



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:49 PM UTC

PDB ID : 1WUO / pdb_00001wuo
Title : Crystal structure of metallo-beta-lactamase IMP-1 mutant (D81A)
Authors : Yamaguchi, Y.; Yamagata, Y.; Goto, M.
Deposited on : 2004-12-08
Resolution : 2.01 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

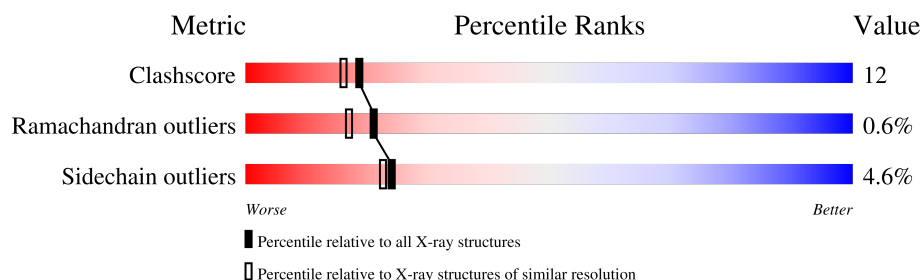
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.01 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	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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	A	228	 68% 24% 5% 3%
1	B	228	 67% 28% 3% 2%
1	C	228	 68% 24% 5% 3%
1	D	228	 71% 21% 5% 3%

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
1	CSD	D	158	-	-	X	-
3	ACY	B	402	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7223 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 Beta-lactamase IMP-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	219	Total	C	N	O	S	0	0	0
			1711	1109	282	319	1			
1	B	219	Total	C	N	O	S	0	0	0
			1711	1109	282	319	1			
1	C	219	Total	C	N	O	S	0	0	0
			1711	1109	282	319	1			
1	D	219	Total	C	N	O	S	0	0	0
			1711	1109	282	319	1			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	81	ALA	ASP	engineered mutation	UNP P52699
B	81	ALA	ASP	engineered mutation	UNP P52699
C	81	ALA	ASP	engineered mutation	UNP P52699
D	81	ALA	ASP	engineered mutation	UNP P52699

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		

- Molecule 3 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is water.

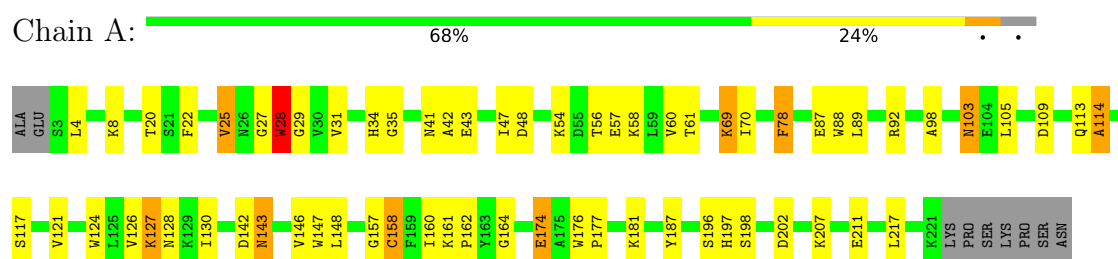
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	73	Total	O	0	0
			73	73		
4	B	88	Total	O	0	0
			88	88		
4	C	108	Total	O	0	0
			108	108		
4	D	90	Total	O	0	0
			90	90		

3 Residue-property plots

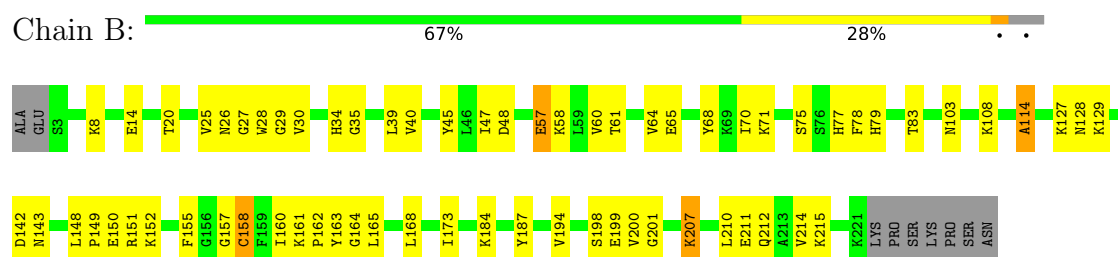
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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

