



Full wwPDB X-ray Structure Validation Report ⓘ

May 8, 2019 – 04:56 PM EDT

PDB ID : 2W2X
Title : Complex of Rac2 and PLCg2 spPH Domain
Authors : Opaleye, O.; Bunney, T.D.; Roe, S.M.; Pearl, L.H.
Deposited on : 2008-11-04
Resolution : 2.30 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.0 (224370), CSD as540be (2019)
Xtriage (Phenix) : 1.13
EDS : rb-20031633
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20031633

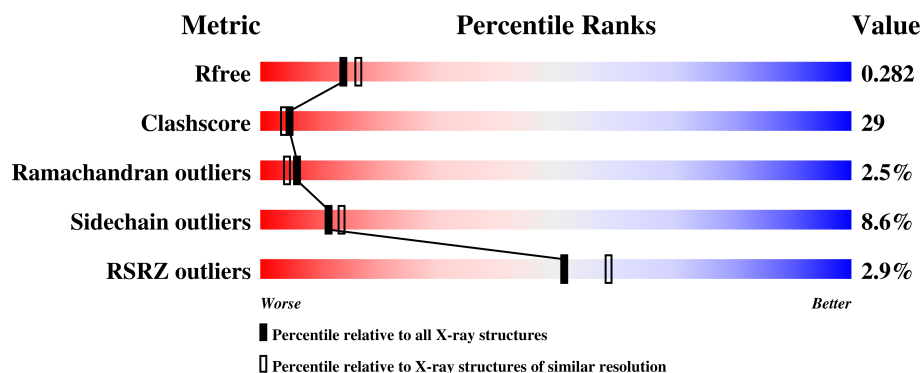
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
R_{free}	111664	4477 (2.30-2.30)
Clashscore	122126	5072 (2.30-2.30)
Ramachandran outliers	120053	5022 (2.30-2.30)
Sidechain outliers	120020	5021 (2.30-2.30)
RSRZ outliers	108989	4374 (2.30-2.30)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	185	<div> <div>3%</div> <div>53% 31% 10% . .</div> </div>
1	B	185	<div> <div>2%</div> <div>59% 25% 8% 8%</div> </div>
2	C	124	<div> <div>2%</div> <div>40% 36% 10% . 12%</div> </div>
3	D	124	<div> <div>3%</div> <div>55% 21% 6% . 15%</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4380 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 RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	177	Total	C	N	O	S	0	0	0
			1333	859	216	252	6			
1	B	170	Total	C	N	O	S	0	0	0
			1250	806	200	239	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	VAL	GLY	engineered mutation	UNP P15153
B	12	VAL	GLY	engineered mutation	UNP P15153

- Molecule 2 is a protein called 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	109	Total	C	N	O	S	0	0	0
			860	553	143	160	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	26	PHE	TYR	conflict	UNP P16885
C	88	ASP	TYR	conflict	UNP P16885

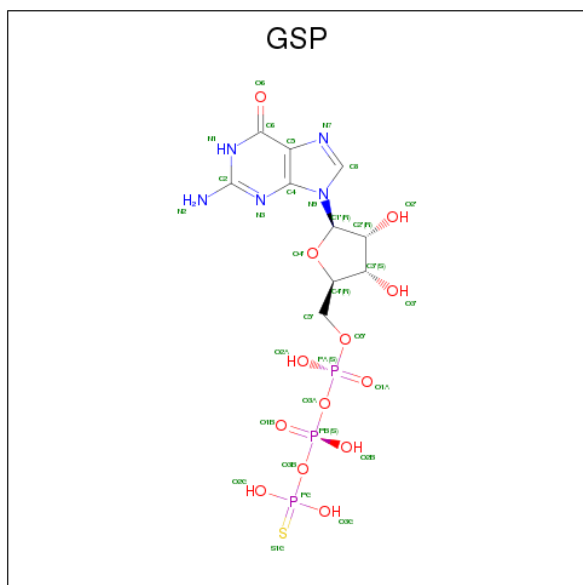
- Molecule 3 is a protein called 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	105	Total	C	N	O	S	0	0	0
			834	536	136	158	4			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	26	PHE	TYR	conflict	UNP P16885
D	88	ASP	TYR	conflict	UNP P16885
D	97	LYS	ARG	conflict	UNP P16885

- Molecule 4 is 5'-GUANOSINE-DIPHOSPHATE-MONOTHIOPHOSPHATE (three-letter code: GSP) (formula: C₁₀H₁₆N₅O₁₃P₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total 32	C 10	N 5	O 13	P 3	S 1	0	0
4	B	1	Total 32	C 10	N 5	O 13	P 3	S 1	0	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Mg	0	0
			1	1		
5	A	1	Total	Mg	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	12	Total	O	0	0
			12	12		

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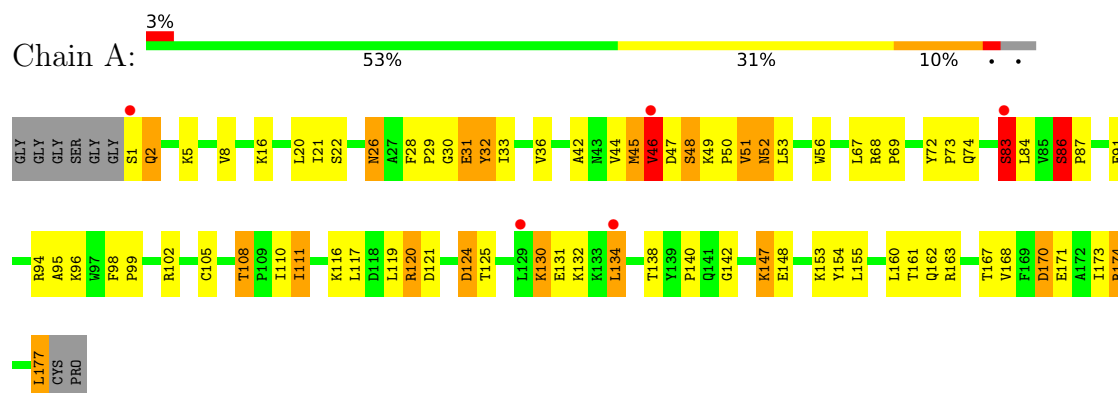
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	11	Total 11	O 11	0	0
6	C	6	Total 6	O 6	0	0
6	D	8	Total 8	O 8	0	0

