



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 2, 2026 – 01:51 AM UTC

PDB ID : 1P04 / pdb_00001p04
Title : STRUCTURE ANALYSIS OF SPECIFICITY. ALPHA-LYTIC PROTEASE
COMPLEXES WITH ANALOGUES OF REACTION INTERMEDIATES
Authors : Bone, R.; Agard, D.A.
Deposited on : 1989-04-24
Resolution : 2.55 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

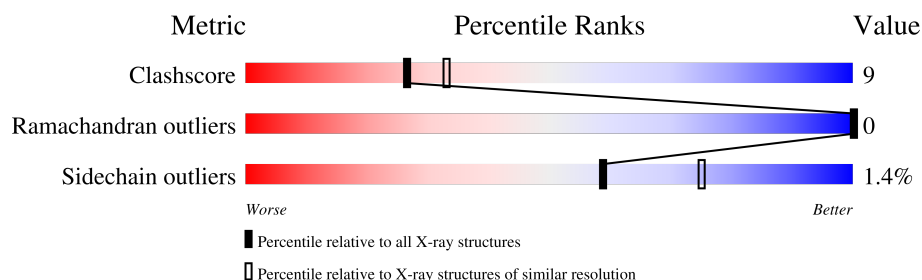
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)

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	198	49% 41% 9%
2	P	5	40% 40% 20%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 1563 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.

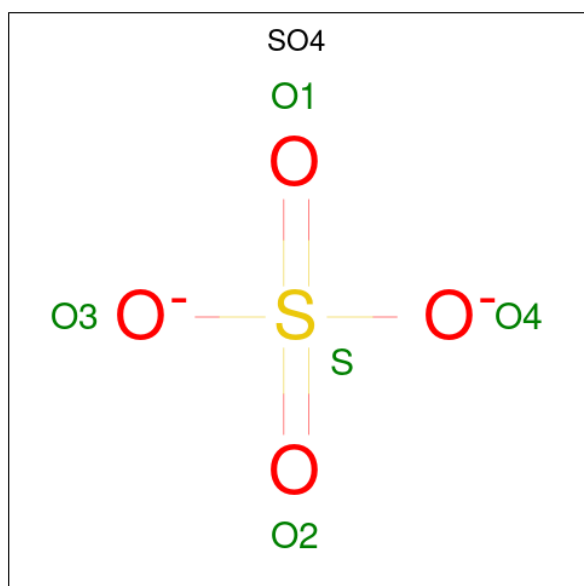
- Molecule 1 is a protein called ALPHA-LYTIC PROTEASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	198	Total	C	N	O	S	0	0	0
			1391	846	262	275	8			

- Molecule 2 is a protein called METHOXYSUCCINYL-ALA-ALA-PRO-ISOLEUCINE BORONIC ACID INHIBITOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	4	Total	B	C	N	O	0	0	0
			26	1	16	4	5			

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 4 is water.

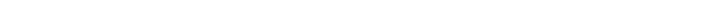
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	136	Total 136	O 136	0	0
4	P	5	Total 5	O 5	0	0

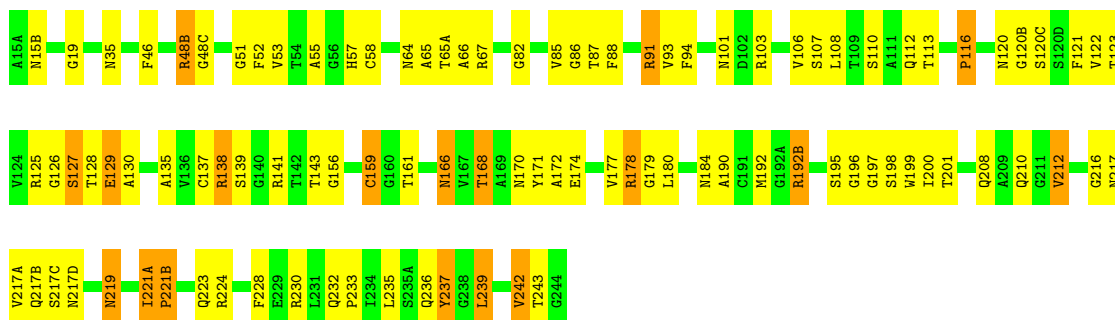
3 Residue-property plots

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: ALPHA-LYTIC PROTEASE

Chain A:  49% 41% 9%



● Molecule 2: METHOXYSUCCINYL-ALA-ALA-PRO-ISOLEUCINE BORONIC ACID INHIBITOR

Chain P: 40% 40% 20%



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	66.30 Å 66.30 Å 80.31 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 2.55	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.55)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.134 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1563	wwPDB-VP
Average B, all atoms (Å ²)	11.0	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: B2I, SO4

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	1.41	0/1409	2.70	127/1909 (6.7%)
2	P	0.94	0/17	2.33	1/23 (4.3%)
All	All	1.40	0/1426	2.69	128/1932 (6.6%)

There are no bond length outliers.

