:H	2:2:131:GLN:HE21	1.47	0.62
2:2:219:GLU:H	2:2:219:GLU:CD	2.06	0.62
2:2:152:PHE:HD2	2:2:159:GLU:HG2	1.64	0.61
1:1:257:LYS:HE2	1:1:265:SER:HB2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:145:TYR:HB2	6:1:900:MYR:H141	1.84	0.59
2:2:152:PHE:CD2	2:2:159:GLU:HG2	2.38	0.59
1:1:204:THR:HG23	1:1:204:THR:O	2.02	0.58
1:1:275:ARG:HD3	3:3:57:ASN:OD1	2.04	0.58
2:2:119:GLN:HB3	3:3:122:THR:HG22	1.86	0.58
2:2:220:THR:C	2:2:221:THR:HG22	2.25	0.57
1:1:145:TYR:CD1	6:1:900:MYR:H132	2.39	0.57
3:3:115:ILE:HG21	3:3:216:MET:HE3	1.87	0.57
3:3:89:GLY:O	3:3:90:GLY:O	2.23	0.57
3:3:104:LYS:O	3:3:230:LYS:HE2	2.05	0.56
3:3:122:THR:OG1	3:3:125:THR:CG2	2.53	0.56
1:1:137:GLN:O	1:1:173:THR:CG2	2.53	0.56
2:2:89:THR:CG2	7:2:962:HOH:O	2.51	0.56
3:3:186:TYR:C	3:3:188:TYR:H	2.14	0.56
1:1:86:LEU:O	1:1:231:GLN:O	2.23	0.56
2:2:5:GLU:O	2:2:6:ALA:HB2	2.06	0.55
4:4:28:ASN:HD22	4:4:28:ASN:N	2.04	0.55
2:2:119:GLN:HE21	3:3:122:THR:HG23	1.72	0.54
3:3:173:SER:O	3:3:174:HIS:CB	2.36	0.54
1:1:61:VAL:O	1:1:63:THR:HG22	2.08	0.54
1:1:204:THR:O	1:1:204:THR:CG2	2.55	0.54
1:1:96:ARG:HD3	1:1:260:TYR:OH	2.07	0.54
1:1:195:TYR:H	2:2:131:GLN:NE2	2.05	0.54
3:3:185:ASN:HA	3:3:187:GLN:HE21	1.72	0.54
1:1:96:ARG:NH1	7:1:965:HOH:O	2.34	0.53
4:4:28:ASN:N	4:4:28:ASN:ND2	2.56	0.53
2:2:20:ASN:OD1	2:2:62:ARG:NH1	2.37	0.52
1:1:270:ARG:HB2	3:3:66:ARG:NH1	2.25	0.52
1:1:257:LYS:CE	1:1:265:SER:HB2	2.40	0.52
1:1:16:ALA:HA	4:4:45:ASP:HB2	1.92	0.51
2:2:27:GLU:HB2	2:2:181:ASN:CB	2.35	0.51
1:1:16:ALA:HB2	4:4:43:LYS:O	2.11	0.51
3:3:129:VAL:HG22	3:3:155:TRP:HB3	1.93	0.51
3:3:182:ASP:HA	3:3:187:GLN:HE22	1.75	0.51
3:3:53:LEU:HD12	3:3:216:MET:HE2	1.94	0.50
1:1:24:SER:O	1:1:57:THR:HG23	2.11	0.50
3:3:235:MET:HE2	3:3:235:MET:CA	2.36	0.50
3:3:94:LEU:HD21	3:3:218:ILE:HD13	1.94	0.49
1:1:98:ASP:HB3	1:1:100:ARG:H	1.78	0.49
3:3:235:MET:CE	3:3:235:MET:CA	2.89	0.49
1:1:279:THR:HG23	1:1:279:THR:O	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:195:MET:HE1	2:2:238:ASN:OD1	2.13	0.49
1:1:206:PRO:O	2:2:137:GLN:HG2	2.13	0.48
3:3:94:LEU:HD21	3:3:218:ILE:CD1	2.44	0.48
2:2:63:PHE:CD1	2:2:231:ALA:HB2	2.48	0.48
2:2:163:SER:HB2	7:2:1000:HOH:O	2.14	0.48
3:3:80:GLN:HB2	3:3:197:TRP:CZ3	2.48	0.48
3:3:107:THR:HG22	3:3:230:LYS:HB3	1.95	0.48
2:2:110:VAL:O	2:2:182:SER:HB2	2.13	0.47
3:3:175:PHE:CZ	3:3:227:ARG:HD3	2.49	0.47
1:1:270:ARG:HH11	1:1:270:ARG:HG3	1.80	0.47
2:2:32:CYS:HB3	2:2:185:LEU:HD13	1.97	0.47
3:3:130:LEU:C	3:3:130:LEU:HD23	2.40	0.47
3:3:143:ASN:ND2	3:3:146:GLU:H	2.13	0.47
1:1:96:ARG:HG2	7:1:965:HOH:O	2.15	0.46
3:3:181:ASP:OD1	3:3:183:VAL:CG1	2.58	0.46
3:3:181:ASP:OD2	3:3:184:LEU:HB2	2.15	0.46