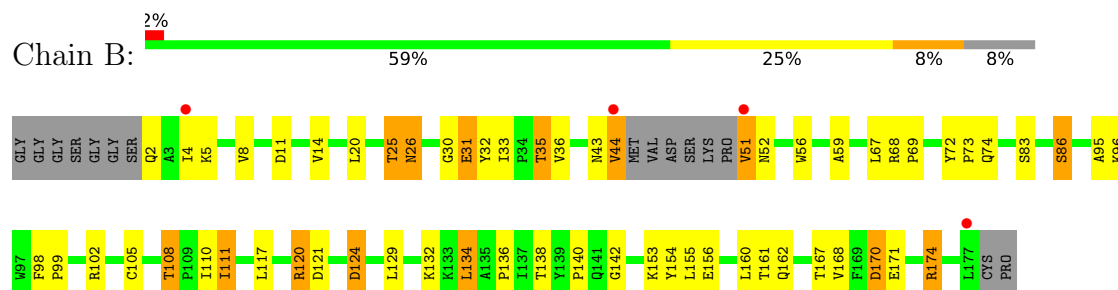
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

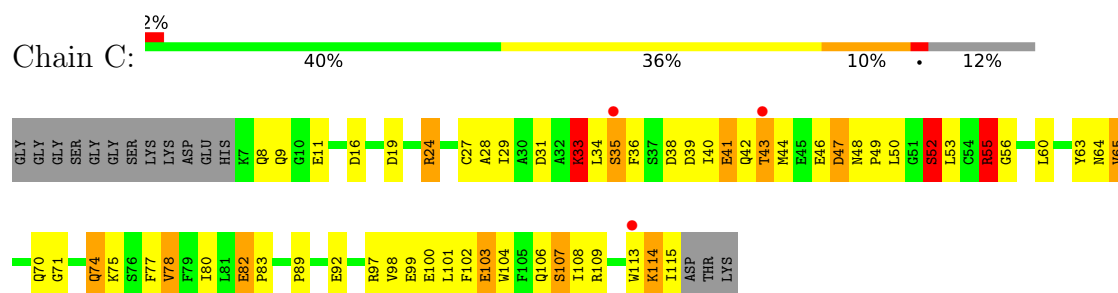
• Molecule 1: RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2



• Molecule 1: RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2

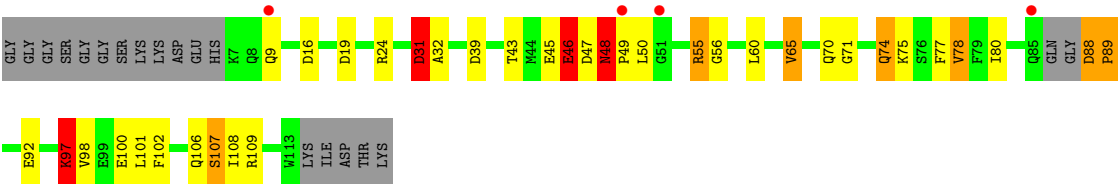


• Molecule 2: 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA-2



• Molecule 3: 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE GAMMA-2





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	131.57Å 84.46Å 74.20Å 90.00° 112.21° 90.00°	Depositor
Resolution (Å)	69.41 – 2.30 68.69 – 2.30	Depositor EDS
% Data completeness (in resolution range)	83.5 (69.41-2.30) 80.0 (68.69-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 2.29Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.234 , 0.294 0.222 , 0.282	Depositor DCC
R_{free} test set	1359 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	49.3	Xtriage
Anisotropy	0.818	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 66.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4380	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.11% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GSP, MG

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	9.42	18/1358 (1.3%)	1.85	29/1856 (1.6%)
1	B	7.19	7/1276 (0.5%)	1.58	13/1753 (0.7%)
2	C	8.69	13/875 (1.5%)	1.64	19/1178 (1.6%)
3	D	6.68	8/851 (0.9%)	1.33	11/1150 (1.0%)
All	All	8.16	46/4360 (1.1%)	1.64	72/5937 (1.2%)