All (128) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	170	ASN	CA-CB-CG	-12.10	100.50	112.60
1	A	106	VAL	CA-C-O	-11.55	108.24	120.48
1	A	91	ARG	NH1-CZ-NH2	-11.41	104.47	119.30
1	A	91	ARG	NE-CZ-NH2	11.14	129.22	119.20
1	A	48(B)	ARG	NH1-CZ-NH2	10.62	133.10	119.30
1	A	217(B)	GLN	CG-CD-NE2	9.93	131.30	116.40
1	A	143	THR	CA-C-O	-9.91	107.96	119.56
1	A	48(B)	ARG	NE-CZ-NH1	-9.88	111.62	121.50
1	A	170	ASN	CA-C-O	-9.65	111.27	122.37
1	A	224	ARG	CD-NE-CZ	-9.52	111.07	124.40
1	A	65(A)	THR	CA-CB-OG1	-9.35	95.57	109.60
1	A	221(B)	PRO	CA-C-O	-8.95	110.76	121.67
1	A	48(B)	ARG	N-CA-CB	-8.53	97.77	111.58
1	A	64	ASN	CA-C-O	-8.30	108.12	119.16
1	A	208	GLN	CG-CD-NE2	-8.26	104.01	116.40
1	A	48(B)	ARG	CD-NE-CZ	8.26	135.96	124.40
1	A	177	VAL	N-CA-CB	8.01	122.36	112.10
1	A	210	GLN	CG-CD-NE2	7.88	128.22	116.40
1	A	107	SER	CA-CB-OG	-7.75	95.61	111.10
2	P	3	ALA	O-C-N	7.69	127.34	121.88
1	A	103	ARG	CA-C-O	-7.52	112.90	121.40
1	A	57	HIS	CA-C-O	-7.49	110.42	119.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	166	ASN	CB-CG-ND2	7.40	127.49	116.40
1	A	127	SER	N-CA-C	7.37	119.82	110.61
1	A	239	LEU	CA-C-O	-7.27	112.70	121.28
1	A	139	SER	N-CA-CB	-7.14	98.44	110.80
1	A	125	ARG	NH1-CZ-NH2	7.12	128.56	119.30
1	A	130	ALA	N-CA-C	-7.02	101.07	110.55
1	A	199	TRP	N-CA-C	-7.00	96.86	108.34
1	A	88	PHE	CA-C-O	-6.96	112.81	120.81
1	A	237	TYR	CA-C-O	-6.89	111.29	119.35
1	A	192(B)	ARG	CA-C-O	-6.86	113.48	120.96
1	A	48(C)	GLY	N-CA-C	-6.81	99.75	111.47
1	A	184	ASN	OD1-CG-ND2	-6.79	115.81	122.60
1	A	195	SER	N-CA-CB	6.70	120.34	109.69
1	A	196	GLY	CA-C-O	-6.68	112.58	119.20
1	A	67	ARG	NE-CZ-NH1	6.65	128.15	121.50
1	A	58	CYS	N-CA-C	6.58	118.45	111.28
1	A	123	THR	O-C-N	6.55	130.70	123.04
1	A	230	ARG	NE-CZ-NH1	6.50	128.00	121.50
1	A	243	THR	CA-CB-CG2	6.49	121.53	110.50
1	A	121	PHE	CA-CB-CG	6.47	120.27	113.80
1	A	135	ALA	N-CA-C	-6.45	100.94	110.48
1	A	208	GLN	OE1-CD-NE2	6.43	129.03	122.60
1	A	48(B)	ARG	CB-CG-CD	-6.43	96.52	111.30
1	A	85	VAL	CA-CB-CG2	6.42	121.31	110.40
1	A	112	GLN	CA-C-N	6.41	132.21	123.11
1	A	112	GLN	C-N-CA	6.41	132.21	123.11
1	A	161	THR	CA-CB-OG1	-6.39	100.01	109.60
1	A	110	SER	CB-CA-C	-6.36	98.13	110.46
1	A	221(A)	ILE	N-CA-CB	6.30	120.03	111.21
1	A	129	GLU	CG-CD-OE2	-6.28	103.96	118.40
1	A	128	THR	CA-CB-OG1	-6.25	100.22	109.60
1	A	125	ARG	CA-C-N	6.15	128.91	120.72
1	A	125	ARG	C-N-CA	6.15	128.91	120.72
1	A	86	GLY	CA-C-O	-6.14	114.94	121.38
1	A	82	GLY	CA-C-O	-6.08	112.93	118.95
1	A	242	VAL	CA-C-O	-6.08	113.92	120.85
1	A	223	GLN	CA-C-O	-6.04	112.14	119.32
1	A	166	ASN	OD1-CG-ND2	-6.03	116.57	122.60
1	A	35	ASN	OD1-CG-ND2	6.01	128.61	122.60
1	A	200	ILE	CA-C-O	-6.00	115.45	121.45
1	A	199	TRP	N-CA-CB	5.98	120.16	110.77