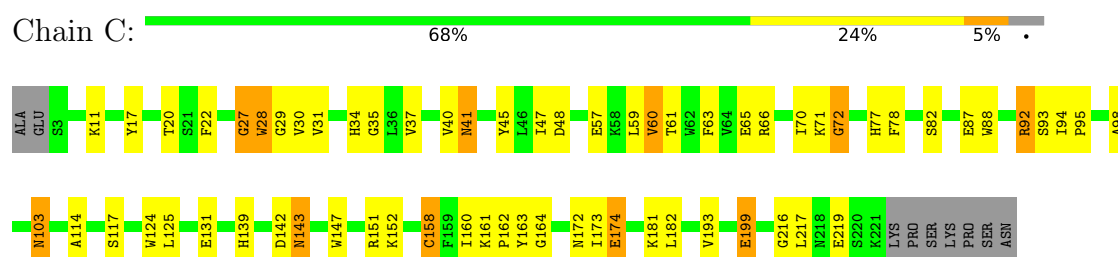
• Molecule 1: Beta-lactamase IMP-1



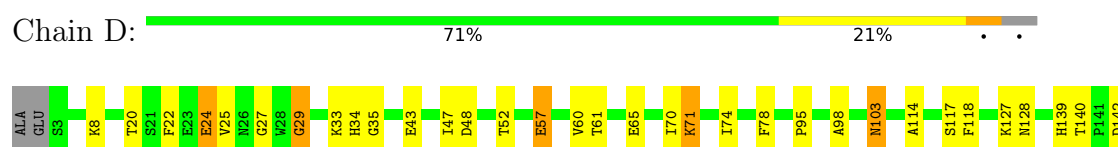
• Molecule 1: Beta-lactamase IMP-1

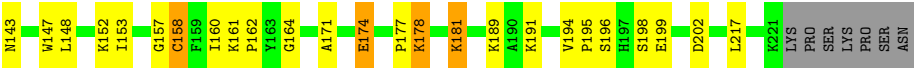


• Molecule 1: Beta-lactamase IMP-1



• Molecule 1: Beta-lactamase IMP-1





4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	49.73Å 73.02Å 82.45Å 85.37° 75.53° 73.62°	Depositor
Resolution (Å)	46.35 – 2.01	Depositor
% Data completeness (in resolution range)	94.9 (46.35-2.01)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.212 , 0.218	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7223	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, ACY, CSD

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	1.31	6/1747 (0.3%)	1.26	9/2371 (0.4%)
1	B	1.15	0/1747	1.23	8/2371 (0.3%)
1	C	1.28	3/1747 (0.2%)	1.25	11/2371 (0.5%)
1	D	1.26	3/1747 (0.2%)	1.27	10/2371 (0.4%)
All	All	1.25	12/6988 (0.2%)	1.25	38/9484 (0.4%)

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	114	ALA	CA-CB	7.29	1.65	1.53
1	D	140	THR	CA-CB	6.83	1.62	1.53
1	A	87	GLU	C-O	-6.21	1.17	1.24
1	C	60	VAL	CA-CB	6.01	1.61	1.54
1	D	33	LYS	CB-CG	5.94	1.70	1.52
1	A	89	LEU	CA-C	5.94	1.60	1.52
1	C	87	GLU	C-O	-5.36	1.18	1.24
1	A	146	VAL	C-O	5.31	1.29	1.24
1	A	56	THR	N-CA	5.21	1.52	1.46
1	A	121	VAL	C-O	-5.09	1.18	1.24
1	C	94	ILE	CA-C	5.01	1.57	1.53
1	D	153	ILE	C-O	-5.01	1.18	1.24

