Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 08:51 AM UTC

PDB ID	:	1P06 / pdb_00001p06
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	:	2.34 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:

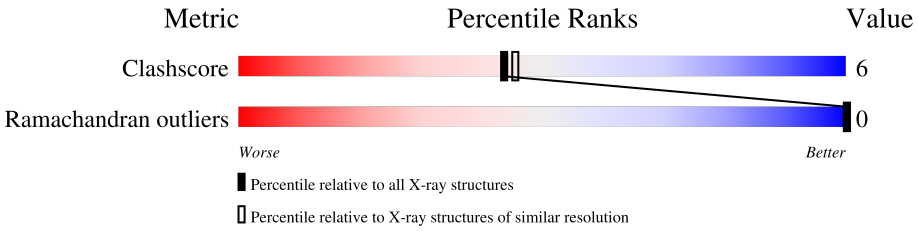
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al.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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.34 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	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	198	41% 51% 8%
2	P	5	40% 40% 20%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 1587 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.

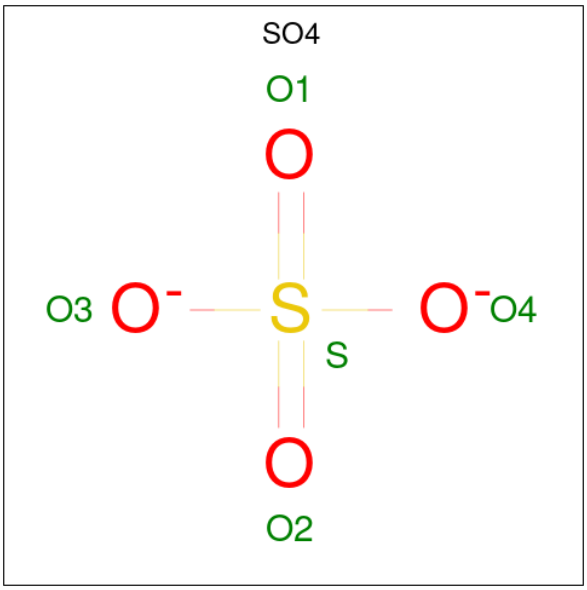
- Molecule 1 is a protein called ALPHA-LYTIC PROTEASE.

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-PHENYLALANIN E BORONIC ACID INHIBITOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	4	Total	B	C	N	O	0	0	0
			28	1	19	4	4			

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



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	161	Total O 161 161	0	0
4	P	2	Total O 2 2	0	0

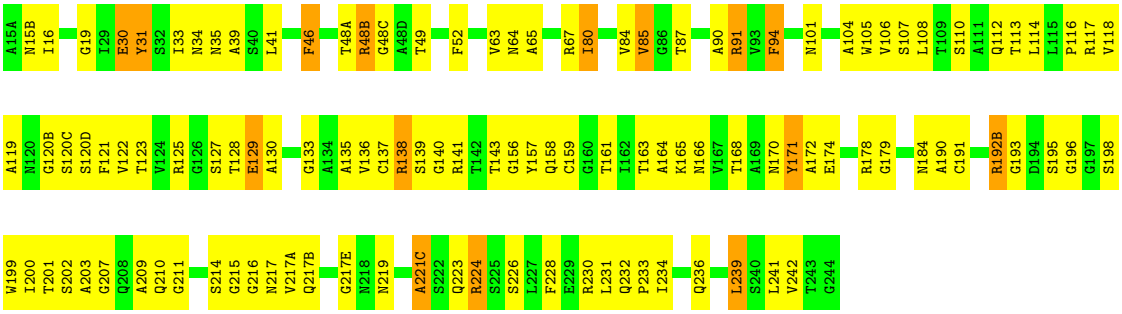
3 Residue-property plots (i)

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:



• Molecule 2: METHOXYSUCCINYL-ALA-ALA-PRO-PHENYLALANINE BORONIC ACID INHIBITOR

Chain P:

4 Data and refinement statistics (i)

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	66.62Å 66.62Å 80.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	(Not available) – 2.34	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.34)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.140 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1587	wwPDB-VP
Average B, all atoms (Å^2)	8.0	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: B2F, 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	1.65	8/1409 (0.6%)	3.16	185/1909 (9.7%)
2	P	1.50	0/17	3.10	1/23 (4.3%)
All	All	1.65	8/1426 (0.6%)	3.16	186/1932 (9.6%)

