



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:53 AM UTC

PDB ID : 1B7H / pdb_00001b7h
Title : OLIGO-PEPTIDE BINDING PROTEIN COMPLEXED WITH LYSYL-NO
RLEUCYL-LYSINE
Authors : Davies, T.G.; Tame, J.R.H.
Deposited on : 1998-11-16
Resolution : 2.00 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

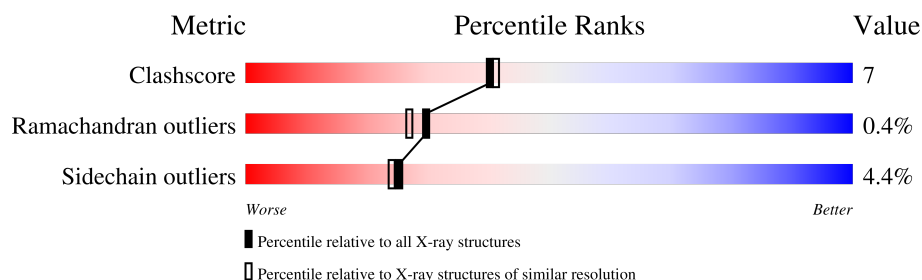
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	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	517	 70% 25% . .
2	B	3	 67% 33%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4467 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 Periplasmic oligopeptide-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	517	Total	C	N	O	S	9	0	0
			4165	2666	700	794	5			

- Molecule 2 is a protein called LYS-NLE-LYS PEPTIDE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	3	Total	C	N	O	0	0	0
			27	18	5	4			

- Molecule 3 is URANIUM ATOM (CCD ID: U1) (formula: U).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	U	0	0
			2	2		

- Molecule 4 is water.

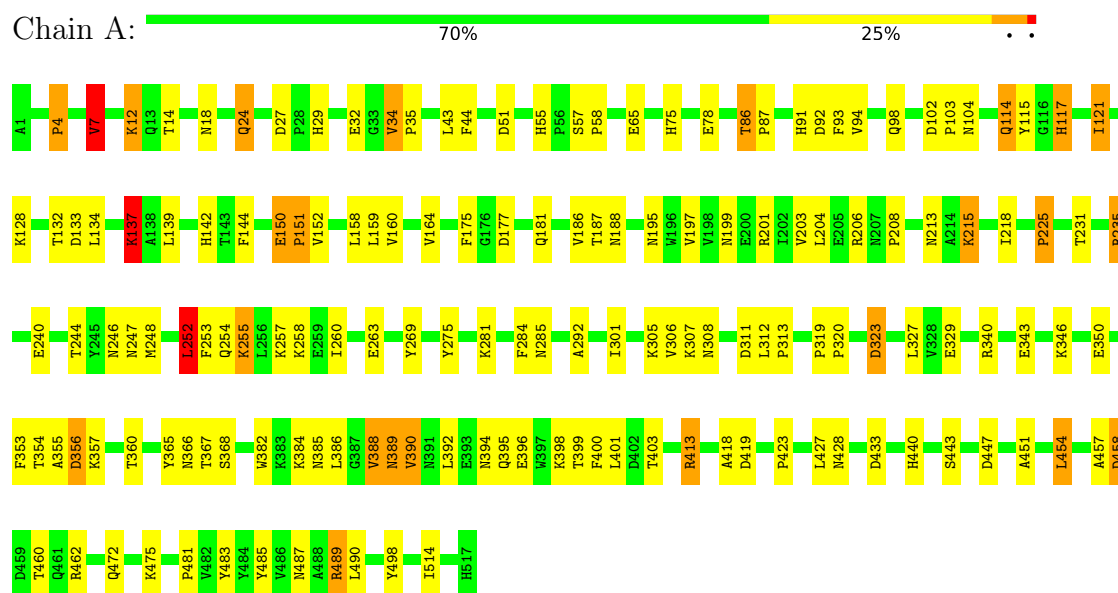
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	270	Total	O	0	0
			270	270		
4	B	3	Total	O	0	0
			3	3		