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	2
1	B	0	2
All	All	0	4

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	83	SER	CA-CB	159.79	3.92	1.52
1	B	44	VAL	C-O	159.16	4.25	1.23
1	B	51	VAL	C-O	134.19	3.78	1.23
1	A	48	SER	C-O	129.12	3.68	1.23
1	B	35	THR	C-O	113.69	3.39	1.23
2	C	41	GLU	C-O	112.56	3.37	1.23
1	A	124	ASP	C-O	110.91	3.34	1.23
3	D	55	ARG	C-O	109.74	3.31	1.23
1	A	86	SER	CA-CB	109.54	3.17	1.52
1	A	52	ASN	C-O	109.12	3.30	1.23
2	C	52	SER	CA-CB	108.32	3.15	1.52
2	C	55	ARG	C-O	105.26	3.23	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	46	VAL	C-O	83.52	2.82	1.23
3	D	74	GLN	C-O	83.18	2.81	1.23
2	C	74	GLN	C-O	78.28	2.72	1.23
1	A	130	LYS	CA-CB	75.80	3.20	1.53
3	D	97	LYS	CA-CB	75.19	3.19	1.53
1	A	83	SER	C-O	74.85	2.65	1.23
2	C	35	SER	C-O	74.72	2.65	1.23
2	C	103	GLU	CA-CB	74.27	3.17	1.53
1	A	32	TYR	C-O	72.32	2.60	1.23
1	B	25	THR	C-O	70.49	2.57	1.23
2	C	43	THR	C-O	67.38	2.51	1.23
3	D	31	ASP	C-O	66.81	2.50	1.23
1	A	86	SER	C-O	64.80	2.46	1.23
1	A	46	VAL	CA-CB	63.68	2.88	1.54
2	C	107	SER	C-O	62.20	2.41	1.23
1	A	147	LYS	C-O	61.58	2.40	1.23
3	D	107	SER	C-O	60.61	2.38	1.23
3	D	88	ASP	C-O	58.27	2.34	1.23
1	B	170	ASP	C-O	54.97	2.27	1.23
1	A	170	ASP	C-O	51.20	2.20	1.23
2	C	82	GLU	C-O	42.84	2.04	1.23
2	C	33	LYS	C-O	37.82	1.95	1.23
1	A	86	SER	C-N	31.95	1.95	1.34
3	D	88	ASP	C-N	29.43	1.90	1.34
1	B	35	THR	C-N	27.37	1.97	1.34
1	A	52	ASN	C-N	27.23	1.96	1.34
1	B	25	THR	C-N	26.98	1.96	1.34
3	D	31	ASP	C-N	26.84	1.95	1.34
1	A	147	LYS	C-N	26.46	1.94	1.34
1	A	130	LYS	C-N	24.82	1.91	1.34
1	A	83	SER	C-N	23.41	1.88	1.34
2	C	103	GLU	C-N	23.24	1.87	1.34
2	C	33	LYS	C-N	22.97	1.86	1.34
2	C	52	SER	C-N	21.70	1.83	1.34

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	83	SER	CA-CB-OG	-34.16	18.98	111.20
1	B	51	VAL	CA-C-O	-31.50	53.94	120.10
1	B	44	VAL	CA-C-O	-31.48	53.99	120.10
1	A	86	SER	N-CA-CB	29.93	155.40	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	86	SER	CA-CB-OG	-20.70	55.30	111.20
3	D	88	ASP	CA-C-O	20.30	162.72	120.10
2	C	52	SER	CB-CA-C	20.28	148.62	110.10
2	C	52	SER	CA-CB-OG	-20.27	56.47	111.20
1	A	83	SER	CA-C-O	19.43	160.91	120.10
2	C	33	LYS	O-C-N	-19.34	91.75	122.70
1	A	147	LYS	CA-C-O	19.15	160.31	120.10
1	B	25	THR	CA-C-O	-18.39	81.48	120.10
1	A	147	LYS	O-C-N	-17.49	94.71	122.70
2	C	103	GLU	CA-CB-CG	-17.20	75.57	113.40
1	B	35	THR	O-C-N	16.65	149.34	122.70
1	B	25	THR	O-C-N	-16.43	96.41	122.70
3	D	88	ASP	O-C-N	-16.32	90.09	121.10
1	A	83	SER	O-C-N	-14.84	98.95	122.70
3	D	97	LYS	N-CA-CB	-13.28	86.69	110.60
1	A	102	ARG	NE-CZ-NH2	13.11	126.86	120.30
1	A	102	ARG	NE-CZ-NH1	-12.74	113.93	120.30
2	C	24	ARG	NE-CZ-NH1	-12.67	113.97	120.30
2	C	24	ARG	NE-CZ-NH2	12.46	126.53	120.30
1	A	174	ARG	NE-CZ-NH1	-12.32	114.14	120.30
1	A	46	VAL	CA-CB-CG1	-12.23	92.55	110.90
1	B	174	ARG	NE-CZ-NH2	-12.12	114.24	120.30
3	D	55	ARG	NE-CZ-NH2	12.01	126.31	120.30
1	B	174	ARG	NE-CZ-NH1	11.94	126.27	120.30
3	D	55	ARG	NE-CZ-NH1	-11.62	114.49	120.30
1	B	102	ARG	NE-CZ-NH2	-11.46	114.57	120.30
1	A	174	ARG	NE-CZ-NH2	11.38	125.99	120.30
2	C	55	ARG	NE-CZ-NH1	11.20	125.90	120.30
1	B	102	ARG	NE-CZ-NH1	11.17	125.88	120.30
1	B	35	THR	CA-C-N	-10.78	93.50	117.20
2	C	55	ARG	NE-CZ-NH2	-10.27	115.17	120.30
1	A	86	SER	CB-CA-C	-10.14	90.83	110.10
1	A	52	ASN	CA-C-N	-9.90	95.41	117.20
3	D	24	ARG	NE-CZ-NH2	-9.80	115.40	120.30
2	C	41	GLU	CA-C-O	9.47	139.98	120.10
1	A	52	ASN	O-C-N	-9.35	107.73	122.70
1	A	130	LYS	CB-CA-C	-9.16	92.09	110.40
2	C	52	SER	N-CA-CB	-8.87	97.20	110.50
1	A	86	SER	CA-C-O	8.46	137.88	120.10
1	A	83	SER	CA-C-N	-7.92	99.78	117.20
2	C	103	GLU	CA-C-N	-7.84	99.95	117.20
1	A	83	SER	N-CA-CB	7.68	122.03	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	86	SER	O-C-N	-7.65	106.57	121.10
3	D	24	ARG	NE-CZ-NH1	7.62	124.11	120.30
1	A	147	LYS	CA-C-N	-7.40	100.93	117.20
2	C	74	GLN	CA-C-O	7.36	135.55	120.10
2	C	107	SER	CA-C-O	-7.23	104.92	120.10
3	D	74	GLN	CA-C-O	7.16	135.13	120.10
3	D	107	SER	CA-C-O	-7.04	105.33	120.10
1	A	48	SER	CA-C-O	6.78	134.34	120.10
1	A	170	ASP	CA-C-O	6.78	134.33	120.10
1	A	174	ARG	CD-NE-CZ	6.61	132.85	123.60
2	C	103	GLU	CB-CA-C	6.56	123.51	110.40
1	A	102	ARG	CD-NE-CZ	6.53	132.74	123.60
2	C	33	LYS	CA-C-N	-6.50	102.89	117.20
1	B	35	THR	C-N-CA	-6.38	105.75	121.70
2	C	24	ARG	CD-NE-CZ	6.27	132.38	123.60
1	A	52	ASN	C-N-CA	-6.25	106.07	121.70
2	C	103	GLU	N-CA-CB	-5.88	100.01	110.60
1	B	174	ARG	CD-NE-CZ	5.87	131.82	123.60
3	D	97	LYS	CA-CB-CG	-5.68	100.91	113.40
1	B	102	ARG	CD-NE-CZ	5.66	131.53	123.60
2	C	55	ARG	CD-NE-CZ	5.57	131.39	123.60
3	D	55	ARG	CD-NE-CZ	5.48	131.27	123.60
2	C	103	GLU	C-N-CA	-5.47	108.04	121.70
1	A	83	SER	CB-CA-C	-5.35	99.93	110.10
1	A	130	LYS	O-C-N	-5.31	114.20	122.70
1	A	86	SER	CA-C-N	-5.21	102.50	117.10