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	78	PHE	N-CA-C	8.98	123.50	112.54
1	A	42	ALA	N-CA-C	-8.26	101.64	113.21
1	D	78	PHE	N-CA-C	7.53	122.22	112.89
1	D	148	LEU	CA-C-N	7.47	129.18	119.84
1	D	148	LEU	C-N-CA	7.47	129.18	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	148	LEU	CA-C-N	6.92	128.49	119.84
1	B	148	LEU	C-N-CA	6.92	128.49	119.84
1	A	142	ASP	N-CA-C	6.71	121.62	113.17
1	C	125	LEU	N-CA-C	-6.62	103.55	111.69
1	A	148	LEU	CA-C-N	6.38	126.59	119.32
1	A	148	LEU	C-N-CA	6.38	126.59	119.32
1	C	139	HIS	N-CA-C	-6.30	104.42	111.28
1	A	78	PHE	N-CA-C	6.26	119.08	111.82
1	D	139	HIS	N-CA-C	-6.25	104.47	111.28
1	A	197	HIS	N-CA-C	6.01	121.53	113.72
1	D	142	ASP	N-CA-C	5.99	120.72	113.17
1	C	40	VAL	N-CA-C	5.97	116.95	111.81
1	D	194	VAL	N-CA-C	5.94	113.43	107.55
1	B	35	GLY	N-CA-C	-5.83	102.43	111.12
1	B	142	ASP	N-CA-C	5.81	120.49	113.17
1	C	35	GLY	N-CA-C	-5.76	102.54	111.12
1	C	41	ASN	N-CA-C	-5.64	98.79	110.80
1	B	114	ALA	N-CA-C	-5.60	102.60	110.50
1	A	142	ASP	CB-CA-C	-5.58	100.78	110.09
1	C	72	GLY	N-CA-C	5.54	118.46	111.09
1	C	193	VAL	N-CA-C	-5.49	100.22	108.12
1	C	78	PHE	N-CA-C	5.47	119.22	112.54
1	B	187	TYR	N-CA-C	5.40	119.39	112.26
1	D	29	GLY	N-CA-C	-5.39	106.72	111.67
1	B	150	GLU	N-CA-C	5.30	117.05	111.28
1	C	143	ASN	N-CA-C	5.27	117.67	110.24
1	D	35	GLY	N-CA-C	-5.25	100.81	110.83
1	D	52	THR	N-CA-C	5.24	118.13	109.85
1	C	142	ASP	N-CA-C	5.20	119.63	113.28
1	D	171	ALA	N-CA-C	5.09	118.02	110.48
1	C	63	PHE	N-CA-C	5.07	116.89	111.36
1	A	35	GLY	N-CA-C	-5.06	101.19	113.18
1	A	143	ASN	N-CA-C	5.02	117.32	110.24

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	1711	0	1725	41	1
1	B	1711	0	1724	49	0
1	C	1711	0	1724	43	0
1	D	1711	0	1725	35	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	4	0	3	0	0
3	B	4	0	3	3	0
3	C	4	0	3	0	0
3	D	4	0	3	0	0
4	A	73	0	0	1	0
4	B	88	0	0	5	0
4	C	108	0	0	1	1
4	D	90	0	0	2	0
All	All	7223	0	6910	164	1

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 12.