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
1	A	0	1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	113	THR	CA-CB	7.20	1.63	1.53
1	A	140	GLY	N-CA	6.54	1.52	1.45
1	A	101	ASN	N-CA	5.68	1.53	1.46
1	A	91	ARG	CD-NE	-5.37	1.38	1.46
1	A	135	ALA	C-N	-5.35	1.28	1.33
1	A	138	ARG	CA-C	5.25	1.59	1.52
1	A	168	THR	CA-CB	5.17	1.60	1.53
1	A	215	GLY	C-O	5.15	1.29	1.23

All (186) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	125	ARG	CD-NE-CZ	21.27	154.18	124.40
1	A	125	ARG	NE-CZ-NH2	-20.13	101.08	119.20
1	A	138	ARG	NE-CZ-NH1	-14.54	106.95	121.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	116	PRO	CA-C-O	-14.36	110.69	121.31
1	A	64	ASN	CB-CG-ND2	13.39	136.48	116.40
1	A	228	PHE	CA-CB-CG	12.26	126.06	113.80
1	A	125	ARG	NE-CZ-NH1	12.15	133.65	121.50
1	A	48(B)	ARG	NE-CZ-NH1	-11.54	109.96	121.50
1	A	91	ARG	CD-NE-CZ	11.37	140.32	124.40
1	A	49	THR	CA-CB-OG1	-11.27	92.70	109.60
1	A	138	ARG	NE-CZ-NH2	11.26	129.33	119.20
1	A	156	GLY	CA-C-N	10.70	137.72	122.85
1	A	156	GLY	C-N-CA	10.70	137.72	122.85
1	A	117	ARG	NE-CZ-NH2	-10.49	109.76	119.20
1	A	91	ARG	NE-CZ-NH2	10.37	128.53	119.20
1	A	90	ALA	CA-C-O	-10.30	110.21	121.23
1	A	200	ILE	CA-C-O	-10.04	110.85	121.19
1	A	91	ARG	NH1-CZ-NH2	-9.98	106.33	119.30
2	P	3	ALA	O-C-N	9.87	128.89	121.88
1	A	166	ASN	CA-CB-CG	-9.69	102.91	112.60
1	A	125	ARG	N-CA-CB	-9.66	96.45	110.65
1	A	64	ASN	CB-CG-OD1	-9.66	101.48	120.80
1	A	192(B)	ARG	CD-NE-CZ	-9.52	111.07	124.40
1	A	161	THR	CA-CB-CG2	9.32	126.34	110.50
1	A	112	GLN	OE1-CD-NE2	-9.29	113.31	122.60
1	A	118	VAL	CA-C-N	9.11	133.67	120.82
1	A	118	VAL	C-N-CA	9.11	133.67	120.82
1	A	106	VAL	O-C-N	9.10	132.73	123.18
1	A	117	ARG	O-C-N	9.07	134.15	123.17
1	A	106	VAL	CA-C-O	-8.97	110.97	120.48
1	A	63	VAL	O-C-N	8.91	132.28	122.75
1	A	184	ASN	CA-C-O	-8.87	109.13	119.59
1	A	135	ALA	CA-C-O	-8.68	111.49	121.47
1	A	168	THR	CA-C-O	-8.44	111.23	120.43
1	A	106	VAL	CA-C-N	-8.36	109.72	122.09
1	A	106	VAL	C-N-CA	-8.36	109.72	122.09
1	A	166	ASN	OD1-CG-ND2	-8.34	114.26	122.60
1	A	114	LEU	CA-C-O	-8.27	111.41	120.92
1	A	143	THR	CA-CB-CG2	8.18	124.40	110.50
1	A	120(D)	SER	N-CA-CB	-8.14	96.13	110.14
1	A	84	VAL	CA-C-O	-8.11	111.80	121.04
1	A	80	ILE	CA-C-O	8.00	128.15	120.31
1	A	201	THR	CA-CB-CG2	7.95	124.02	110.50
1	A	41	LEU	O-C-N	7.95	132.96	123.27
1	A	211	GLY	CA-C-O	-7.90	113.05	121.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	143	THR	CA-CB-OG1	-7.86	97.81	109.60
1	A	178	ARG	NH1-CZ-NH2	-7.77	109.20	119.30
1	A	195	SER	CB-CA-C	-7.74	96.87	109.72
1	A	199	TRP	N-CA-CB	7.72	123.66	110.68
1	A	198	SER	CA-C-O	-7.68	112.75	121.19
1	A	192(B)	ARG	CA-C-O	-7.66	112.61	120.96
1	A	120(D)	SER	CB-CA-C	7.59	126.94	112.43
1	A	190	ALA	CA-C-O	-7.57	112.68	121.16
1	A	216	GLY	CA-C-O	-7.48	114.52	121.63
1	A	63	VAL	CA-C-O	-7.47	112.54	121.28
1	A	214	SER	O-C-N	7.45	130.66	121.95