3 Residue-property plots

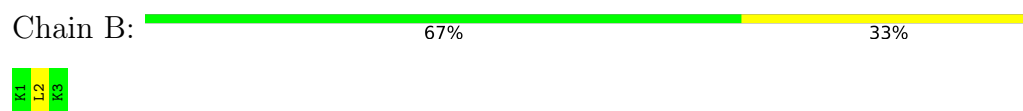
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded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



- Molecule 2: LYS-NLE-LYS PEPTIDE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 2 A	Depositor
Cell constants a, b, c, α , β , γ	104.01Å 74.08Å 69.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	99.0 (20.00-2.00)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.210 , 0.260	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4467	wwPDB-VP
Average B, all atoms (Å ²)	38.0	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: NLE, U1

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	1.01	2/4276 (0.0%)	2.00	126/5830 (2.2%)
2	B	1.07	0/17	1.95	0/16
All	All	1.01	2/4293 (0.0%)	2.00	126/5846 (2.2%)

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	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	160	VAL	C-O	5.58	1.30	1.24
1	A	384	LYS	CD-CE	-5.15	1.37	1.52

All (126) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	201	ARG	CD-NE-CZ	25.49	160.09	124.40
1	A	413	ARG	NE-CZ-NH2	-14.54	106.12	119.20
1	A	413	ARG	NE-CZ-NH1	14.09	135.59	121.50
1	A	114	GLN	CA-CB-CG	11.88	137.87	114.10
1	A	235	ARG	CD-NE-CZ	11.33	140.26	124.40
1	A	91	HIS	CA-CB-CG	-9.45	104.35	113.80
1	A	356	ASP	CB-CG-OD1	-9.09	97.50	118.40
1	A	400	PHE	CA-CB-CG	8.95	122.75	113.80
1	A	356	ASP	CB-CG-OD2	8.77	138.56	118.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	12	LYS	CA-CB-CG	8.76	131.61	114.10
1	A	489	ARG	NE-CZ-NH1	8.73	130.23	121.50
1	A	385	ASN	CA-CB-CG	7.91	120.51	112.60
1	A	117	HIS	CA-CB-CG	-7.61	106.19	113.80
1	A	323	ASP	CA-CB-CG	7.49	120.09	112.60
1	A	177	ASP	CA-CB-CG	7.23	119.83	112.60
1	A	366	ASN	N-CA-CB	7.15	121.03	109.95
1	A	489	ARG	CD-NE-CZ	7.12	134.37	124.40
1	A	252	LEU	N-CA-C	7.12	121.99	113.16
1	A	395	GLN	OE1-CD-NE2	-7.07	115.53	122.60
1	A	427	LEU	CA-C-O	-7.02	112.17	120.10
1	A	231	THR	CA-CB-OG1	-7.02	99.07	109.60
1	A	114	GLN	CB-CG-CD	6.93	124.39	112.60
1	A	443	SER	CA-C-O	6.93	126.63	119.49
1	A	195	ASN	CA-CB-CG	6.90	119.50	112.60