3:3:113:VAL:HG11	3:3:218:ILE:HD11	1.98	0.46
2:2:173:GLN:NE2	2:2:184:THR:H	2.14	0.46
3:3:107:THR:C	3:3:178:VAL:HG13	2.41	0.45
1:1:211:ILE:HD11	1:1:260:TYR:HB3	1.97	0.45
3:3:81:ILE:HG12	3:3:198:TYR:CE2	2.52	0.45
3:3:105:HIS:HE1	7:3:258:HOH:O	1.97	0.45
3:3:143:ASN:HD22	3:3:146:GLU:H	1.65	0.45
1:1:205:ASP:HA	1:1:206:PRO:HD3	1.84	0.44
1:1:241:LYS:HE3	4:4:37:ALA:O	2.16	0.44
3:3:114:GLU:HG2	3:3:164:THR:HG23	2.00	0.44
1:1:198:TYR:CE1	1:1:209:TYR:HB2	2.52	0.44
2:2:195:MET:HE1	2:2:238:ASN:CG	2.42	0.44
1:1:131:GLN:H	1:1:131:GLN:CD	2.26	0.44
1:1:85:LEU:O	1:1:93:THR:CG2	2.66	0.44
1:1:46:THR:HG23	3:3:50:GLU:HG3	2.00	0.43
3:3:42:ASN:ND2	3:3:44:LEU:HB2	2.33	0.43
3:3:186:TYR:C	3:3:188:TYR:N	2.71	0.43
3:3:173:SER:HB3	3:3:175:PHE:O	2.18	0.43
1:1:42:GLU:HA	2:2:174:TRP:HB2	2.01	0.43
3:3:132:ALA:O	3:3:194:VAL:HA	2.18	0.43
1:1:96:ARG:HD3	7:1:965:HOH:O	2.18	0.43
1:1:103:VAL:H	3:3:237:GLN:NE2	2.17	0.43
1:1:275:ARG:HG3	1:1:277:SER:O	2.19	0.43
3:3:51:SER:HB3	3:3:98:LEU:HD22	2.01	0.43
3:3:159:LEU:HD12	3:3:159:LEU:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:127:ILE:HA	2:2:128:PRO:HD3	1.84	0.42
2:2:219:GLU:CD	2:2:219:GLU:N	2.76	0.42
2:2:107:ALA:HB3	2:2:231:ALA:HB3	2.01	0.42
3:3:131:LEU:HD12	3:3:131:LEU:N	2.34	0.42
1:1:101:GLU:HG2	3:3:240:ILE:HG23	2.02	0.42
1:1:253:GLN:NE2	3:3:101:THR:HG21	2.25	0.42
3:3:110:SER:O	3:3:224:PHE:HA	2.20	0.42
3:3:199:GLN:HA	3:3:199:GLN:NE2	2.29	0.42
2:2:5:GLU:O	2:2:6:ALA:CB	2.68	0.42
1:1:274:ASN:HD21	3:3:66:ARG:NH2	2.06	0.42
2:2:221:THR:HA	2:2:222:PRO:HD3	1.88	0.41
3:3:75:ASP:OD1	3:3:75:ASP:N	2.52	0.41
1:1:85:LEU:O	1:1:93:THR:HG21	2.19	0.41
2:2:101:LEU:HA	2:2:101:LEU:HD23	1.76	0.41
2:2:163:SER:CB	7:2:1000:HOH:O	2.68	0.41
1:1:247:ILE:HA	1:1:248:PRO:HD2	1.93	0.41
2:2:142:ARG:NH2	2:2:151:THR:O	2.53	0.41
3:3:221:GLN:HB3	3:3:222:PRO:CD	2.49	0.41
1:1:103:VAL:H	3:3:237:GLN:HE22	1.68	0.41
1:1:33:ASP:CG	1:1:34:SER:N	2.78	0.41
1:1:131:GLN:H	1:1:131:GLN:NE2	2.19	0.41
1:1:204:THR:HG23	2:2:140:PHE:HB2	2.03	0.41
2:2:83:PRO:O	2:2:84:ASP:C	2.64	0.40
2:2:241:ARG:HG3	2:2:241:ARG:HH11	1.86	0.40
3:3:42:ASN:HD22	3:3:44:LEU:HB2	1.86	0.40
3:3:98:LEU:HD12	3:3:98:LEU:HA	1.87	0.40
1:1:226:GLU:OE1	1:1:226:GLU:HA	2.21	0.40
2:2:115:THR:C	2:2:117:PHE:H	2.30	0.40
1:1:131:GLN:NE2	1:1:131:GLN:N	2.69	0.40
2:2:209:ILE:HA	2:2:210:PRO:HD3	1.93	0.40
1:1:22:GLY:CA	1:1:62:PRO:HG3	2.51	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	1	266/281 (95%)	252 (95%)	11 (4%)	3 (1%)	11	43
2	2	242/248 (98%)	220 (91%)	19 (8%)	3 (1%)	10	40
3	3	240/242 (99%)	225 (94%)	10 (4%)	5 (2%)	5	27
4	4	38/68 (56%)	32 (84%)	2 (5%)	4 (10%)	0	2
All	All	786/839 (94%)	729 (93%)	42 (5%)	15 (2%)	6	30