1	A	224	ARG	CA-C-O	-5.94	114.09	120.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	192(B)	ARG	O-C-N	5.90	130.14	123.06
1	A	108	LEU	CA-C-O	-5.89	114.47	121.66
1	A	228	PHE	CA-CB-CG	5.88	119.68	113.80
1	A	192(B)	ARG	CD-NE-CZ	-5.88	116.17	124.40
1	A	200	ILE	O-C-N	5.81	129.15	122.82
1	A	217(D)	ASN	OD1-CG-ND2	5.79	128.39	122.60
1	A	195	SER	O-C-N	5.79	130.03	122.97
1	A	190	ALA	CA-C-O	-5.77	114.70	121.16
1	A	217(C)	SER	CA-C-O	-5.75	112.53	119.49
1	A	174	GLU	N-CA-C	5.75	119.55	112.54
1	A	224	ARG	NE-CZ-NH2	-5.72	114.05	119.20
1	A	122	VAL	N-CA-CB	5.69	118.63	111.46
1	A	53	VAL	O-C-N	5.68	129.17	122.69
1	A	184	ASN	CA-CB-CG	-5.68	106.92	112.60
1	A	190	ALA	N-CA-C	-5.67	101.89	110.28
1	A	210	GLN	OE1-CD-NE2	-5.66	116.94	122.60
1	A	236	GLN	CG-CD-NE2	-5.66	107.91	116.40
1	A	106	VAL	CA-C-N	-5.64	113.74	122.09
1	A	106	VAL	C-N-CA	-5.64	113.74	122.09
1	A	123	THR	CA-CB-OG1	-5.57	101.25	109.60
1	A	94	PHE	CA-CB-CG	-5.52	108.28	113.80
1	A	217	ASN	N-CA-C	5.51	118.14	108.56
1	A	168	THR	N-CA-CB	5.50	119.59	110.52
1	A	57	HIS	N-CA-C	-5.49	105.69	112.38
1	A	242	VAL	CG1-CB-CG2	5.48	122.86	110.80
1	A	35	ASN	CA-CB-CG	5.46	118.06	112.60
1	A	172	ALA	CA-C-O	-5.43	114.77	120.63
1	A	19	GLY	N-CA-C	5.41	121.12	114.69
1	A	120(B)	GLY	N-CA-C	-5.39	101.00	111.02
1	A	159	CYS	CA-C-N	5.36	131.92	121.41
1	A	159	CYS	C-N-CA	5.36	131.92	121.41
1	A	113	THR	O-C-N	5.36	129.88	123.13
1	A	219	ASN	N-CA-CB	5.33	119.99	111.20
1	A	192(B)	ARG	CA-C-N	-5.32	117.66	123.30
1	A	192(B)	ARG	C-N-CA	-5.32	117.66	123.30
1	A	55	ALA	CA-C-N	5.31	125.88	119.98
1	A	55	ALA	C-N-CA	5.31	125.88	119.98
1	A	199	TRP	CA-C-O	-5.31	114.61	120.24
1	A	180	LEU	O-C-N	5.29	128.88	122.85
1	A	48(B)	ARG	CG-CD-NE	-5.28	100.38	112.00
1	A	120	ASN	OD1-CG-ND2	-5.28	117.32	122.60
1	A	66	ALA	CA-C-O	-5.28	114.94	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	201	THR	O-C-N	-5.25	117.06	122.94
1	A	235	LEU	CA-C-O	-5.25	114.99	120.55
1	A	107	SER	CA-C-O	-5.24	114.90	120.92
1	A	192(B)	ARG	NE-CZ-NH1	-5.20	116.30	121.50
1	A	156	GLY	CA-C-N	5.19	129.68	122.77
1	A	156	GLY	C-N-CA	5.19	129.68	122.77
1	A	212	VAL	CA-C-N	5.17	128.10	120.82
1	A	212	VAL	C-N-CA	5.17	128.10	120.82
1	A	138	ARG	NE-CZ-NH2	5.12	123.81	119.20
1	A	171	TYR	CB-CG-CD2	5.11	128.47	120.80
1	A	128	THR	N-CA-C	-5.10	102.31	109.96
1	A	15(B)	ASN	O-C-N	5.10	128.99	123.13
1	A	51	GLY	CA-C-O	5.08	126.53	121.60
1	A	108	LEU	N-CA-CB	-5.08	102.64	110.56
1	A	125	ARG	NE-CZ-NH1	-5.06	116.44	121.50
1	A	192(B)	ARG	NE-CZ-NH2	5.05	123.75	119.20
1	A	120(C)	SER	CA-CB-OG	-5.04	101.02	111.10
1	A	217(B)	GLN	CG-CD-OE1	-5.04	110.73	120.80
1	A	172	ALA	O-C-N	5.03	127.45	122.12
1	A	121	PHE	O-C-N	-5.03	117.65	123.33
1	A	178	ARG	NE-CZ-NH2	5.03	123.72	119.20
1	A	126	GLY	O-C-N	-5.02	119.11	123.88