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	30	GLY	Peptide
1	A	31	GLU	Peptide
1	B	30	GLY	Peptide
1	B	31	GLU	Peptide

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	1333	0	1282	91	0
1	B	1250	0	1164	54	0
2	C	860	0	783	60	0
3	D	834	0	760	41	0
4	A	32	0	12	3	0
4	B	32	0	12	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	12	0	0	0	0
6	B	11	0	0	0	0
6	C	6	0	0	0	0
6	D	8	0	0	0	0
All	All	4380	0	4013	243	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 29.

All (243) 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)
2:C:52:SER:C	2:C:53:LEU:N	1.84	1.30
2:C:33:LYS:C	2:C:34:LEU:N	1.86	1.28
1:A:83:SER:C	1:A:84:LEU:N	1.87	1.27
2:C:103:GLU:C	2:C:104:TRP:N	1.87	1.27
1:A:130:LYS:C	1:A:131:GLU:N	1.91	1.23
3:D:88:ASP:C	3:D:89:PRO:N	1.90	1.23
1:A:86:SER:C	1:A:87:PRO:N	1.95	1.20
1:B:25:THR:C	1:B:26:ASN:N	1.96	1.19
1:A:52:ASN:C	1:A:53:LEU:N	1.96	1.19
1:A:147:LYS:C	1:A:148:GLU:N	1.94	1.19
3:D:31:ASP:C	3:D:32:ALA:N	1.95	1.19
1:B:35:THR:C	1:B:36:VAL:N	1.97	1.18
2:C:82:GLU:C	2:C:83:PRO:N	2.01	1.14
1:A:124:ASP:C	1:A:125:THR:N	2.00	1.14
1:A:32:TYR:C	1:A:33:ILE:N	2.01	1.12
2:C:35:SER:C	2:C:36:PHE:N	2.05	1.10
1:B:51:VAL:C	1:B:52:ASN:N	2.05	1.08
1:A:120:ARG:HH21	1:A:120:ARG:HG2	1.20	1.07
2:C:33:LYS:O	2:C:33:LYS:C	1.95	1.04
1:B:120:ARG:HG2	1:B:120:ARG:HH21	1.23	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:74:GLN:C	2:C:75:LYS:N	2.09	1.04
2:C:107:SER:C	2:C:108:ILE:N	2.15	0.99
3:D:74:GLN:C	3:D:75:LYS:N	2.18	0.97
2:C:82:GLU:O	2:C:82:GLU:C	2.04	0.95
3:D:107:SER:C	3:D:108:ILE:N	2.22	0.93
1:B:31:GLU:HB3	1:B:32:TYR:HA	1.50	0.90
1:A:46:VAL:HA	1:A:47:ASP:N	1.87	0.88
1:A:87:PRO:O	1:A:91:GLU:HG3	1.79	0.82
1:B:120:ARG:HG2	1:B:120:ARG:NH2	1.97	0.80
2:C:55:ARG:C	2:C:56:GLY:N	2.36	0.79
3:D:55:ARG:C	3:D:56:GLY:N	2.35	0.79
1:A:170:ASP:O	1:A:170:ASP:C	2.20	0.78
2:C:11:GLU:OE1	2:C:24:ARG:HD2	1.84	0.78
1:A:1:SER:O	1:A:51:VAL:HA	1.85	0.77
1:A:46:VAL:O	1:A:177:LEU:HD11	1.86	0.75
1:B:120:ARG:HG3	1:B:121:ASP:OD1	1.86	0.75
1:A:120:ARG:HG2	1:A:120:ARG:NH2	1.95	0.75
1:A:120:ARG:HG3	1:A:121:ASP:OD1	1.87	0.74
2:C:63:TYR:HA	2:C:82:GLU:O	1.89	0.72
1:B:170:ASP:C	1:B:170:ASP:O	2.27	0.72
1:B:44:VAL:O	1:B:51:VAL:HG12	1.90	0.71
2:C:52:SER:HA	2:C:53:LEU:N	2.06	0.70
1:A:46:VAL:CA	1:A:47:ASP:N	2.56	0.69
1:B:35:THR:CA	1:B:36:VAL:N	2.57	0.67
2:C:29:ILE:HA	2:C:33:LYS:O	1.94	0.67
1:A:95:ALA:O	1:A:99:PRO:HG2	1.94	0.67
3:D:88:ASP:O	3:D:88:ASP:C	2.34	0.66
1:A:32:TYR:CA	1:A:33:ILE:N	2.58	0.66
2:C:52:SER:HB3	2:C:55:ARG:HH22	1.60	0.66
1:A:32:TYR:CD2	4:A:1178:GSP:H5'2	2.31	0.66
1:B:155:LEU:HD13	1:B:168:VAL:HA	1.77	0.65
1:B:5:LYS:HE3	1:B:56:TRP:CE2	2.32	0.65
1:B:95:ALA:O	1:B:99:PRO:HG2	1.94	0.65
1:A:170:ASP:O	1:A:174:ARG:N	2.27	0.65