All (164) 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:C:158:CSD:SG	1:C:158:CSD:OD1	1.91	1.28
1:A:158:CSD:OD1	1:A:158:CSD:SG	1.93	1.26
1:D:158:CSD:OD1	1:D:158:CSD:SG	1.94	1.25
1:B:158:CSD:SG	1:B:158:CSD:OD1	1.96	1.23
1:A:103:ASN:HD21	1:A:114:ALA:H	1.22	0.87
1:C:88:TRP:CZ2	1:C:92:ARG:HD2	2.11	0.85
1:B:103:ASN:HD21	1:B:114:ALA:H	1.23	0.83
1:B:168:LEU:HD13	1:B:173:ILE:HD11	1.61	0.82
1:C:103:ASN:HD21	1:C:114:ALA:H	1.31	0.78
1:D:103:ASN:HD21	1:D:114:ALA:H	1.32	0.75
1:D:158:CSD:HB2	1:D:161:LYS:NZ	2.02	0.74
1:A:92:ARG:HH11	1:A:92:ARG:HB3	1.53	0.73
1:B:160:ILE:HG22	1:B:162:PRO:HD3	1.71	0.72
1:D:181:LYS:HD3	1:D:181:LYS:C	2.15	0.71
1:C:181:LYS:HD3	1:C:181:LYS:C	2.18	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:ILE:HG22	1:A:162:PRO:HD3	1.75	0.69
1:C:181:LYS:HD3	1:C:182:LEU:N	2.08	0.69
1:A:28:TRP:HB3	1:A:31:VAL:HG22	1.76	0.67
1:D:158:CSD:HB2	1:D:161:LYS:HZ2	1.62	0.65
1:C:98:ALA:O	1:C:117:SER:HA	1.96	0.65
1:B:57:GLU:HG3	1:B:58:LYS:N	2.12	0.64
1:B:14:GLU:HB3	1:B:151:ARG:HH11	1.63	0.64
1:B:158:CSD:SG	3:B:402:ACY:OXT	2.57	0.63
1:B:151:ARG:HE	1:B:151:ARG:HA	1.64	0.63
1:A:92:ARG:HB3	1:A:92:ARG:NH1	2.14	0.62
1:B:45:TYR:OH	1:B:71:LYS:HG2	1.99	0.62
1:B:103:ASN:ND2	1:B:114:ALA:H	1.95	0.62
1:A:174:GLU:H	1:A:174:GLU:CD	2.08	0.62
1:D:160:ILE:HG22	1:D:162:PRO:HD3	1.81	0.62
1:A:103:ASN:HD21	1:A:114:ALA:N	1.96	0.62
1:D:20:THR:OG1	1:D:34:HIS:HD2	1.85	0.60
1:B:199:GLU:HG2	1:C:199:GLU:HB3	1.83	0.60
1:A:127:LYS:HG3	1:A:128:ASN:ND2	2.16	0.59
1:C:11:LYS:HB2	1:C:17:TYR:CE2	2.37	0.59
1:A:103:ASN:ND2	1:A:114:ALA:H	1.99	0.59
1:B:40:VAL:HG13	1:B:129:LYS:HD2	1.86	0.58
1:A:88:TRP:CZ2	1:A:92:ARG:HD2	2.39	0.57
1:D:161:LYS:HB3	1:D:164:GLY:O	2.04	0.57
1:D:158:CSD:CB	1:D:161:LYS:NZ	2.67	0.57
1:D:25:VAL:HG22	1:D:29:GLY:O	2.05	0.57
1:A:25:VAL:HG23	1:A:27:GLY:H	1.70	0.56
1:A:198:SER:HB3	4:A:424:HOH:O	2.06	0.56
1:B:199:GLU:OE2	1:C:34:HIS:HE1	1.88	0.56
1:B:210:LEU:O	1:B:214:VAL:HG13	2.06	0.56
1:C:31:VAL:O	1:C:31:VAL:HG23	2.06	0.56
1:D:174:GLU:HA	1:D:217:LEU:HD13	1.88	0.55
1:B:207:LYS:O	1:B:211:GLU:HG3	2.07	0.55
1:B:25:VAL:HG22	1:B:29:GLY:O	2.06	0.55
1:B:27:GLY:C	1:B:29:GLY:H	2.15	0.54
1:B:155:PHE:CZ	1:B:157:GLY:HA2	2.43	0.53
1:B:60:VAL:HG13	1:B:70:ILE:HG13	1.90	0.53
1:C:199:GLU:H	1:C:199:GLU:CD	2.17	0.53
1:D:147:TRP:CH2	1:D:152:LYS:HA	2.43	0.53
1:B:127:LYS:HG3	1:B:128:ASN:ND2	2.24	0.53
