



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 05:14 AM UTC

PDB ID : 3D3X / pdb_00003d3x
Title : Crystal structure of botulinum neurotoxin serotype E catalytic domain in complex with SNAP-25 substrate peptide
Authors : Agarwal, R.; Swaminathan, S.
Deposited on : 2008-05-13
Resolution : 2.25 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) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

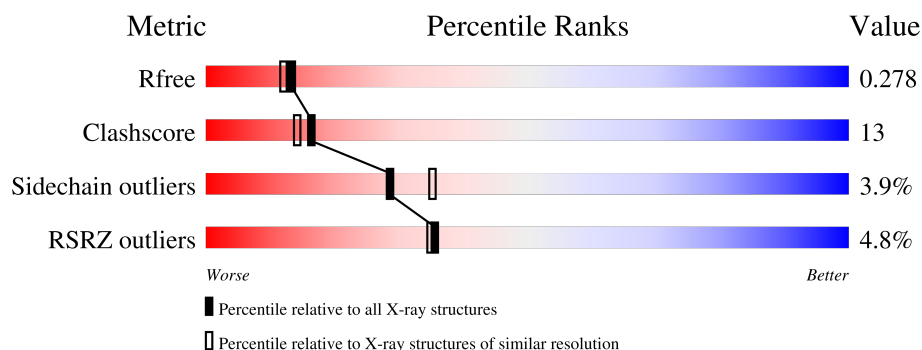
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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}	180053	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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 $\leq 5\%$. 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	427	 3% 69% 23% • 5%
1	B	427	 5% 67% 25% • 5%
2	C	5	 40% 20% 40% 40%
2	D	5	 40% 60%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6883 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 Type E botulinum toxin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	407	Total	C	N	O	S	0	0	0
			3263	2086	545	624	8			
1	B	407	Total	C	N	O	S	0	0	0
			3265	2085	548	625	7			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	422	HIS	-	expression tag	UNP Q9K395
A	423	HIS	-	expression tag	UNP Q9K395
A	424	HIS	-	expression tag	UNP Q9K395
A	425	HIS	-	expression tag	UNP Q9K395
A	426	HIS	-	expression tag	UNP Q9K395
A	427	HIS	-	expression tag	UNP Q9K395
B	422	HIS	-	expression tag	UNP Q9K395
B	423	HIS	-	expression tag	UNP Q9K395
B	424	HIS	-	expression tag	UNP Q9K395
B	425	HIS	-	expression tag	UNP Q9K395
B	426	HIS	-	expression tag	UNP Q9K395
B	427	HIS	-	expression tag	UNP Q9K395

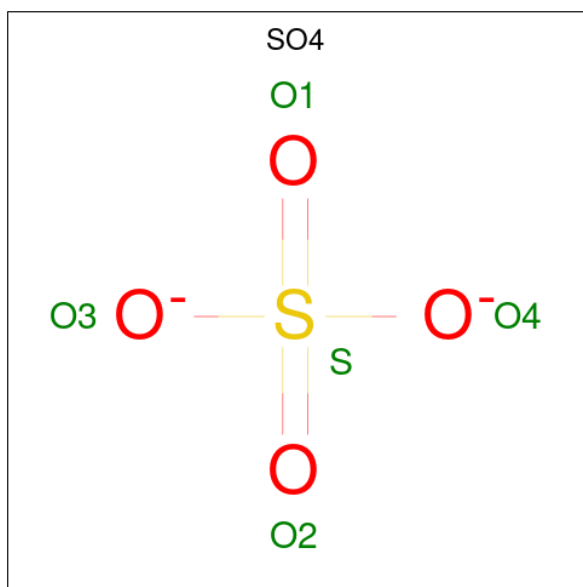
- Molecule 2 is a protein called SNAP-25 substrate peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	S	0	0	0
			21	14	3	3	1			
2	D	5	Total	C	N	O	S	0	1	1
			41	24	8	8	1			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