1:A:52:ASN:CA	1:A:53:LEU:N	2.60	0.65
2:C:35:SER:CA	2:C:36:PHE:N	2.60	0.65
1:B:31:GLU:HB3	1:B:32:TYR:CA	2.25	0.64
2:C:34:LEU:HG	2:C:35:SER:O	1.97	0.64
1:A:155:LEU:HD13	1:A:168:VAL:HA	1.80	0.64
1:A:5:LYS:HE3	1:A:56:TRP:CE2	2.32	0.64
3:D:97:LYS:HA	3:D:98:VAL:N	2.13	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:31:GLU:HG2	1:B:33:ILE:HD12	1.80	0.64
1:A:83:SER:CA	1:A:84:LEU:N	2.62	0.63
2:C:103:GLU:CA	2:C:104:TRP:N	2.61	0.63
3:D:39:ASP:O	3:D:43:THR:HG23	1.98	0.63
2:C:27:CYS:HB3	2:C:35:SER:O	1.99	0.63
3:D:97:LYS:C	3:D:98:VAL:N	2.53	0.63
3:D:65:VAL:HG22	3:D:108:ILE:HG22	1.81	0.62
1:B:105:CYS:HB3	1:B:108:THR:HG23	1.81	0.62
1:A:32:TYR:HA	1:A:33:ILE:N	2.14	0.62
2:C:77:PHE:HB3	2:C:101:LEU:HD22	1.80	0.62
3:D:77:PHE:HB3	3:D:101:LEU:HD22	1.80	0.62
1:A:140:PRO:HG3	1:B:26:ASN:HB2	1.82	0.62
2:C:43:THR:N	2:C:44:MET:N	2.48	0.62
3:D:107:SER:C	3:D:107:SER:O	2.38	0.62
3:D:106:GLN:OE1	3:D:109:ARG:NH1	2.33	0.61
1:B:170:ASP:O	1:B:174:ARG:N	2.29	0.61
1:B:124:ASP:N	1:B:124:ASP:OD1	2.33	0.60
1:A:160:LEU:C	1:A:160:LEU:HD23	2.21	0.60
1:A:147:LYS:O	1:A:147:LYS:C	2.40	0.60
1:B:68:ARG:HB3	1:B:69:PRO:HD3	1.84	0.60
1:B:138:THR:OG1	1:B:140:PRO:HD2	2.02	0.59
1:A:105:CYS:HB3	1:A:108:THR:HG23	1.84	0.59
2:C:114:LYS:HA	2:C:115:ILE:CG1	2.33	0.59
1:A:47:ASP:OD1	1:A:174:ARG:NH2	2.36	0.59
2:C:103:GLU:C	2:C:104:TRP:CA	2.71	0.59
2:C:107:SER:O	2:C:107:SER:C	2.41	0.58
2:C:64:ASN:N	2:C:82:GLU:O	2.32	0.58
2:C:33:LYS:CA	2:C:34:LEU:N	2.64	0.58
1:B:2:GLN:O	1:B:51:VAL:O	2.21	0.58
1:B:160:LEU:C	1:B:160:LEU:HD23	2.24	0.58
1:A:68:ARG:HB3	1:A:69:PRO:HD3	1.86	0.58
1:A:140:PRO:CG	1:B:26:ASN:HB2	2.33	0.57
3:D:55:ARG:C	3:D:56:GLY:CA	2.72	0.57
1:B:170:ASP:C	1:B:171:GLU:N	2.57	0.57
1:A:49:LYS:N	1:A:50:PRO:HD3	2.20	0.57
3:D:46:GLU:HG3	3:D:48:ASN:CG	2.24	0.57
1:B:35:THR:C	1:B:36:VAL:CA	2.73	0.56
1:A:52:ASN:C	1:A:53:LEU:CA	2.74	0.56
3:D:71:GLY:HA2	3:D:78:VAL:HG13	1.86	0.56
1:A:1:SER:O	1:A:50:PRO:O	2.23	0.56
1:A:96:LYS:C	1:A:99:PRO:HD2	2.26	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:106:GLN:OE1	2:C:109:ARG:NH1	2.39	0.56
1:A:138:THR:OG1	1:A:140:PRO:HD2	2.05	0.56
1:A:147:LYS:CA	1:A:148:GLU:N	2.69	0.55
2:C:107:SER:CA	2:C:108:ILE:N	2.69	0.55
2:C:48:ASN:OD1	2:C:49:PRO:HD2	2.07	0.55
2:C:55:ARG:C	2:C:56:GLY:CA	2.75	0.55
3:D:80:ILE:HG12	3:D:92:GLU:HG2	1.88	0.55
1:A:86:SER:C	1:A:86:SER:O	2.46	0.54
1:A:96:LYS:O	1:A:99:PRO:HD2	2.07	0.54
3:D:107:SER:CA	3:D:108:ILE:N	2.69	0.54
1:A:32:TYR:CE2	4:A:1178:GSP:H5'2	2.42	0.54
1:B:96:LYS:C	1:B:99:PRO:HD2	2.29	0.54
2:C:71:GLY:HA2	2:C:78:VAL:HG13	1.90	0.54
2:C:63:TYR:CA	2:C:82:GLU:O	2.53	0.54
3:D:48:ASN:OD1	3:D:48:ASN:N	2.42	0.53
1:A:86:SER:C	1:A:86:SER:OG	2.47	0.53
3:D:71:GLY:HA2	3:D:78:VAL:CG1	2.39	0.53