1:A:78:PHE:CD1	1:A:105:LEU:HD13	2.44	0.53
1:A:98:ALA:O	1:A:117:SER:HA	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:25:VAL:HG23	1:D:27:GLY:H	1.74	0.52
1:D:178:LYS:O	1:D:178:LYS:HE3	2.10	0.52
1:C:161:LYS:HB3	1:C:164:GLY:O	2.10	0.51
1:B:214:VAL:HG23	1:B:215:LYS:N	2.24	0.51
1:C:88:TRP:CH2	1:C:92:ARG:HD2	2.46	0.51
1:B:199:GLU:OE2	1:C:34:HIS:CE1	2.63	0.51
1:A:27:GLY:C	1:A:29:GLY:H	2.18	0.51
1:A:174:GLU:HA	1:A:217:LEU:HD13	1.91	0.51
1:D:98:ALA:O	1:D:117:SER:HA	2.10	0.51
1:D:157:GLY:HA2	1:D:196:SER:OG	2.11	0.51
1:C:124:TRP:CZ3	1:C:131:GLU:HB2	2.45	0.51
1:B:149:PRO:O	1:B:152:LYS:HD2	2.12	0.50
1:C:160:ILE:HG22	1:C:162:PRO:HD3	1.93	0.50
1:B:200:VAL:HG12	1:B:201:GLY:N	2.28	0.49
1:D:127:LYS:HG3	1:D:128:ASN:ND2	2.27	0.49
1:B:161:LYS:HE2	1:B:165:LEU:O	2.12	0.49
1:B:198:SER:HB3	4:B:453:HOH:O	2.12	0.49
1:B:20:THR:OG1	1:B:34:HIS:HD2	1.96	0.49
1:D:24:GLU:H	1:D:24:GLU:CD	2.19	0.49
1:C:20:THR:OG1	1:C:34:HIS:HD2	1.95	0.49
1:C:27:GLY:C	1:C:29:GLY:H	2.20	0.49
1:C:173:ILE:HD11	1:C:216:GLY:C	2.38	0.49
1:C:60:VAL:HG21	1:C:88:TRP:HZ3	1.78	0.49
1:A:176:TRP:HB3	1:A:177:PRO:HD3	1.95	0.48
1:A:20:THR:OG1	1:A:34:HIS:HD2	1.96	0.48
1:C:61:THR:O	1:C:65:GLU:HG3	2.12	0.48
1:B:60:VAL:O	1:B:64:VAL:HG23	2.14	0.48
1:C:28:TRP:CD1	1:C:31:VAL:HG12	2.49	0.48
1:C:47:ILE:O	1:C:48:ASP:HB2	2.14	0.48
1:C:103:ASN:ND2	1:C:114:ALA:H	2.06	0.48
1:B:30:VAL:HB	1:C:163:TYR:HB3	1.95	0.47
1:B:184:LYS:HE3	1:B:207:LYS:NZ	2.29	0.47
1:C:174:GLU:H	1:C:174:GLU:CD	2.21	0.47
1:A:47:ILE:O	1:A:48:ASP:HB2	2.14	0.47
1:C:72:GLY:HA2	1:C:95:PRO:O	2.15	0.47
1:C:92:ARG:O	1:C:93:SER:HB2	2.12	0.47
1:D:152:LYS:HB2	1:D:191:LYS:HD3	1.96	0.47
1:C:60:VAL:HG13	1:C:70:ILE:HG13	1.96	0.47
1:D:57:GLU:O	1:D:61:THR:HG23	2.14	0.47
1:D:199:GLU:HG2	4:D:474:HOH:O	2.13	0.46
1:A:4:LEU:HD12	1:A:4:LEU:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:195:PRO:HG2	1:D:198:SER:O	2.15	0.46
1:D:57:GLU:CD	1:D:57:GLU:C	2.83	0.46
1:A:60:VAL:HG13	1:A:70:ILE:HG13	1.96	0.46
1:A:43:GLU:HG2	1:A:69:LYS:NZ	2.30	0.46
1:A:207:LYS:O	1:A:211:GLU:HG3	2.15	0.46
1:C:66:ARG:HG3	1:C:66:ARG:HH11	1.80	0.46
1:D:22:PHE:CD1	1:D:22:PHE:N	2.83	0.46
1:B:26:ASN:HA	4:B:486:HOH:O	2.15	0.46
1:D:178:LYS:HA	1:D:178:LYS:HD2	1.81	0.46
1:B:47:ILE:O	1:B:48:ASP:HB2	2.16	0.45
1:C:22:PHE:CD1	1:C:22:PHE:N	2.85	0.45
1:B:61:THR:O	1:B:65:GLU:HG3	2.15	0.45
1:C:77:HIS:CE1	1:C:82:SER:OG	2.69	0.45