1	A	353	PHE	CA-CB-CG	-6.87	106.93	113.80
1	A	329	GLU	CB-CG-CD	-6.86	100.94	112.60
1	A	284	PHE	CA-CB-CG	-6.84	106.96	113.80
1	A	433	ASP	CA-CB-CG	-6.83	105.77	112.60
1	A	55	HIS	CA-CB-CG	-6.79	107.01	113.80
1	A	103	PRO	N-CA-CB	6.77	110.25	103.48
1	A	457	ALA	N-CA-CB	-6.72	100.24	109.98
1	A	275	TYR	CA-CB-CG	-6.69	101.86	113.90
1	A	186	VAL	CA-C-O	-6.61	113.60	120.27
1	A	18	ASN	CA-CB-CG	-6.54	106.06	112.60
1	A	481	PRO	N-CA-CB	6.52	109.11	103.31
1	A	102	ASP	O-C-N	-6.51	116.39	121.47
1	A	320	PRO	N-CA-CB	6.39	109.87	103.48
1	A	253	PHE	N-CA-C	6.39	118.24	111.28
1	A	458	ASP	N-CA-C	6.38	120.30	110.42
1	A	164	VAL	CA-C-O	-6.37	113.77	120.14
1	A	355	ALA	N-CA-C	-6.37	104.20	112.23
1	A	440	HIS	CA-CB-CG	-6.36	107.44	113.80
1	A	102	ASP	CA-C-N	6.33	126.02	119.56
1	A	102	ASP	C-N-CA	6.33	126.02	119.56
1	A	396	GLU	CB-CG-CD	6.29	123.29	112.60
1	A	150	GLU	O-C-N	6.27	125.72	121.71
1	A	254	GLN	N-CA-C	-6.25	104.47	111.28
1	A	485	TYR	CA-CB-CG	6.22	125.09	113.90
1	A	29	HIS	CA-CB-CG	-6.21	107.59	113.80
1	A	319	PRO	O-C-N	-6.20	114.15	121.46
1	A	114	GLN	OE1-CD-NE2	-6.17	116.43	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	419	ASP	CA-C-O	6.14	125.90	119.14
1	A	4	PRO	N-CA-CB	6.13	108.62	103.17
1	A	12	LYS	CB-CA-C	6.12	120.45	110.22
1	A	142	HIS	CA-CB-CG	-6.11	107.69	113.80
1	A	104	ASN	CA-CB-CG	6.10	118.70	112.60
1	A	319	PRO	CA-C-N	6.09	125.77	119.56
1	A	319	PRO	C-N-CA	6.09	125.77	119.56
1	A	114	GLN	O-C-N	-6.05	115.26	122.15
1	A	353	PHE	CA-C-O	-6.03	114.10	120.80
1	A	281	LYS	CA-CB-CG	6.03	126.15	114.10
1	A	292	ALA	CA-C-O	-5.97	114.23	120.55
1	A	128	LYS	CA-C-O	5.94	125.33	118.97
1	A	311	ASP	CA-C-O	-5.92	115.11	121.56
1	A	181	GLN	CA-C-N	5.90	126.04	119.32
1	A	181	GLN	C-N-CA	5.90	126.04	119.32
1	A	121	ILE	O-C-N	-5.83	116.18	121.89
1	A	246	ASN	CA-C-N	5.77	130.94	122.39
1	A	246	ASN	C-N-CA	5.77	130.94	122.39
1	A	447	ASP	O-C-N	5.72	128.19	122.12
1	A	308	ASN	OD1-CG-ND2	5.71	128.31	122.60
1	A	313	PRO	N-CA-CB	5.69	108.37	103.31
1	A	32	GLU	CA-C-N	-5.67	115.91	122.77
1	A	32	GLU	C-N-CA	-5.67	115.91	122.77
1	A	472	GLN	CA-C-O	5.66	126.41	120.42
1	A	114	GLN	CA-C-O	5.64	126.39	120.42