1:A:170:ASP:C	1:A:171:GLU:N	2.62	0.53
3:D:65:VAL:HG22	3:D:108:ILE:CG2	2.38	0.53
1:B:8:VAL:HG21	1:B:20:LEU:HD21	1.89	0.53
2:C:35:SER:C	2:C:36:PHE:CA	2.76	0.52
1:B:35:THR:O	1:B:59:ALA:HB1	2.09	0.52
2:C:65:VAL:HG22	2:C:108:ILE:HG22	1.90	0.52
3:D:107:SER:C	3:D:108:ILE:CA	2.78	0.52
1:A:116:LYS:HB3	1:A:119:LEU:HD12	1.92	0.51
1:B:161:THR:O	1:B:162:GLN:HB2	2.09	0.51
1:B:142:GLY:HA3	1:B:154:TYR:CZ	2.46	0.51
2:C:114:LYS:N	2:C:115:ILE:HA	2.26	0.51
1:A:46:VAL:CB	1:A:46:VAL:CA	2.88	0.51
3:D:97:LYS:CA	3:D:98:VAL:N	2.73	0.51
1:A:142:GLY:HA3	1:A:154:TYR:CZ	2.46	0.51
1:A:86:SER:CA	1:A:87:PRO:N	2.71	0.51
1:B:51:VAL:O	1:B:51:VAL:HG13	2.11	0.51
2:C:114:LYS:HA	2:C:115:ILE:HG13	1.93	0.50
3:D:31:ASP:O	3:D:31:ASP:C	2.50	0.50
2:C:65:VAL:HG22	2:C:108:ILE:CG2	2.42	0.49
2:C:71:GLY:HA2	2:C:78:VAL:CG1	2.42	0.49
3:D:77:PHE:CE1	3:D:98:VAL:HB	2.47	0.49
1:B:132:LYS:O	1:B:134:LEU:HD22	2.12	0.49
2:C:40:ILE:O	2:C:42:GLN:N	2.45	0.49
1:A:46:VAL:C	1:A:47:ASP:HB2	2.32	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:97:ARG:HD2	2:C:100:GLU:OE1	2.13	0.49
1:A:46:VAL:C	1:A:47:ASP:N	2.66	0.49
2:C:43:THR:C	2:C:43:THR:O	2.51	0.49
1:A:73:PRO:O	1:A:74:GLN:HB2	2.12	0.49
1:B:73:PRO:O	1:B:74:GLN:HB2	2.12	0.49
1:B:96:LYS:O	1:B:99:PRO:HD2	2.12	0.49
2:C:77:PHE:CE1	2:C:98:VAL:HB	2.48	0.49
1:A:161:THR:O	1:A:162:GLN:HB2	2.11	0.49
1:A:45:MET:HE3	1:A:46:VAL:H	1.77	0.48
1:B:167:THR:O	1:B:171:GLU:N	2.46	0.48
1:A:45:MET:HE1	1:A:48:SER:C	2.33	0.48
1:A:69:PRO:HA	1:A:72:TYR:CD2	2.47	0.48
1:A:167:THR:O	1:A:171:GLU:N	2.47	0.48
2:C:107:SER:C	2:C:108:ILE:CA	2.81	0.48
2:C:113:TRP:O	2:C:114:LYS:CB	2.62	0.48
1:A:44:VAL:HG12	1:A:45:MET:O	2.12	0.48
1:A:52:ASN:HA	1:A:53:LEU:N	2.29	0.48
1:A:83:SER:CA	1:A:83:SER:OG	2.61	0.48
2:C:80:ILE:HG12	2:C:92:GLU:HG2	1.94	0.48
2:C:48:ASN:C	2:C:50:LEU:H	2.17	0.48
3:D:55:ARG:C	3:D:56:GLY:HA2	2.34	0.48
3:D:88:ASP:O	3:D:89:PRO:HA	2.13	0.48
1:A:21:ILE:HG21	1:A:29:PRO:HG3	1.96	0.48
1:B:69:PRO:HA	1:B:72:TYR:CD2	2.49	0.47
2:C:28:ALA:N	2:C:35:SER:O	2.47	0.47
3:D:65:VAL:CG2	3:D:108:ILE:HG22	2.44	0.47
1:A:94:ARG:NE	1:A:148:GLU:OE2	2.34	0.47
3:D:31:ASP:C	3:D:32:ALA:CA	2.81	0.47
1:B:51:VAL:CA	1:B:52:ASN:N	2.77	0.47
3:D:97:LYS:O	3:D:98:VAL:N	2.48	0.47
3:D:97:LYS:HB3	3:D:100:GLU:OE1	2.15	0.46
1:A:86:SER:CA	1:A:86:SER:OG	2.63	0.46
1:B:4:ILE:HG13	1:B:51:VAL:O	2.15	0.46
1:A:48:SER:O	1:A:49:LYS:CB	2.63	0.46
1:A:8:VAL:HG21	1:A:20:LEU:HD21	1.97	0.45
2:C:60:LEU:HD23	2:C:60:LEU:HA	1.70	0.45
1:A:153:LYS:HB2	1:A:153:LYS:HE2	1.63	0.45
1:A:1:SER:O	1:A:2:GLN:HB3	2.17	0.45
1:A:147:LYS:C	1:A:148:GLU:CA	2.82	0.45
1:B:134:LEU:HA	1:B:134:LEU:HD13	1.78	0.45
2:C:39:ASP:OD1	2:C:39:ASP:C	2.54	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:LEU:O	1:A:160:LEU:HD23	2.17	0.45