1:D:47:ILE:O	1:D:48:ASP:HB2	2.16	0.45
1:A:28:TRP:HB3	1:A:31:VAL:CG2	2.44	0.45
1:B:194:VAL:HG13	4:B:456:HOH:O	2.16	0.45
1:C:57:GLU:HA	1:C:88:TRP:CH2	2.51	0.45
1:C:172:ASN:OD1	1:C:174:GLU:HG2	2.17	0.45
1:A:147:TRP:CG	1:A:187:TYR:CE2	3.05	0.45
1:B:161:LYS:HB3	1:B:164:GLY:O	2.16	0.45
1:A:57:GLU:HG3	1:A:58:LYS:N	2.32	0.44
1:B:40:VAL:HG13	1:B:129:LYS:CD	2.47	0.44
1:D:202:ASP:C	1:D:202:ASP:OD1	2.61	0.44
1:B:77:HIS:NE2	1:B:79:HIS:HB2	2.33	0.44
1:A:4:LEU:HD23	1:A:22:PHE:O	2.17	0.44
1:A:43:GLU:HG2	1:A:69:LYS:HZ2	1.83	0.44
1:D:71:LYS:O	1:D:71:LYS:HD2	2.17	0.44
1:A:157:GLY:HA2	1:A:196:SER:OG	2.17	0.44
1:C:20:THR:OG1	1:C:34:HIS:CD2	2.72	0.43
1:A:124:TRP:CE3	1:A:127:LYS:O	2.71	0.43
3:B:402:ACY:CH3	4:B:413:HOH:O	2.66	0.43
1:A:103:ASN:CG	1:A:113:GLN:HB3	2.43	0.43
1:D:20:THR:OG1	1:D:34:HIS:CD2	2.70	0.43
1:B:214:VAL:CG2	1:B:215:LYS:N	2.82	0.43
1:D:174:GLU:CD	1:D:174:GLU:H	2.27	0.42
1:A:54:LYS:HZ3	1:A:54:LYS:HG2	1.72	0.42
1:B:211:GLU:O	1:B:214:VAL:HG22	2.19	0.42
1:A:202:ASP:OD1	1:A:202:ASP:C	2.63	0.42
1:C:181:LYS:HD2	4:C:486:HOH:O	2.20	0.42
1:B:25:VAL:HG23	1:B:27:GLY:H	1.83	0.42
1:C:45:TYR:OH	1:C:71:LYS:HG2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:151:ARG:HA	1:C:151:ARG:HD3	1.81	0.42
1:A:78:PHE:CE1	1:A:105:LEU:HD13	2.54	0.42
1:B:14:GLU:CB	1:B:151:ARG:HH11	2.33	0.42
1:D:27:GLY:C	1:D:29:GLY:N	2.78	0.42
1:D:74:ILE:HD11	1:D:118:PHE:CE2	2.54	0.42
1:A:161:LYS:HB3	1:A:164:GLY:O	2.19	0.41
1:C:147:TRP:CH2	1:C:152:LYS:HA	2.55	0.41
1:A:28:TRP:CD1	1:A:31:VAL:HG22	2.56	0.41
1:B:39:LEU:HD13	1:B:68:TYR:CE1	2.56	0.41
1:A:43:GLU:HG2	1:A:69:LYS:HG2	2.03	0.41
1:B:163:TYR:HB3	1:C:30:VAL:HB	2.03	0.41
1:D:61:THR:O	1:D:65:GLU:HB2	2.21	0.41
1:A:4:LEU:N	1:A:4:LEU:CD1	2.84	0.41
1:A:57:GLU:OE2	1:A:61:THR:HG21	2.21	0.41
1:B:75:SER:CB	1:B:83:THR:HG22	2.51	0.41
1:C:37:VAL:HG21	1:C:59:LEU:HD11	2.03	0.41
1:C:57:GLU:OE2	1:C:88:TRP:CZ2	2.74	0.41
1:C:174:GLU:HA	1:C:217:LEU:HD13	2.03	0.41
1:D:57:GLU:HG3	4:D:432:HOH:O	2.21	0.41
1:B:79:HIS:CG	3:B:402:ACY:H3	2.56	0.41
1:B:212:GLN:NE2	4:B:482:HOH:O	2.53	0.40
1:D:60:VAL:HG13	1:D:70:ILE:HG13	2.03	0.40
1:B:64:VAL:HA	1:B:68:TYR:O	2.21	0.40
1:B:27:GLY:C	1:B:29:GLY:N	2.79	0.40
1:A:126:VAL:CG2	1:A:130:ILE:HD12	2.52	0.40
1:B:57:GLU:OE2	1:B:61:THR:HG21	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:ASN:O	4:C:439:HOH:O[1_654]	2.08	0.12