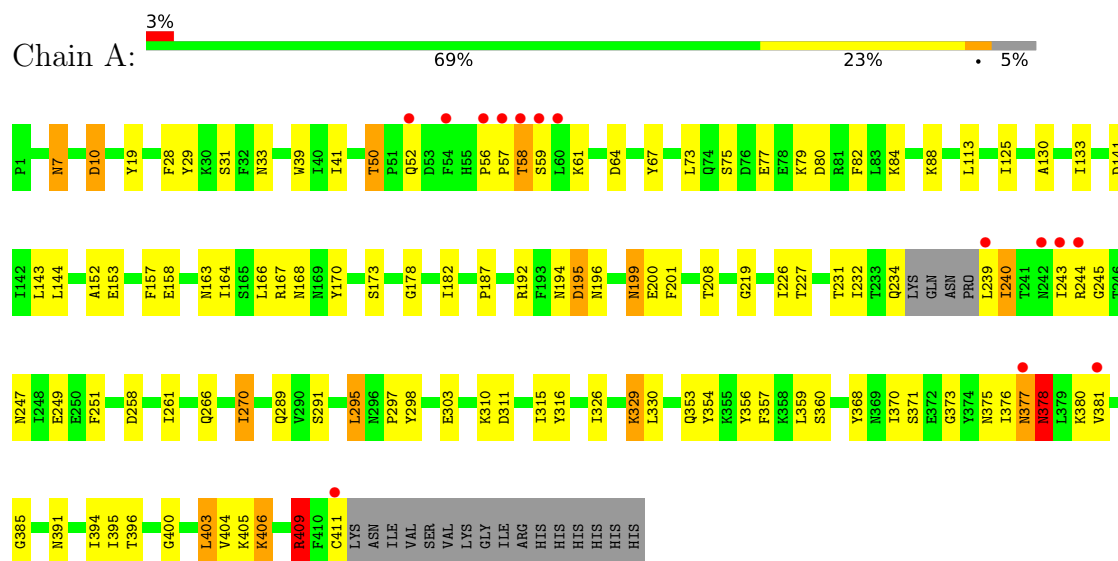
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	148	Total 148	O 148	0	0
5	B	102	Total 102	O 102	0	0
5	D	1	Total 1	O 1	0	0

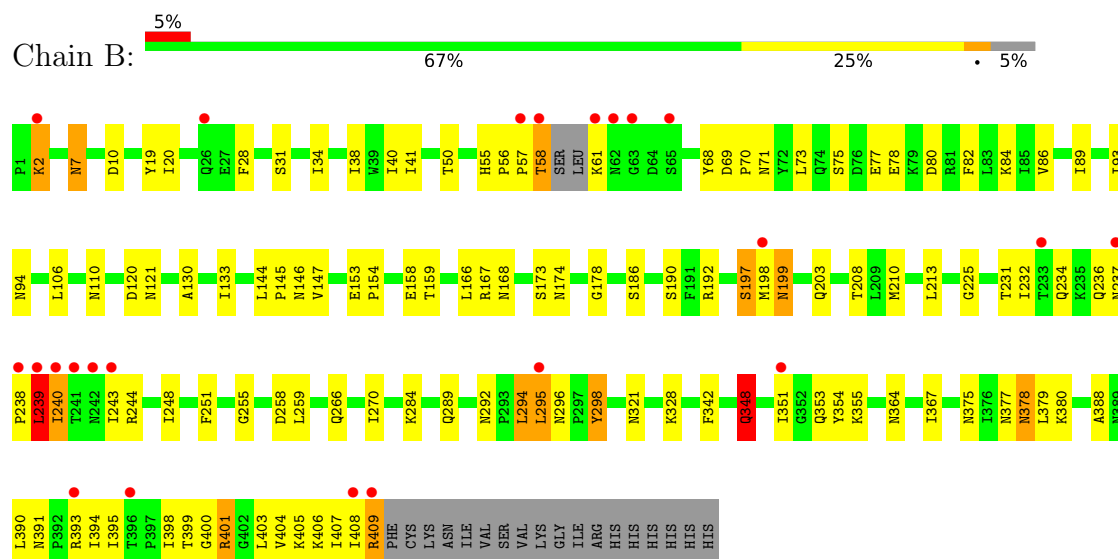
3 Residue-property plots [i](#)

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 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.

