



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:36 PM UTC

PDB ID : 3K7W / pdb_00003k7w
Title : Protein phosphatase 2A core complex bound to dinophysistoxin-2
Authors : Jeffrey, P.D.; Huhn, J.; Shi, Y.
Deposited on : 2009-10-13
Resolution : 2.96 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

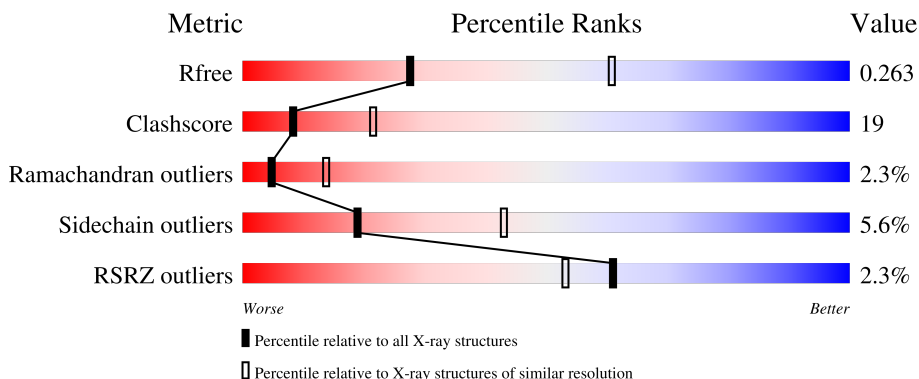
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.96 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	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)

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	589	 3% 58% 34% 6% •
2	C	309	 54% 35% • 7%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6948 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.

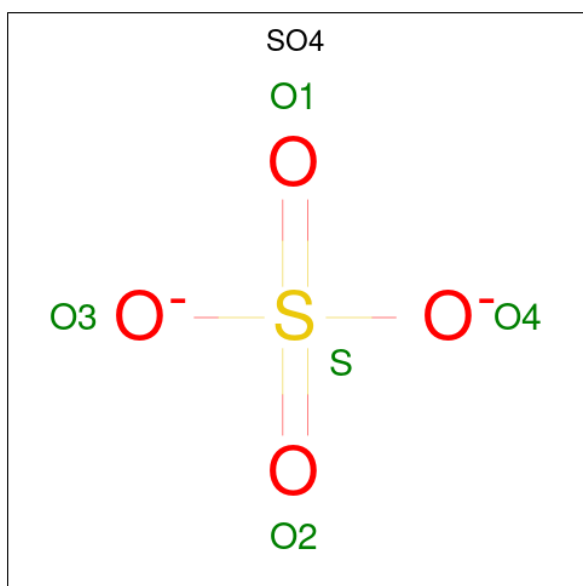
- Molecule 1 is a protein called Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	581	Total	C	N	O	S	0	0	0
			4527	2877	763	860	27			

- Molecule 2 is a protein called Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	288	Total	C	N	O	S	0	0	0
			2322	1471	396	440	15			

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



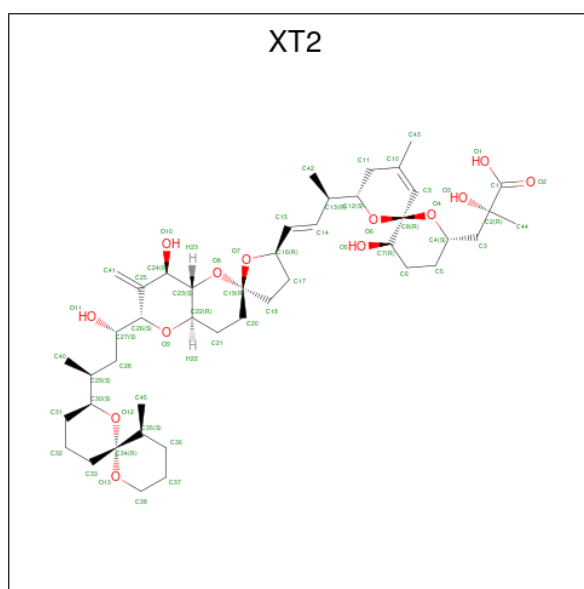
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		

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

- Molecule 4 is (2R)-2-hydroxy-3-[(2S,5R,6R,8S)-5-hydroxy-8-[(1R,2E)-3-[(2R,4a'R,5R,6'S,8'R,8a'S)-8'-hydroxy-6'-[(1S,3S)-1-hydroxy-3-[(2S,6R,11S)-11-methyl-1,7-dioxaspiro[5.5]undec-2-yl]butyl]-7'-methylideneoctahydro-3H,3'H-spiro[furan-2,2'-pyrano[3,2-b]pyran]-5-yl]-1-methylprop-2-en-1-yl]-10-methyl-1,7-dioxaspiro[5.5]undec-10-en-2-yl]-2-methylpropanoic acid (CCD ID: XT2) (formula: C₄₄H₆₈O₁₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			57	44	13		