1	A	158	LEU	CB-CA-C	-5.62	100.22	110.63
1	A	98	GLN	O-C-N	-5.61	116.17	122.12
1	A	152	VAL	CA-C-N	5.61	125.71	119.32
1	A	152	VAL	C-N-CA	5.61	125.71	119.32
1	A	418	ALA	CA-C-O	-5.55	115.66	121.55
1	A	159	LEU	N-CA-C	5.53	119.51	112.87
1	A	104	ASN	OD1-CG-ND2	-5.41	117.19	122.60
1	A	389	ASN	CA-C-O	-5.40	114.38	120.32
1	A	203	VAL	O-C-N	5.37	129.06	123.26
1	A	151	PRO	N-CA-CB	5.35	108.07	103.31
1	A	158	LEU	N-CA-CB	5.34	118.44	110.22
1	A	34	VAL	CA-C-N	5.34	124.52	118.97
1	A	34	VAL	C-N-CA	5.34	124.52	118.97
1	A	7	VAL	N-CA-CB	5.33	117.56	110.26
1	A	144	PHE	CA-C-N	-5.33	115.48	122.99
1	A	144	PHE	C-N-CA	-5.33	115.48	122.99
1	A	137	LYS	O-C-N	5.32	129.44	123.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	197	VAL	N-CA-CB	5.32	118.60	111.90
1	A	285	ASN	O-C-N	-5.29	115.06	122.37
1	A	247	ASN	CA-CB-CG	5.28	117.88	112.60
1	A	399	THR	CA-C-O	5.28	126.01	120.42
1	A	384	LYS	O-C-N	-5.27	116.53	122.12
1	A	93	PHE	CA-CB-CG	-5.26	108.53	113.80
1	A	327	LEU	O-C-N	5.24	128.81	122.94
1	A	340	ARG	NE-CZ-NH1	-5.23	116.27	121.50
1	A	260	ILE	CA-C-N	5.22	126.37	119.84
1	A	260	ILE	C-N-CA	5.22	126.37	119.84
1	A	175	PHE	CA-CB-CG	-5.21	108.59	113.80
1	A	343	GLU	CA-C-N	5.20	127.20	120.44
1	A	343	GLU	C-N-CA	5.20	127.20	120.44
1	A	44	PHE	CA-CB-CG	-5.18	108.62	113.80
1	A	86	THR	CA-C-N	5.17	124.93	119.76
1	A	86	THR	C-N-CA	5.17	124.93	119.76
1	A	403	THR	O-C-N	-5.12	116.76	122.09
1	A	188	ASN	O-C-N	5.12	127.81	122.23
1	A	489	ARG	NH1-CZ-NH2	-5.12	112.65	119.30
1	A	399	THR	CA-C-N	5.11	127.38	120.38
1	A	399	THR	C-N-CA	5.11	127.38	120.38
1	A	327	LEU	CA-C-O	-5.10	115.70	121.72
1	A	367	THR	CA-CB-OG1	-5.09	101.96	109.60
1	A	386	LEU	N-CA-CB	-5.08	103.73	111.15
1	A	94	VAL	O-C-N	-5.06	116.73	121.94
1	A	92	ASP	CA-C-N	5.05	127.47	120.29
1	A	92	ASP	C-N-CA	5.05	127.47	120.29
1	A	208	PRO	N-CA-CB	5.05	108.84	103.39
1	A	385	ASN	CA-C-O	5.05	125.17	119.27
1	A	27	ASP	CA-C-N	5.04	125.32	119.47
1	A	27	ASP	C-N-CA	5.04	125.32	119.47
1	A	390	VAL	N-CA-CB	-5.02	99.96	111.81
1	A	235	ARG	NE-CZ-NH2	5.01	123.71	119.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	24	GLN	Mainchain