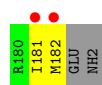
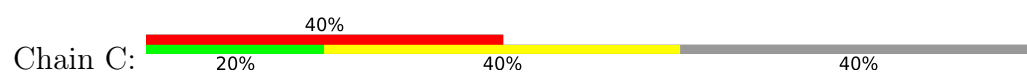
• Molecule 1: Type E botulinum toxin



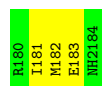
• Molecule 1: Type E botulinum toxin



• Molecule 2: SNAP-25 substrate peptide



- Molecule 2: SNAP-25 substrate peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	89.41Å 144.74Å 83.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.48 – 2.25 33.48 – 2.25	Depositor EDS
% Data completeness (in resolution range)	91.6 (33.48-2.25) 91.7 (33.48-2.25)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.66 (at 2.24Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.235 , 0.288 (Not available) , 0.278	Depositor DCC
R_{free} test set	1426 reflections (2.90%)	wwPDB-VP
Wilson B-factor (Å ²)	31.8	Xtriage
Anisotropy	0.741	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 32.6	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	0.93	EDS
Total number of atoms	6883	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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: SO4, ZN, NH2

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	0.52	0/3335	1.04	19/4516 (0.4%)
1	B	0.49	0/3337	0.99	17/4519 (0.4%)
2	C	0.68	0/20	1.05	0/25
2	D	0.73	0/43	0.91	0/53
All	All	0.51	0/6735	1.02	36/9113 (0.4%)

There are no bond length outliers.

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	401	ARG	N-CA-C	-11.60	98.36	111.82
1	B	240	ILE	N-CA-C	-10.98	102.38	113.47
1	A	56	PRO	N-CA-C	9.04	121.73	110.70
1	B	197	SER	N-CA-C	-7.84	103.78	112.72
1	A	409	ARG	N-CA-C	7.61	127.01	110.80
1	A	7	ASN	N-CA-C	-7.30	98.35	109.95
1	A	240	ILE	N-CA-C	-7.12	105.79	112.83
1	A	378	ASN	N-CA-C	-6.88	96.15	110.80
1	B	7	ASN	N-CA-C	-6.72	98.76	109.59
1	A	303	GLU	N-CA-C	-6.69	103.92	111.07
1	B	158	GLU	N-CA-C	6.35	119.68	110.28
1	A	10	ASP	N-CA-C	-6.33	100.37	109.48
1	A	330	LEU	N-CA-C	6.15	117.98	111.28
1	A	232	ILE	N-CA-C	-6.14	99.56	108.71
1	A	371	SER	N-CA-C	6.06	120.40	112.89
1	B	239	LEU	N-CA-C	-6.05	105.15	113.56
1	A	57	PRO	N-CA-C	-5.99	100.14	112.47
1	A	195	ASP	N-CA-C	-5.93	100.63	109.94
1	A	58	THR	N-CA-C	5.83	123.22	110.80
1	B	348	GLN	N-CA-C	-5.80	106.36	113.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	270	ILE	N-CA-C	-5.70	105.17	110.53
1	B	398	ILE	N-CA-C	-5.61	100.99	108.96
1	B	377	ASN	CB-CA-C	-5.61	110.09	116.54
1	A	152	ALA	N-CA-C	5.58	118.11	110.24
1	A	158	GLU	N-CA-C	5.50	118.26	110.50
1	A	391	ASN	CA-C-N	5.49	125.16	119.56
1	A	391	ASN	C-N-CA	5.49	125.16	119.56
1	B	94	ASN	N-CA-C	5.45	116.90	111.07
1	B	146	ASN	N-CA-C	-5.26	106.92	113.55
1	B	121	ASN	N-CA-C	5.24	119.43	113.19
1	B	186	SER	CA-C-N	5.21	125.02	119.28
1	B	186	SER	C-N-CA	5.21	125.02	119.28
1	B	259	LEU	N-CA-C	-5.18	106.81	113.23
1	A	199	ASN	N-CA-C	-5.15	103.24	110.50
1	B	110	ASN	N-CA-C	5.08	115.82	109.57
1	B	399	THR	N-CA-C	5.05	119.47	112.45

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	3263	0	3216	87	0
1	B	3265	0	3220	86	0
2	C	21	0	21	3	0
2	D	41	0	40	3	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	30	0	0	1	0
4	B	10	0	0	0	0
5	A	148	0	0	4	0
5	B	102	0	0	4	0
5	D	1	0	0	0	0
All	All	6883	0	6497	171	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 13.