1:B:110:ILE:CG2	1:B:111:ILE:N	2.79	0.45
1:A:16:LYS:NZ	4:A:1178:GSP:O1B	2.46	0.45
2:C:82:GLU:CA	2:C:83:PRO:N	2.77	0.45
2:C:8:GLN:NE2	2:C:8:GLN:HA	2.31	0.45
3:D:88:ASP:CA	3:D:89:PRO:N	2.75	0.45
2:C:41:GLU:C	2:C:42:GLN:N	2.70	0.45
2:C:52:SER:CA	2:C:52:SER:OG	2.64	0.45
3:D:16:ASP:OD2	3:D:19:ASP:HB2	2.17	0.45
1:B:98:PHE:N	1:B:99:PRO:CD	2.80	0.45
1:B:25:THR:HA	1:B:25:THR:O	2.17	0.44
3:D:97:LYS:C	3:D:100:GLU:H	2.20	0.44
1:A:53:LEU:HD22	1:A:173:ILE:HD11	2.00	0.44
1:A:132:LYS:O	1:A:134:LEU:HD22	2.17	0.44
1:B:83:SER:HB3	1:B:86:SER:HB3	1.99	0.44
2:C:48:ASN:C	2:C:50:LEU:N	2.69	0.44
1:A:48:SER:C	1:A:49:LYS:N	2.71	0.44
3:D:45:GLU:O	3:D:46:GLU:C	2.56	0.44
1:A:110:ILE:CG2	1:A:111:ILE:N	2.80	0.44
1:A:120:ARG:CG	1:A:120:ARG:NH2	2.72	0.44
2:C:38:ASP:OD1	2:C:55:ARG:HD2	2.17	0.44
1:B:129:LEU:HD13	1:B:136:PRO:HD3	2.00	0.43
1:B:25:THR:O	1:B:25:THR:C	2.57	0.43
1:B:35:THR:HA	1:B:36:VAL:N	2.33	0.43
3:D:39:ASP:OD1	3:D:39:ASP:C	2.57	0.43
1:A:22:SER:O	1:A:26:ASN:HA	2.19	0.43
1:A:45:MET:CE	1:A:46:VAL:H	2.31	0.42
1:B:43:ASN:HA	1:B:44:VAL:O	2.19	0.42
1:B:51:VAL:C	1:B:52:ASN:CA	2.85	0.42
2:C:102:PHE:O	2:C:103:GLU:C	2.57	0.42
1:A:28:PHE:HA	1:A:29:PRO:HD3	1.74	0.42
1:A:134:LEU:HD13	1:A:134:LEU:HA	1.77	0.42
1:A:170:ASP:O	1:A:174:ARG:HG3	2.19	0.42
1:A:46:VAL:CG2	1:A:173:ILE:HD13	2.49	0.42
1:B:105:CYS:HB3	1:B:108:THR:CG2	2.48	0.42
1:B:110:ILE:HG22	1:B:111:ILE:N	2.34	0.42
2:C:16:ASP:OD2	2:C:19:ASP:HB2	2.19	0.42
2:C:55:ARG:C	2:C:56:GLY:HA2	2.39	0.42
2:C:99:GLU:H	2:C:99:GLU:CD	2.23	0.42
1:A:110:ILE:HG22	1:A:111:ILE:N	2.34	0.42
1:A:98:PHE:N	1:A:99:PRO:CD	2.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:60:LEU:HD23	3:D:60:LEU:HA	1.77	0.42
3:D:102:PHE:O	3:D:106:GLN:HG2	2.20	0.41
1:B:11:ASP:O	1:B:14:VAL:HG13	2.20	0.41
1:A:117:LEU:O	1:A:117:LEU:HD12	2.20	0.41
1:B:120:ARG:NH1	1:B:156:GLU:OE2	2.53	0.41
1:A:130:LYS:C	1:A:131:GLU:CA	2.83	0.41
3:D:32:ALA:O	3:D:60:LEU:HB2	2.21	0.41
1:B:153:LYS:HB2	1:B:153:LYS:HE2	1.68	0.41
1:A:124:ASP:C	1:A:125:THR:CA	2.86	0.41
1:A:45:MET:HE3	1:A:49:LYS:O	2.21	0.40
2:C:53:LEU:HA	2:C:53:LEU:HD23	1.84	0.40
1:A:45:MET:HA	1:A:45:MET:HE3	2.03	0.40
3:D:46:GLU:C	3:D:48:ASN:N	2.75	0.40
1:A:130:LYS:HA	1:A:134:LEU:O	2.21	0.40
1:A:47:ASP:O	1:A:48:SER:C	2.58	0.40
1:A:36:VAL:HG11	3:D:98:VAL:HG21	2.03	0.40
1:A:42:ALA:O	1:A:53:LEU:N	2.55	0.40
1:A:44:VAL:HG12	1:A:45:MET:N	2.36	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	165/185 (89%)	148 (90%)	14 (8%)	3 (2%)	9	8
1	B	163/185 (88%)	151 (93%)	11 (7%)	1 (1%)	27	33
2	C	93/124 (75%)	86 (92%)	4 (4%)	3 (3%)	4	2
3	D	93/124 (75%)	84 (90%)	3 (3%)	6 (6%)	1	0
All	All	514/618 (83%)	469 (91%)	32 (6%)	13 (2%)	6	4