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	216/228 (95%)	202 (94%)	11 (5%)	3 (1%)	9	4
1	B	216/228 (95%)	204 (94%)	12 (6%)	0	100	100
1	C	216/228 (95%)	204 (94%)	10 (5%)	2 (1%)	14	9
1	D	216/228 (95%)	206 (95%)	10 (5%)	0	100	100
All	All	864/912 (95%)	816 (94%)	43 (5%)	5 (1%)	21	17

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	127	LYS
1	C	41	ASN
1	A	28	TRP
1	A	25	VAL
1	C	27	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	186/194 (96%)	178 (96%)	8 (4%)	26	25
1	B	186/194 (96%)	180 (97%)	6 (3%)	34	35
1	C	186/194 (96%)	179 (96%)	7 (4%)	29	29
1	D	186/194 (96%)	173 (93%)	13 (7%)	14	10
All	All	744/776 (96%)	710 (95%)	34 (5%)	24	22

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	LYS
1	A	28	TRP
1	A	69	LYS

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Mol	Chain	Res	Type
1	A	103	ASN
1	A	109	ASP
1	A	143	ASN
1	A	174	GLU
1	A	181	LYS
1	B	8	LYS
1	B	28	TRP
1	B	57	GLU
1	B	108	LYS
1	B	143	ASN
1	B	207	LYS
1	C	28	TRP
1	C	92	ARG
1	C	103	ASN
1	C	143	ASN
1	C	174	GLU
1	C	199	GLU
1	C	219	GLU
1	D	8	LYS
1	D	24	GLU
1	D	43	GLU
1	D	57	GLU
1	D	71	LYS
1	D	95	PRO
1	D	103	ASN
1	D	143	ASN
1	D	174	GLU
1	D	177	PRO
1	D	178	LYS
1	D	181	LYS
1	D	189	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	ASN
1	A	34	HIS
1	A	90	ASN
1	A	103	ASN
1	A	113	GLN
1	A	128	ASN
1	A	212	GLN

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Mol	Chain	Res	Type
1	B	34	HIS
1	B	90	ASN
1	B	103	ASN
1	B	113	GLN
1	B	128	ASN
1	B	212	GLN
1	C	34	HIS
1	C	90	ASN
1	C	103	ASN
1	C	122	ASN
1	C	128	ASN
1	D	19	HIS
1	D	26	ASN
1	D	34	HIS
1	D	41	ASN
1	D	103	ASN
1	D	113	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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$
1	CSD	D	158	1	4,7,8	25.73	1 (25%)	1,8,10	2.72	1 (100%)
1	CSD	A	158	1	4,7,8	25.02	1 (25%)	1,8,10	1.28	0
1	CSD	C	158	1	4,7,8	24.00	1 (25%)	1,8,10	0.19	0
1	CSD	B	158	1	4,7,8	26.86	2 (50%)	1,8,10	1.62	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
1	CSD	D	158	1	-	2/2/6/8	-
1	CSD	A	158	1	-	2/2/6/8	-
1	CSD	C	158	1	-	2/2/6/8	-
1	CSD	B	158	1	-	2/2/6/8	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	158	CSD	OD1-SG	53.62	1.96	1.47
1	D	158	CSD	OD1-SG	51.41	1.94	1.47
1	A	158	CSD	OD1-SG	49.99	1.93	1.47
1	C	158	CSD	OD1-SG	47.95	1.91	1.47
1	B	158	CSD	CB-SG	-2.28	1.66	1.79

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	158	CSD	OD1-SG-CB	2.72	110.61	105.60

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	158	CSD	N-CA-CB-SG
1	A	158	CSD	CA-CB-SG-OD1
1	B	158	CSD	CA-CB-SG-OD1
1	C	158	CSD	N-CA-CB-SG
1	C	158	CSD	CA-CB-SG-OD1
1	D	158	CSD	N-CA-CB-SG
1	D	158	CSD	CA-CB-SG-OD1
1	B	158	CSD	N-CA-CB-SG

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	158	CSD	4	0
1	A	158	CSD	1	0
1	C	158	CSD	1	0
1	B	158	CSD	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 for Mogul analysis.

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	$\# Z > 2$
3	ACY	D	404	2	3,3,3	0.76	0	3,3,3	0.77	0
3	ACY	A	401	2	3,3,3	1.05	0	3,3,3	0.95	0
3	ACY	B	402	2	3,3,3	0.97	0	3,3,3	0.79	0
3	ACY	C	403	2	3,3,3	0.99	0	3,3,3	0.73	0

There are no bond length outliers.

There are no bond angle outliers.

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
3	B	402	ACY	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.