All (171) 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:B:237:ASN:H	1:B:238:PRO:HD2	1.31	0.95
1:A:409:ARG:HH11	1:A:409:ARG:HG2	1.36	0.90
1:B:2:LYS:HD3	1:B:2:LYS:H	1.37	0.90
1:B:56:PRO:HG3	1:B:68:TYR:HB2	1.57	0.85
1:A:58:THR:HG23	1:A:59:SER:H	1.44	0.82
1:B:153:GLU:HB2	1:B:154:PRO:HD2	1.63	0.79
1:B:408:ILE:C	1:B:409:ARG:HD2	2.09	0.78
1:A:409:ARG:HG2	1:A:409:ARG:NH1	1.97	0.75
1:B:237:ASN:N	1:B:238:PRO:HD2	2.02	0.73
1:A:404:VAL:HG23	1:A:405:LYS:H	1.51	0.73
1:B:130:ALA:HB2	1:B:144:LEU:HD23	1.70	0.73
1:A:377:ASN:HB2	1:A:380:LYS:HD3	1.74	0.70
1:B:353:GLN:HE22	2:D:182:MET:HE3	1.57	0.69
1:B:353:GLN:NE2	2:D:182:MET:HE3	2.07	0.69
1:A:58:THR:HG23	1:A:59:SER:N	2.07	0.68
1:B:409:ARG:CA	1:B:409:ARG:HH11	2.07	0.68
1:B:409:ARG:HH11	1:B:409:ARG:N	1.92	0.67
1:A:226:ILE:HB	1:A:270:ILE:HD13	1.78	0.66
1:B:243:ILE:O	1:B:244:ARG:HG2	1.96	0.65
1:B:58:THR:OG1	1:B:61:LYS:HB2	1.99	0.63
1:A:258:ASP:HA	1:A:261:ILE:HD12	1.80	0.61
1:B:237:ASN:C	1:B:237:ASN:HD22	2.08	0.61
1:A:7:ASN:HB2	1:A:10:ASP:OD1	2.01	0.60
1:A:409:ARG:HH11	1:A:409:ARG:CG	2.10	0.60
1:B:31:SER:OG	1:B:41:ILE:HG12	2.02	0.60
1:B:106:LEU:HD11	1:B:213:LEU:HB3	1.84	0.60
1:A:231:THR:HG22	1:A:247:ASN:HD22	1.65	0.60
1:A:295:LEU:HD22	5:A:981:HOH:O	2.03	0.59
1:B:295:LEU:H	1:B:295:LEU:HD23	1.67	0.59
1:B:248:ILE:HA	1:B:251:PHE:HD1	1.66	0.59
1:A:130:ALA:HB2	1:A:144:LEU:HD23	1.85	0.58
1:B:2:LYS:H	1:B:2:LYS:CD	2.14	0.58
1:B:210:MET:HE1	1:B:342:PHE:CE2	2.38	0.58
1:A:243:ILE:O	1:A:245:GLY:N	2.37	0.58
1:A:406:LYS:HB2	1:A:406:LYS:NZ	2.19	0.57
1:B:231:THR:O	1:B:232:ILE:HD13	2.05	0.56
1:B:239:LEU:HD13	1:B:239:LEU:N	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:409:ARG:N	1:B:409:ARG:NH1	2.54	0.56
1:B:55:HIS:ND1	1:B:70:PRO:HG2	2.20	0.56
1:A:404:VAL:HG23	1:A:405:LYS:N	2.20	0.56
1:B:197:SER:O	1:B:198:MET:HG2	2.05	0.55
1:A:50:THR:HG22	1:A:52:GLN:H	1.72	0.55
1:A:73:LEU:HD21	1:A:82:PHE:HB2	1.89	0.55
1:A:163:ASN:ND2	1:A:219:GLY:HA3	2.22	0.54
1:B:7:ASN:HB2	1:B:10:ASP:OD1	2.07	0.54
1:B:401:ARG:O	1:B:405:LYS:HG3	2.08	0.54
1:B:400:GLY:O	1:B:404:VAL:HG23	2.09	0.53
1:A:182:ILE:HD12	1:A:182:ILE:N	2.24	0.52
1:B:409:ARG:NH1	1:B:409:ARG:H	2.07	0.52
1:A:244:ARG:O	1:A:244:ARG:HG2	2.08	0.52
1:A:311:ASP:OD2	1:A:315:ILE:HB	2.09	0.52
1:B:19:TYR:HB3	1:B:28:PHE:HB3	1.91	0.52
1:B:364:ASN:ND2	1:B:367:ILE:HG13	2.25	0.51
1:A:394:ILE:HG13	1:A:395:ILE:HG12	1.92	0.51
1:B:375:ASN:HB3	1:B:380:LYS:HA	1.91	0.51
1:A:231:THR:HG22	1:A:247:ASN:ND2	2.26	0.51
1:A:163:ASN:HD21	1:A:219:GLY:HA3	1.76	0.51
1:B:239:LEU:N	1:B:239:LEU:CD1	2.74	0.51