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	4165	0	4076	55	0
2	B	27	0	38	2	0
3	A	2	0	0	0	0
4	A	270	0	0	12	0
4	B	3	0	0	0	0
All	All	4467	0	4114	55	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 7.

All (55) 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:A:199:ASN:CB	4:A:779:HOH:O	1.87	1.19
1:A:451:ALA:CA	4:A:754:HOH:O	1.78	1.16
1:A:451:ALA:HA	4:A:754:HOH:O	1.29	1.15
1:A:199:ASN:CA	4:A:779:HOH:O	1.93	1.14
1:A:451:ALA:C	4:A:754:HOH:O	1.96	1.04
1:A:215:LYS:HE3	4:A:777:HOH:O	0.82	1.00
1:A:451:ALA:O	4:A:754:HOH:O	1.80	0.99
1:A:199:ASN:HA	4:A:779:HOH:O	1.62	0.89
1:A:199:ASN:HB3	4:A:779:HOH:O	1.58	0.87
1:A:252:LEU:HA	1:A:255:LYS:HE2	1.58	0.84
1:A:248:MET:HA	1:A:248:MET:HE2	1.63	0.81
1:A:401:LEU:HD22	2:B:2:NLE:HD2	1.67	0.76
1:A:215:LYS:CE	4:A:777:HOH:O	1.66	0.65
1:A:255:LYS:H	1:A:255:LYS:NZ	1.95	0.64
1:A:150:GLU:HB3	1:A:151:PRO:HD2	1.82	0.61
1:A:255:LYS:H	1:A:255:LYS:HZ3	1.49	0.60
1:A:218:ILE:HD11	1:A:514:ILE:HG12	1.84	0.59
1:A:137:LYS:HG3	1:A:139:LEU:HD23	1.87	0.56
1:A:252:LEU:HA	1:A:255:LYS:CE	2.35	0.55
1:A:24:GLN:O	1:A:398:LYS:HE3	2.09	0.53
1:A:199:ASN:ND2	4:A:779:HOH:O	2.41	0.52
1:A:218:ILE:CD1	1:A:514:ILE:HG12	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:307:LYS:HE3	1:A:483:TYR:OH	2.09	0.51
1:A:382:TRP:HB3	1:A:388:VAL:HG22	1.92	0.51
1:A:115:TYR:CE1	1:A:428:ASN:HB3	2.48	0.49
1:A:365:TYR:O	1:A:394:ASN:HA	2.13	0.49
1:A:458:ASP:OD2	1:A:460:THR:HB	2.12	0.49
1:A:117:HIS:ND1	1:A:454:LEU:HD11	2.27	0.49
1:A:244:THR:HG23	1:A:490:LEU:HB2	1.95	0.49
1:A:401:LEU:HD22	2:B:2:NLE:CD	2.40	0.49
1:A:4:PRO:O	1:A:7:VAL:HG13	2.13	0.49
1:A:360:THR:HA	1:A:389:ASN:O	2.13	0.48
1:A:43:LEU:O	1:A:187:THR:HB	2.14	0.47
1:A:323:ASP:O	1:A:423:PRO:HD3	2.15	0.47
1:A:235:ARG:HD3	1:A:240:GLU:OE1	2.14	0.47
1:A:199:ASN:CG	4:A:779:HOH:O	2.40	0.47
1:A:354:THR:OG1	1:A:357:LYS:N	2.48	0.47
1:A:114:GLN:HA	1:A:121:ILE:HG21	1.97	0.46
1:A:263:GLU:O	1:A:490:LEU:HA	2.15	0.46
1:A:346:LYS:HE2	1:A:350:GLU:OE2	2.15	0.46
1:A:301:ILE:HA	1:A:305:LYS:HG3	1.97	0.45
1:A:137:LYS:HB3	1:A:137:LYS:HE2	1.57	0.45
1:A:269:TYR:HB2	1:A:487:ASN:HB2	1.99	0.45
1:A:489:ARG:HD2	1:A:498:TYR:CZ	2.53	0.43
1:A:43:LEU:HD21	1:A:204:LEU:HD22	2.01	0.42
1:A:206:ARG:HD3	1:A:213:ASN:OD1	2.19	0.42
1:A:57:SER:HB3	1:A:58:PRO:HD2	2.00	0.42
1:A:34:VAL:HB	1:A:35:PRO:HD3	2.02	0.42
1:A:51:ASP:HB3	1:A:57:SER:OG	2.20	0.42
1:A:269:TYR:CG	1:A:487:ASN:HB2	2.55	0.41
1:A:240:GLU:O	1:A:240:GLU:HG2	2.19	0.41
1:A:12:LYS:HD2	1:A:14:THR:HG23	2.03	0.41
1:A:65:GLU:OE2	1:A:75:HIS:NE2	2.48	0.41
1:A:133:ASP:O	1:A:134:LEU:C	2.64	0.41
1:A:86:THR:HA	1:A:87:PRO:HD3	1.85	0.40

There are no symmetry-related clashes.

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	515/517 (100%)	492 (96%)	21 (4%)	2 (0%)	30	27

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	225	PRO
1	A	368	SER

5.3.2 Protein sidechains [i](#)

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	455/455 (100%)	435 (96%)	20 (4%)	25	24
2	B	2/2 (100%)	2 (100%)	0	100	100
All	All	457/457 (100%)	437 (96%)	20 (4%)	25	24

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	VAL
1	A	78	GLU
1	A	132	THR
1	A	137	LYS
1	A	215	LYS
1	A	225	PRO
1	A	252	LEU

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Mol	Chain	Res	Type
1	A	255	LYS
1	A	257	LYS
1	A	258	LYS
1	A	306	VAL
1	A	312	LEU
1	A	356	ASP
1	A	388	VAL
1	A	390	VAL
1	A	392	LEU
1	A	413	ARG
1	A	454	LEU
1	A	462	ARG
1	A	475	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	279	ASN
1	A	304	ASN
1	A	308	ASN
1	A	338	GLN
1	A	385	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	NLE	B	2	2	6,7,8	0.98	0	2,7,9	0.84	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
2	NLE	B	2	2	-	1/5/6/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2	NLE	CE-CD-CG-CB

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2	NLE	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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.