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	1391	0	1360	26	0
2	P	26	0	28	5	0
3	A	5	0	0	1	0
4	A	136	0	0	3	1
4	P	5	0	0	0	0
All	All	1563	0	1388	26	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 9.

All (26) 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:217(A):VAL:HG11	2:P:1:B2I:HD11	1.45	0.95
1:A:93:VAL:HG11	1:A:101:ASN:HD22	1.66	0.60
1:A:192(B):ARG:HA	2:P:1:B2I:HD13	1.89	0.55
1:A:197:GLY:O	1:A:212:VAL:HA	2.07	0.54
1:A:129:GLU:HG3	4:A:361:HOH:O	2.08	0.54
1:A:221(A):ILE:HB	1:A:221(B):PRO:HD2	1.89	0.54
1:A:217(A):VAL:CG1	2:P:1:B2I:HD11	2.28	0.52
1:A:116:PRO:HB3	1:A:242:VAL:HG12	1.91	0.51
1:A:48(B):ARG:HG3	1:A:239:LEU:HD23	1.93	0.49
1:A:127:SER:O	1:A:232:GLN:NE2	2.44	0.49
1:A:217(A):VAL:HG11	2:P:1:B2I:CD1	2.30	0.48
1:A:48(B):ARG:CZ	4:A:377:HOH:O	2.62	0.48
1:A:166:ASN:HD22	1:A:179:GLY:HA2	1.78	0.48
1:A:46:PHE:O	1:A:52:PHE:HA	2.15	0.47
1:A:168:THR:HG23	1:A:178:ARG:HG2	1.98	0.46
1:A:141:ARG:HD3	1:A:141:ARG:C	2.41	0.46
1:A:192(B):ARG:CA	2:P:1:B2I:HD13	2.45	0.46
1:A:192:MET:HE2	1:A:216:GLY:HA3	1.98	0.45
1:A:138:ARG:HA	1:A:198:SER:O	2.17	0.44
1:A:232:GLN:N	1:A:233:PRO:HD2	2.33	0.44
1:A:65:ALA:O	1:A:87:THR:HA	2.18	0.43
1:A:192:MET:HE3	1:A:219:ASN:ND2	2.34	0.43
1:A:137:CYS:HA	1:A:159:CYS:HA	2.00	0.42
1:A:233:PRO:HB3	3:A:1:SO4:O4	2.20	0.42
1:A:237:TYR:HB2	1:A:239:LEU:HG	2.03	0.41
1:A:48(B):ARG:HD2	4:A:352:HOH:O	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)
4:A:254:HOH:O	4:A:347:HOH:O[5_665]	0.41	1.79

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	196/198 (99%)	187 (95%)	9 (5%)	0	100	100
2	P	2/5 (40%)	2 (100%)	0	0	100	100
All	All	198/203 (98%)	189 (96%)	9 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	142/142 (100%)	140 (99%)	2 (1%)	59	75
2	P	1/1 (100%)	1 (100%)	0	100	100
All	All	143/143 (100%)	141 (99%)	2 (1%)	59	75

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	91	ARG
1	A	116	PRO

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

Mol	Chain	Res	Type
1	A	101	ASN

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Mol	Chain	Res	Type
1	A	112	GLN
1	A	120	ASN
1	A	166	ASN
1	A	182	GLN
1	A	223	GLN

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	B2I	P	1	1,2	3,8,8	0.35	0	2,10,10	1.50	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	B2I	P	1	1,2	-	1/4/10/10	-

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	P	1	B2I	CG2-CB-CG1-CD1

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	P	1	B2I	5	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand 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	$\# Z > 2$
3	SO4	A	1	-	4,4,4	0.73	0	6,6,6	0.41	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 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1	SO4	1	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.