1:A:153:GLU:HG3	5:A:907:HOH:O	2.12	0.50
1:A:251:PHE:CE2	1:A:261:ILE:HD13	2.46	0.50
1:B:409:ARG:HH11	1:B:409:ARG:HA	1.74	0.50
1:B:61:LYS:N	1:B:61:LYS:HD3	2.27	0.50
1:B:238:PRO:C	1:B:239:LEU:HD13	2.36	0.50
1:A:33:ASN:HB2	1:A:39:TRP:CH2	2.46	0.50
1:A:196:ASN:HB2	4:A:897:SO4:O2	2.12	0.50
1:B:2:LYS:HD3	1:B:2:LYS:N	2.16	0.50
1:B:173:SER:HA	1:B:178:GLY:HA2	1.94	0.50
1:B:406:LYS:C	1:B:408:ILE:H	2.19	0.50
1:B:120:ASP:OD1	1:B:284:LYS:HE2	2.12	0.49
1:B:34:ILE:HD12	1:B:40:ILE:HD11	1.95	0.49
1:B:292:ASN:O	1:B:295:LEU:HD23	2.13	0.49
1:B:405:LYS:HB3	1:B:405:LYS:NZ	2.28	0.49
1:A:208:THR:HG23	2:C:181:ILE:HG12	1.94	0.49
1:B:407:ILE:HG22	1:B:407:ILE:O	2.14	0.48
1:A:58:THR:CG2	1:A:59:SER:H	2.22	0.48
1:A:289:GLN:HG3	1:A:291:SER:H	1.79	0.48
1:A:297:PRO:HG2	1:B:298:TYR:CD2	2.49	0.48
1:B:394:ILE:HG13	1:B:395:ILE:HG13	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:409:ARG:HD2	1:B:409:ARG:N	2.28	0.48
1:A:125:ILE:HD11	1:B:294:LEU:HD13	1.96	0.48
1:A:227:THR:HB	1:A:249:GLU:HB2	1.96	0.48
1:B:167:ARG:O	1:B:168:ASN:HB2	2.14	0.48
1:A:19:TYR:HB3	1:A:28:PHE:HB3	1.96	0.48
1:A:194:ASN:ND2	1:A:200:GLU:HG2	2.29	0.47
1:A:378:ASN:H	1:A:380:LYS:HG2	1.79	0.47
1:A:409:ARG:HA	1:A:409:ARG:HD3	1.41	0.47
1:A:234:GLN:O	1:A:239:LEU:HD23	2.14	0.47
1:A:357:PHE:HB3	1:A:395:ILE:HD12	1.95	0.47
1:A:240:ILE:HG22	1:A:240:ILE:O	2.15	0.47
1:A:251:PHE:HE2	1:A:261:ILE:HD13	1.79	0.47
1:B:238:PRO:O	1:B:239:LEU:HB2	2.15	0.47
1:A:80:ASP:O	1:A:84:LYS:HG2	2.15	0.47
1:A:266:GLN:O	1:A:270:ILE:HG12	2.15	0.47
1:A:360:SER:OG	1:A:396:THR:HG23	2.14	0.47
1:B:82:PHE:O	1:B:86:VAL:HG23	2.15	0.47
1:B:400:GLY:HA2	1:B:403:LEU:HB3	1.97	0.47
1:B:234:GLN:C	1:B:236:GLN:H	2.24	0.46
1:A:88:LYS:HG3	1:A:370:ILE:HD11	1.98	0.46
1:A:167:ARG:O	1:A:168:ASN:HB2	2.14	0.46
1:A:375:ASN:HD22	1:A:385:GLY:HA3	1.80	0.46
1:A:378:ASN:O	1:A:381:VAL:HG22	2.15	0.46
1:B:255:GLY:O	1:B:258:ASP:HB2	2.16	0.46
1:B:238:PRO:O	1:B:240:ILE:HG13	2.16	0.46
1:A:377:ASN:CB	1:A:380:LYS:HD3	2.45	0.46
1:B:403:LEU:O	1:B:407:ILE:HG13	2.16	0.46
1:A:368:TYR:HA	1:A:373:GLY:O	2.16	0.45
1:A:406:LYS:HB2	1:A:406:LYS:HZ3	1.82	0.45
1:A:166:LEU:HD12	1:A:170:TYR:HD2	1.82	0.45
1:A:33:ASN:HB2	1:A:39:TRP:CZ2	2.52	0.45
1:A:173:SER:HA	1:A:178:GLY:HA2	1.99	0.45
1:A:192:ARG:HA	1:A:201:PHE:O	2.17	0.45
1:B:174:ASN:HB3	1:B:225:GLY:HA2	1.99	0.44
1:B:38:ILE:CD1	1:B:147:VAL:HB	2.47	0.44
1:B:355:LYS:HA	5:B:938:HOH:O	2.17	0.44
1:A:326:ILE:HA	1:A:329:LYS:HE3	1.99	0.44
1:B:89:ILE:O	1:B:93:ILE:HG13	2.17	0.44
1:A:400:GLY:O	1:A:403:LEU:HB2	2.17	0.44
1:A:67:TYR:HB2	1:A:157:PHE:CZ	2.53	0.44