1	A	34	ASN	N-CA-CB	-7.44	100.98	111.62
1	A	217(A)	VAL	CA-C-O	-7.34	113.29	121.36
1	A	170	ASN	OD1-CG-ND2	-7.32	115.28	122.60
1	A	114	LEU	N-CA-CB	-7.30	98.40	110.23
1	A	234	ILE	N-CA-C	-7.30	103.34	110.72
1	A	122	VAL	N-CA-C	-7.28	97.97	108.17
1	A	48(A)	THR	CA-CB-OG1	-7.28	98.68	109.60
1	A	15(B)	ASN	CA-C-O	-7.22	112.38	120.54
1	A	113	THR	CA-CB-OG1	-7.10	98.95	109.60
1	A	214	SER	CA-C-O	-7.10	110.81	119.61
1	A	217(E)	GLY	CA-C-O	-7.09	110.90	119.06
1	A	67	ARG	CD-NE-CZ	-7.07	114.50	124.40
1	A	161	THR	CA-CB-OG1	-7.04	99.04	109.60
1	A	48(A)	THR	CA-C-O	7.01	129.67	121.46
1	A	48(B)	ARG	CD-NE-CZ	6.93	134.11	124.40
1	A	105	TRP	O-C-N	-6.93	114.94	123.33
1	A	141	ARG	NE-CZ-NH1	-6.88	114.62	121.50
1	A	203	ALA	CA-C-O	-6.83	108.71	119.23
1	A	117	ARG	CD-NE-CZ	-6.83	114.84	124.40
1	A	67	ARG	NE-CZ-NH1	6.82	128.32	121.50
1	A	30	GLU	CA-C-O	-6.73	113.73	121.47
1	A	129	GLU	CB-CG-CD	6.71	124.02	112.60
1	A	216	GLY	O-C-N	6.70	131.38	123.61
1	A	39	ALA	CA-C-N	6.66	133.09	120.97
1	A	39	ALA	C-N-CA	6.66	133.09	120.97
1	A	128	THR	CA-CB-OG1	-6.65	99.62	109.60
1	A	178	ARG	NE-CZ-NH1	6.64	128.14	121.50
1	A	48(B)	ARG	CA-CB-CG	-6.63	100.84	114.10
1	A	196	GLY	N-CA-C	-6.59	107.23	115.08
1	A	129	GLU	CA-C-O	-6.59	113.18	120.69
1	A	19	GLY	CA-C-O	-6.52	112.00	119.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	210	GLN	OE1-CD-NE2	-6.51	116.09	122.60
1	A	105	TRP	CB-CA-C	6.49	122.56	109.38
1	A	224	ARG	CB-CG-CD	-6.47	96.41	111.30
1	A	64	ASN	CA-C-O	-6.43	111.31	120.51
1	A	221(C)	ALA	O-C-N	6.43	128.78	122.09
1	A	158	GLN	CA-C-O	-6.43	113.76	120.70
1	A	122	VAL	CA-CB-CG2	6.42	121.32	110.40
1	A	202	SER	O-C-N	6.35	130.65	122.39
1	A	48(C)	GLY	N-CA-C	-6.28	100.34	112.02
1	A	156	GLY	O-C-N	-6.27	115.66	122.62
1	A	217(B)	GLN	CB-CG-CD	-6.26	101.96	112.60
1	A	234	ILE	O-C-N	6.24	128.25	121.83
1	A	242	VAL	N-CA-CB	-6.21	103.99	110.95
1	A	46	PHE	CA-C-N	6.20	129.62	120.95
1	A	46	PHE	C-N-CA	6.20	129.62	120.95
1	A	138	ARG	O-C-N	6.17	130.31	123.33
1	A	200	ILE	O-C-N	6.16	129.78	123.00
1	A	207	GLY	N-CA-C	6.14	123.92	115.27
1	A	164	ALA	N-CA-CB	-6.10	102.10	111.56
1	A	170	ASN	CA-CB-CG	-6.10	106.50	112.60
1	A	113	THR	O-C-N	6.09	130.81	123.13
1	A	113	THR	CA-C-N	-6.08	113.08	122.09
1	A	113	THR	C-N-CA	-6.08	113.08	122.09
1	A	239	LEU	CA-C-O	-6.05	114.14	121.28
1	A	141	ARG	NE-CZ-NH2	6.01	124.61	119.20
1	A	178	ARG	N-CA-CB	-6.00	101.76	110.70
1	A	120(C)	SER	CA-CB-OG	-5.98	99.15	111.10
1	A	165	LYS	N-CA-CB	-5.97	101.16	111.55
1	A	211	GLY	O-C-N	5.97	129.65	123.92
1	A	234	ILE	CA-C-O	-5.94	114.56	120.85
1	A	30	GLU	O-C-N	5.92	129.65	122.96
1	A	123	THR	CA-CB-OG1	-5.91	100.73	109.60
1	A	163	THR	O-C-N	5.90	130.73	122.36
1	A	105	TRP	CA-C-O	5.89	127.67	120.60
1	A	136	VAL	O-C-N	5.88	128.78	122.67
1	A	139	SER	CA-CB-OG	-5.87	99.36	111.10
1	A	48(B)	ARG	N-CA-CB	-5.87	100.11	110.90
1	A	85	VAL	CA-CB-CG2	5.83	120.31	110.40