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	2	6	ALA
3	3	63	GLY
3	3	90	GLY
4	4	24	THR
4	4	30	ILE
1	1	158	SER
3	3	174	HIS
4	4	29	ASN
2	2	221	THR
1	1	33	ASP
1	1	232	VAL
2	2	9	TYR
3	3	228	ILE
3	3	64	VAL
4	4	25	ILE

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	1	228/239 (95%)	199 (87%)	29 (13%)	4	20
2	2	198/205 (97%)	188 (95%)	10 (5%)	21	55
3	3	206/206 (100%)	181 (88%)	25 (12%)	5	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	4	30/55 (54%)	24 (80%)	6 (20%)	1	7
All	All	662/705 (94%)	592 (89%)	70 (11%)	6	27

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	20	VAL
1	1	27	THR
1	1	32	THR
1	1	48	THR
1	1	50	ARG
1	1	60	ILE
1	1	63	THR
1	1	69	THR
1	1	80	LEU
1	1	85	LEU
1	1	90	THR
1	1	92	ILE
1	1	93	THR
1	1	105	LEU
1	1	128	SER
1	1	131	GLN
1	1	135	THR
1	1	139	THR
1	1	154	SER
1	1	163	SER
1	1	173	THR
1	1	194	VAL
1	1	203	ASP
1	1	204	THR
1	1	220	MET
1	1	226	GLU
1	1	231	GLN
1	1	243	THR
1	1	279	THR
2	2	16	LEU
2	2	22	THR
2	2	62	ARG
2	2	86	LEU
2	2	89	THR
2	2	102	TYR
2	2	111	GLN

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Mol	Chain	Res	Type
2	2	186	ILE
2	2	206	LEU
2	2	219	GLU
3	3	12	GLN
3	3	42	ASN
3	3	44	LEU
3	3	86	LEU
3	3	94	LEU
3	3	98	LEU
3	3	107	THR
3	3	125	THR
3	3	129	VAL
3	3	143	ASN
3	3	162	SER
3	3	171	SER
3	3	173	SER
3	3	174	HIS
3	3	178	VAL
3	3	180	ASN
3	3	184	LEU
3	3	187	GLN
3	3	193	HIS
3	3	194	VAL
3	3	199	GLN
3	3	203	VAL
3	3	227	ARG
3	3	235	MET
3	3	241	LEU
4	4	25	ILE
4	4	28	ASN
4	4	47	THR
4	4	48	GLN
4	4	59	ASP
4	4	60	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	104	GLN
1	1	131	GLN
1	1	162	GLN
1	1	166	ASN

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Mol	Chain	Res	Type
1	1	189	ASN
1	1	230	HIS
1	1	231	GLN
1	1	253	GLN
1	1	274	ASN
2	2	15	GLN
2	2	87	ASN
2	2	88	ASN
2	2	111	GLN
2	2	119	GLN
2	2	130	HIS
2	2	131	GLN
2	2	153	GLN
2	2	173	GLN
2	2	181	ASN
2	2	248	GLN
3	3	12	GLN
3	3	42	ASN
3	3	105	HIS
3	3	143	ASN
3	3	187	GLN
3	3	199	GLN
3	3	201	ASN
3	3	237	GLN
4	4	28	ASN
4	4	42	ASN
4	4	48	GLN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

3 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	SO4	2	950	-	4,4,4	0.35	0	6,6,6	0.19	0
6	MYR	1	900	-	15,15,15	0.83	1 (6%)	15,15,15	0.80	0
5	SO4	1	951	-	4,4,4	0.51	0	6,6,6	0.44	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
6	MYR	1	900	-	-	5/13/13/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	1	900	MYR	O2-C1	-2.02	1.24	1.30

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	1	900	MYR	C1-C2-C3-C4
6	1	900	MYR	C10-C11-C12-C13
6	1	900	MYR	O1-C1-C2-C3
6	1	900	MYR	O2-C1-C2-C3
6	1	900	MYR	C6-C7-C8-C9

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	1	900	MYR	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 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.