1:A:133:ILE:HG21	1:A:143:LEU:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:TYR:HE1	2:C:182:MET:SD	2.41	0.44
1:B:190:SER:OG	1:B:203:GLN:HB3	2.18	0.44
1:A:61:LYS:HB3	1:A:64:ASP:OD1	2.17	0.44
1:B:388:ALA:HB1	1:B:395:ILE:HD11	1.99	0.44
1:A:130:ALA:HB2	1:A:144:LEU:CD2	2.47	0.44
1:B:210:MET:HE1	1:B:342:PHE:CD2	2.52	0.44
1:B:75:SER:OG	1:B:78:GLU:HG3	2.17	0.43
1:B:192:ARG:O	1:B:354:TYR:HB3	2.18	0.43
1:B:73:LEU:HD21	1:B:82:PHE:HB2	1.99	0.43
1:A:19:TYR:HA	1:A:29:TYR:O	2.18	0.43
1:B:153:GLU:HB2	1:B:154:PRO:CD	2.43	0.43
1:B:56:PRO:HA	1:B:57:PRO:HD3	1.76	0.43
1:B:348:GLN:O	1:B:348:GLN:HG3	2.16	0.43
1:B:378:ASN:ND2	5:B:920:HOH:O	2.51	0.43
1:A:381:VAL:O	1:A:381:VAL:HG23	2.19	0.43
1:B:80:ASP:OD1	1:B:84:LYS:HE3	2.19	0.43
1:B:390:LEU:O	1:B:390:LEU:HD23	2.19	0.43
1:A:226:ILE:CB	1:A:270:ILE:HD13	2.47	0.42
1:A:113:LEU:HD22	1:A:125:ILE:HG12	2.00	0.42
1:A:310:LYS:HD3	1:A:316:TYR:CE1	2.54	0.42
1:B:289:GLN:HA	5:B:941:HOH:O	2.19	0.42
1:B:237:ASN:C	1:B:237:ASN:ND2	2.75	0.42
1:A:376:ILE:O	1:A:377:ASN:C	2.62	0.42
1:B:266:GLN:O	1:B:270:ILE:HG12	2.19	0.42
1:B:69:ASP:OD1	1:B:71:ASN:HB2	2.19	0.42
1:B:409:ARG:HH11	1:B:409:ARG:CG	2.32	0.42
1:A:77:GLU:O	1:A:77:GLU:OE1	2.37	0.42
1:A:164:ILE:HD11	1:A:182:ILE:HD11	2.02	0.42
1:B:159:THR:HG21	1:B:208:THR:HG22	2.00	0.42
1:A:375:ASN:HD22	1:A:385:GLY:CA	2.33	0.42
1:B:166:LEU:HB3	5:B:927:HOH:O	2.18	0.42
1:A:133:ILE:HD11	1:A:141:ASP:HB3	2.01	0.41
1:B:153:GLU:O	1:B:154:PRO:C	2.63	0.41
1:B:409:ARG:NH1	1:B:409:ARG:HG3	2.35	0.41
1:A:31:SER:OG	1:A:41:ILE:HG12	2.20	0.41
1:A:59:SER:C	1:A:61:LYS:H	2.27	0.41
1:A:195:ASP:OD1	1:A:199:ASN:HB2	2.21	0.41
1:A:243:ILE:C	1:A:245:GLY:H	2.28	0.41
1:A:378:ASN:C	1:A:380:LYS:H	2.27	0.41
1:B:20:ILE:HG12	1:B:133:ILE:HG22	2.02	0.41
1:B:208:THR:HG23	2:D:181:ILE:HG12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:393:ARG:HH11	1:B:393:ARG:HG3	1.85	0.41
1:A:75:SER:O	1:A:79:LYS:HG3	2.20	0.41
1:A:187:PRO:O	1:A:359:LEU:HD12	2.21	0.41
1:A:354:TYR:HD2	2:C:182:MET:HG3	1.86	0.41
1:A:61:LYS:HE2	5:A:929:HOH:O	2.21	0.41
1:B:199:ASN:HD22	1:B:199:ASN:HA	1.56	0.41
1:A:227:THR:HG23	5:A:958:HOH:O	2.21	0.41
1:A:405:LYS:HB3	1:A:405:LYS:HE2	1.89	0.40
1:A:226:ILE:HB	1:A:270:ILE:CD1	2.50	0.40
1:A:409:ARG:NH1	1:A:409:ARG:CG	2.71	0.40
1:B:379:LEU:CD1	1:B:391:ASN:HD21	2.34	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	367/387 (95%)	356 (97%)	11 (3%)	36	45
1	B	367/387 (95%)	350 (95%)	17 (5%)	24	28
2	C	2/4 (50%)	2 (100%)	0	100	100
2	D	5/4 (125%)	3 (60%)	2 (40%)	0	0
All	All	741/782 (95%)	711 (96%)	30 (4%)	28	34