1	A	120(D)	SER	CA-CB-OG	-5.80	99.50	111.10
1	A	201	THR	N-CA-C	-5.79	101.95	110.52
1	A	172	ALA	CA-C-O	-5.78	113.32	119.97
1	A	166	ASN	CA-C-O	-5.78	115.14	121.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	203	ALA	CA-C-N	-5.73	112.85	122.25
1	A	203	ALA	C-N-CA	-5.73	112.85	122.25
1	A	223	GLN	CB-CG-CD	-5.72	102.87	112.60
1	A	46	PHE	CA-C-O	-5.70	113.53	120.54
1	A	31	TYR	CA-C-O	-5.69	114.62	120.99
1	A	123	THR	O-C-N	5.68	129.69	123.04
1	A	90	ALA	N-CA-CB	-5.68	102.76	111.56
1	A	31	TYR	CB-CA-C	5.63	121.93	109.94
1	A	107	SER	CA-CB-OG	-5.61	99.88	111.10
1	A	241	LEU	N-CA-CB	-5.60	101.73	109.97
1	A	190	ALA	O-C-N	-5.60	116.06	122.89
1	A	127	SER	CA-C-O	-5.59	113.94	120.53
1	A	90	ALA	CB-CA-C	-5.58	100.25	110.62
1	A	199	TRP	N-CA-C	-5.57	99.83	108.90
1	A	16	ILE	CA-C-O	-5.55	114.55	120.59
1	A	117	ARG	CA-C-N	-5.53	115.30	122.99
1	A	117	ARG	C-N-CA	-5.53	115.30	122.99
1	A	139	SER	N-CA-CB	-5.53	101.39	110.68
1	A	105	TRP	N-CA-C	-5.51	99.69	109.06
1	A	198	SER	N-CA-C	5.48	118.18	110.23
1	A	209	ALA	N-CA-CB	-5.46	101.34	109.69
1	A	193	GLY	N-CA-C	-5.45	107.50	114.37
1	A	33	ILE	O-C-N	5.43	128.96	123.20
1	A	226	SER	O-C-N	5.43	130.28	123.12
1	A	224	ARG	O-C-N	5.40	129.43	123.16
1	A	48(B)	ARG	NH1-CZ-NH2	5.40	126.31	119.30
1	A	168	THR	CA-CB-OG1	-5.38	101.53	109.60
1	A	33	ILE	CA-C-O	-5.36	114.81	120.39
1	A	130	ALA	N-CA-CB	-5.36	101.88	110.46
1	A	166	ASN	CB-CG-OD1	5.35	131.51	120.80
1	A	230	ARG	CB-CG-CD	5.35	123.61	111.30
1	A	121	PHE	CA-C-O	-5.34	114.87	121.06
1	A	41	LEU	CA-C-O	-5.33	114.53	120.66
1	A	190	ALA	N-CA-C	-5.33	102.39	110.28
1	A	171	TYR	N-CA-C	-5.29	103.55	110.53
1	A	94	PHE	CA-CB-CG	-5.27	108.53	113.80
1	A	231	LEU	N-CA-CB	-5.26	102.20	110.30
1	A	133	GLY	CA-C-O	-5.25	113.65	119.27
1	A	210	GLN	CA-C-O	-5.23	113.45	119.78
1	A	35	ASN	CA-C-O	-5.22	114.55	121.08
1	A	110	SER	O-C-N	5.22	129.67	122.46
1	A	108	LEU	O-C-N	5.21	128.92	123.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	15(B)	ASN	CA-C-N	-5.19	116.26	122.90
1	A	15(B)	ASN	C-N-CA	-5.19	116.26	122.90
1	A	34	ASN	OD1-CG-ND2	5.19	127.79	122.60
1	A	195	SER	O-C-N	5.18	129.24	122.87
1	A	119	ALA	O-C-N	5.16	129.35	122.95
1	A	196	GLY	CA-C-O	-5.16	113.91	119.27
1	A	105	TRP	N-CA-CB	5.15	120.35	111.13
1	A	201	THR	O-C-N	-5.09	117.24	122.94
1	A	236	GLN	CA-CB-CG	-5.09	103.91	114.10
1	A	179	GLY	O-C-N	5.08	128.54	122.34
1	A	217	ASN	OD1-CG-ND2	-5.08	117.53	122.60
1	A	207	GLY	O-C-N	5.04	128.45	122.50
1	A	15(B)	ASN	N-CA-C	-5.04	101.09	109.46
1	A	120(B)	GLY	N-CA-C	-5.03	101.26	113.18
1	A	139	SER	O-C-N	5.01	129.26	123.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	192(B)	ARG	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	A	1391	0	1360	17	0
2	P	28	0	25	2	0
3	A	5	0	0	0	0
4	A	161	0	0	2	0
4	P	2	0	0	0	0
All	All	1587	0	1385	17	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 6.