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	31	GLU
2	C	47	ASP
2	C	114	LYS
3	D	50	LEU
1	B	26	ASN
3	D	49	PRO
3	D	46	GLU
1	A	26	ASN
3	D	89	PRO
1	A	2	GLN
2	C	89	PRO
3	D	31	ASP
3	D	48	ASN

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	141/159 (89%)	129 (92%)	12 (8%)	12	14
1	B	127/159 (80%)	119 (94%)	8 (6%)	20	26
2	C	87/109 (80%)	77 (88%)	10 (12%)	6	6
3	D	86/109 (79%)	78 (91%)	8 (9%)	10	11
All	All	441/536 (82%)	403 (91%)	38 (9%)	11	14

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	MET
1	A	46	VAL
1	A	51	VAL
1	A	67	LEU
1	A	83	SER
1	A	86	SER
1	A	108	THR
1	A	111	ILE
1	A	120	ARG

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Mol	Chain	Res	Type
1	A	134	LEU
1	A	163	ARG
1	A	177	LEU
1	B	67	LEU
1	B	86	SER
1	B	108	THR
1	B	111	ILE
1	B	117	LEU
1	B	120	ARG
1	B	124	ASP
1	B	134	LEU
2	C	9	GLN
2	C	31	ASP
2	C	33	LYS
2	C	46	GLU
2	C	47	ASP
2	C	52	SER
2	C	55	ARG
2	C	65	VAL
2	C	70	GLN
2	C	78	VAL
3	D	9	GLN
3	D	46	GLU
3	D	47	ASP
3	D	48	ASN
3	D	65	VAL
3	D	70	GLN
3	D	78	VAL
3	D	97	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	GLN
1	A	26	ASN
1	A	162	GLN
1	B	26	ASN
1	B	162	GLN
2	C	8	GLN
2	C	9	GLN
2	C	70	GLN
3	D	8	GLN

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Mol	Chain	Res	Type
3	D	9	GLN
3	D	70	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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
4	GSP	A	1178	5	25,34,34	2.28	2 (8%)	26,54,54	2.14	6 (23%)
4	GSP	B	1178	5	25,34,34	2.36	3 (12%)	26,54,54	1.93	7 (26%)

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
4	GSP	A	1178	5	-	0/17/38/38	0/3/3/3
4	GSP	B	1178	5	-	0/17/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1178	GSP	PG-S1G	-10.55	1.70	1.90
4	A	1178	GSP	PG-S1G	-10.08	1.71	1.90
4	B	1178	GSP	C2-N1	2.01	1.38	1.35
4	A	1178	GSP	C6-N1	3.29	1.38	1.33
4	B	1178	GSP	C6-N1	3.33	1.38	1.33

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1178	GSP	N3-C2-N1	-6.04	119.08	127.25
4	B	1178	GSP	N3-C2-N1	-5.31	120.07	127.25
4	A	1178	GSP	PA-O3A-PB	-4.36	118.73	132.57
4	B	1178	GSP	C5-C6-N1	-2.90	119.43	123.47
4	A	1178	GSP	C5-C6-N1	-2.67	119.75	123.47
4	B	1178	GSP	PA-O3A-PB	-2.61	124.27	132.57
4	A	1178	GSP	C6-C5-C4	-2.04	118.83	120.79
4	B	1178	GSP	N2-C2-N1	2.04	120.45	117.25
4	B	1178	GSP	O3G-PG-O3B	2.15	112.90	104.54
4	B	1178	GSP	C6-N1-C2	2.71	119.92	116.06
4	A	1178	GSP	C6-N1-C2	3.39	120.89	116.06
4	B	1178	GSP	C2-N3-C4	4.42	120.40	115.36
4	A	1178	GSP	C2-N3-C4	4.48	120.48	115.36

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
4	A	1178	GSP	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	10
2	C	10
3	D	6
1	B	4

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	C	43:THR	C	44:MET	N	2.93
1	A	48:SER	C	49:LYS	N	2.71
1	C	41:GLU	C	42:GLN	N	2.70
1	A	46:VAL	C	47:ASP	N	2.66
1	A	170:ASP	C	171:GLU	N	2.62
1	B	170:ASP	C	171:GLU	N	2.57
1	D	97:LYS	C	98:VAL	N	2.53
1	C	55:ARG	C	56:GLY	N	2.36
1	D	55:ARG	C	56:GLY	N	2.35
1	D	107:SER	C	108:ILE	N	2.22
1	D	74:GLN	C	75:LYS	N	2.18
1	C	107:SER	C	108:ILE	N	2.15
1	C	74:GLN	C	75:LYS	N	2.09
1	B	51:VAL	C	52:ASN	N	2.05
1	C	35:SER	C	36:PHE	N	2.05
1	A	32:TYR	C	33:ILE	N	2.01
1	C	82:GLU	C	83:PRO	N	2.01
1	A	124:ASP	C	125:THR	N	2.00
1	B	35:THR	C	36:VAL	N	1.97
1	A	52:ASN	C	53:LEU	N	1.96
1	B	25:THR	C	26:ASN	N	1.96
1	A	86:SER	C	87:PRO	N	1.95
1	D	31:ASP	C	32:ALA	N	1.95
1	A	147:LYS	C	148:GLU	N	1.94
1	A	130:LYS	C	131:GLU	N	1.91
1	D	88:ASP	C	89:PRO	N	1.90
1	A	83:SER	C	84:LEU	N	1.87
1	C	103:GLU	C	104:TRP	N	1.87
1	C	33:LYS	C	34:LEU	N	1.86
1	C	52:SER	C	53:LEU	N	1.84

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2			OWAB(Å ²)	Q < 0.9
1	A	177/185 (95%)	0.30	5 (2%)	53	60	34, 58, 102, 131	8 (4%)
1	B	170/185 (91%)	0.21	4 (2%)	59	66	41, 63, 105, 163	2 (1%)
2	C	109/124 (87%)	0.24	3 (2%)	53	60	44, 63, 96, 109	0
3	D	105/124 (84%)	0.25	4 (3%)	40	47	34, 60, 96, 131	0
All	All	561/618 (90%)	0.25	16 (2%)	51	59	34, 62, 104, 163	10 (1%)

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	51	VAL	8.3
1	A	46	VAL	5.1
1	A	1	SER	4.6
2	C	43	THR	4.2
2	C	113	TRP	3.1
3	D	85	GLN	3.1
1	A	129	LEU	2.9
1	B	177	LEU	2.7
1	A	83	SER	2.7
1	A	134	LEU	2.3
3	D	49	PRO	2.3
3	D	51	GLY	2.3
1	B	44	VAL	2.2
2	C	35	SER	2.2
3	D	9	GLN	2.1
1	B	4	ILE	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	MG	B	1179	1/1	0.89	0.19	46,46,46,46	0
5	MG	A	1179	1/1	0.92	0.13	47,47,47,47	0
4	GSP	A	1178	32/32	0.97	0.14	33,58,91,107	0
4	GSP	B	1178	32/32	0.98	0.14	32,60,83,120	4

6.5 Other polymers [i](#)

There are no such residues in this entry.