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	THR
1	A	295	LEU
1	A	298	TYR
1	A	329	LYS
1	A	353	GLN
1	A	377	ASN
1	A	378	ASN
1	A	403	LEU
1	A	406	LYS
1	A	409	ARG
1	A	411	CYS
1	B	2	LYS
1	B	50	THR
1	B	58	THR
1	B	77	GLU
1	B	145	PRO
1	B	199	ASN
1	B	239	LEU
1	B	294	LEU
1	B	295	LEU
1	B	296	ASN
1	B	298	TYR
1	B	321	ASN
1	B	328	LYS
1	B	348	GLN
1	B	351	ILE
1	B	378	ASN
1	B	409	ARG
2	D	183[A]	GLU
2	D	183[B]	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	121	ASN
1	A	163	ASN
1	A	174	ASN
1	A	194	ASN
1	A	196	ASN
1	A	247	ASN
1	A	266	GLN
1	A	296	ASN

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Mol	Chain	Res	Type
1	A	324	ASN
1	A	353	GLN
1	A	375	ASN
1	A	389	ASN
1	B	9	ASN
1	B	52	GLN
1	B	71	ASN
1	B	95	ASN
1	B	117	ASN
1	B	124	HIS
1	B	163	ASN
1	B	168	ASN
1	B	174	ASN
1	B	199	ASN
1	B	236	GLN
1	B	237	ASN
1	B	268	ASN
1	B	296	ASN
1	B	321	ASN
1	B	353	GLN
1	B	377	ASN
1	B	389	ASN
1	B	391	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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	SO4	A	893	-	4,4,4	0.44	0	6,6,6	0.15	0
4	SO4	A	897	-	4,4,4	0.45	0	6,6,6	0.10	0
4	SO4	B	890	-	4,4,4	0.46	0	6,6,6	0.18	0
4	SO4	A	896	-	4,4,4	0.52	0	6,6,6	0.10	0
4	SO4	A	892	-	4,4,4	0.57	0	6,6,6	0.13	0
4	SO4	A	891	-	4,4,4	0.45	0	6,6,6	0.15	0
4	SO4	A	894	-	4,4,4	0.46	0	6,6,6	0.13	0
4	SO4	B	895	-	4,4,4	0.49	0	6,6,6	0.19	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
4	A	897	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