All (17) 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:80:ILE:HD12	1:A:85:VAL:HG21	1.71	0.73
1:A:94:PHE:CE1	1:A:174:GLU:HG3	2.44	0.52
1:A:221(C):ALA:HA	1:A:224:ARG:HD2	1.90	0.52
1:A:171:TYR:CE1	2:P:2:PRO:HB3	2.48	0.49
1:A:91:ARG:HB3	1:A:104:ALA:HB2	1.95	0.48
1:A:48(B):ARG:HD2	4:A:355:HOH:O	2.15	0.47
1:A:171:TYR:CD1	2:P:2:PRO:HB3	2.51	0.46
1:A:94:PHE:HE1	1:A:174:GLU:HG3	1.81	0.46
1:A:30:GLU:HG2	1:A:31:TYR:N	2.29	0.46
1:A:65:ALA:O	1:A:87:THR:HA	2.15	0.46
1:A:191:CYS:HA	1:A:219:ASN:OD1	2.16	0.46
1:A:232:GLN:N	1:A:233:PRO:HD2	2.32	0.45
1:A:48(B):ARG:HG3	1:A:239:LEU:HD23	1.98	0.45
1:A:137:CYS:HA	1:A:159:CYS:HA	1.99	0.44
1:A:46:PHE:O	1:A:52:PHE:HA	2.21	0.41
1:A:129:GLU:HG3	4:A:364:HOH:O	2.21	0.40
1:A:138:ARG:O	1:A:157:TYR:HA	2.22	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	196/198 (99%)	188 (96%)	8 (4%)	0	100	100
2	P	2/5 (40%)	2 (100%)	0	0	100	100
All	All	198/203 (98%)	190 (96%)	8 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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	B2F	P	1	1,2	7,11,12	0.70	0	8,13,15	0.94	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	B2F	P	1	1,2	-	0/3/6/8	0/1/1/1

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.

5.5 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	0.66	0	6,6,6	0.44	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.

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.