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	407/427 (95%)	0.26	14 (3%) 48 48	21, 35, 46, 58	0
1	B	407/427 (95%)	0.46	23 (5%) 29 27	26, 39, 51, 56	0
2	C	3/5 (60%)	2.54	2 (66%) 0 0	46, 46, 49, 54	0
2	D	4/5 (80%)	0.92	0 100 100	30, 43, 46, 49	1 (25%)
All	All	821/864 (95%)	0.37	39 (4%) 35 35	21, 37, 49, 58	1 (0%)

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	377	ASN	4.3
1	A	57	PRO	4.3
1	A	56	PRO	3.8
1	B	58	THR	3.7
1	A	239	LEU	3.6
1	B	241	THR	3.3
1	B	237	ASN	3.2
1	B	238	PRO	3.2
1	A	59	SER	3.1
1	A	244	ARG	3.0
2	C	181	ILE	3.0
1	B	233	THR	3.0
1	A	243	ILE	2.9
2	C	182	MET	2.8
1	B	57	PRO	2.8
1	B	242	ASN	2.6
1	A	58	THR	2.6
1	B	393	ARG	2.6
1	B	295	LEU	2.5
1	A	411	CYS	2.5
1	B	408	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	63	GLY	2.4
1	B	409	ARG	2.4
1	B	243	ILE	2.4
1	A	242	ASN	2.3
1	B	65	SER	2.3
1	B	198	MET	2.3
1	B	61	LYS	2.3
1	B	2	LYS	2.2
1	B	239	LEU	2.2
1	B	351	ILE	2.2
1	B	62	ASN	2.2
1	A	52	GLN	2.2
1	B	240	ILE	2.1
1	B	26	GLN	2.1
1	B	396	THR	2.1
1	A	381	VAL	2.1
1	A	54	PHE	2.0
1	A	60	LEU	2.0

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 oligosaccharides 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(Å ²)	Q<0.9
4	SO4	A	892	5/5	0.77	0.13	51,51,52,53	5
4	SO4	A	894	5/5	0.82	0.13	50,52,52,53	5
4	SO4	B	895	5/5	0.82	0.21	60,61,61,62	5
4	SO4	A	896	5/5	0.85	0.18	54,54,55,55	5
4	SO4	A	891	5/5	0.88	0.12	40,44,44,45	5

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	SO4	A	897	5/5	0.89	0.12	50,50,51,51	5
4	SO4	B	890	5/5	0.89	0.13	46,46,48,49	4
4	SO4	A	893	5/5	0.89	0.14	52,53,53,54	5
3	ZN	A	428	1/1	0.98	0.05	50,50,50,50	0
3	ZN	B	822	1/1	0.98	0.07	43,43,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.