- Molecule 5 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	2	Total	Mn		0	0
			2	2			

- Molecule 6 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	8	Total	O		0	0
			8	8			

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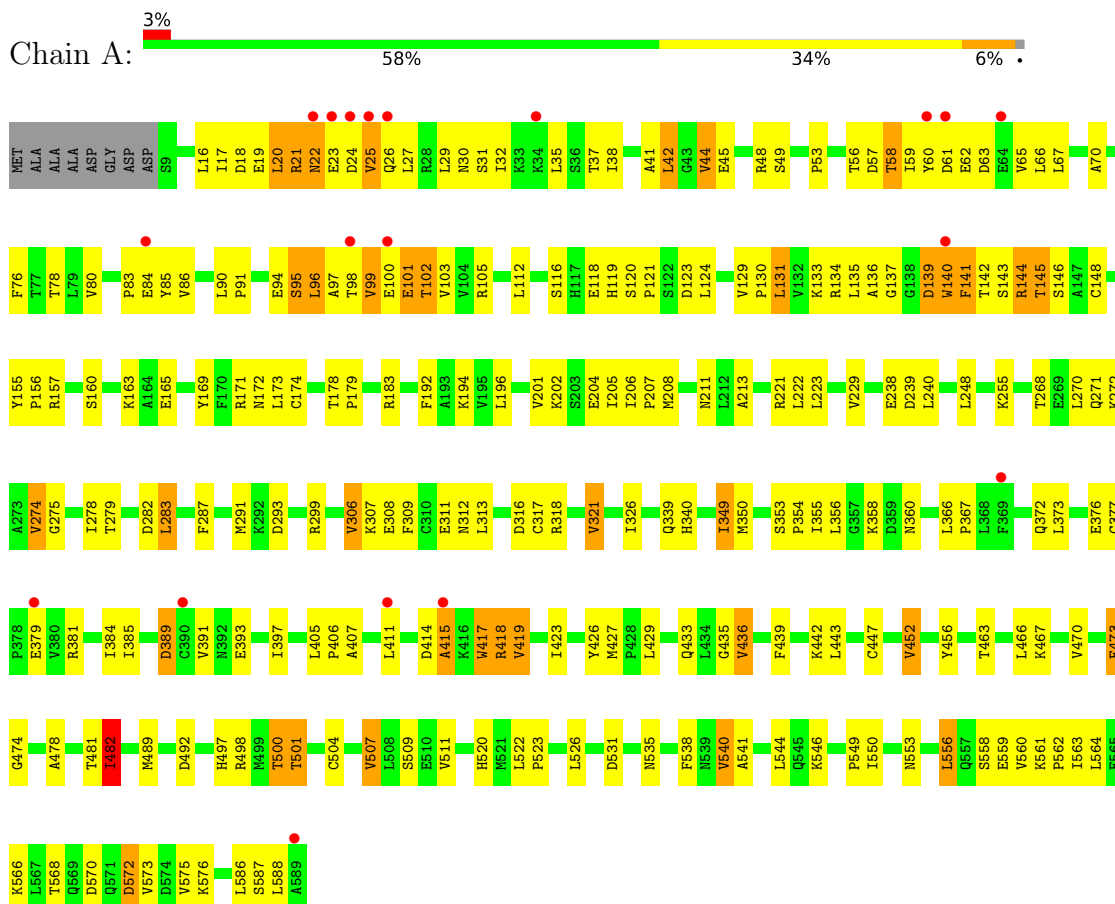
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	17	Total	O	0	0
			17	17		

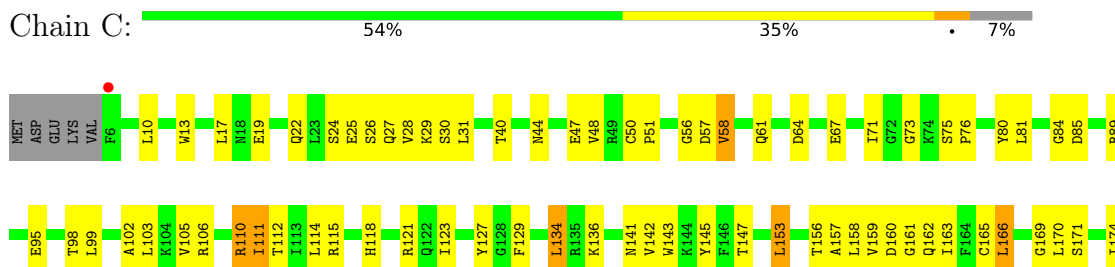
3 Residue-property plots [i](#)

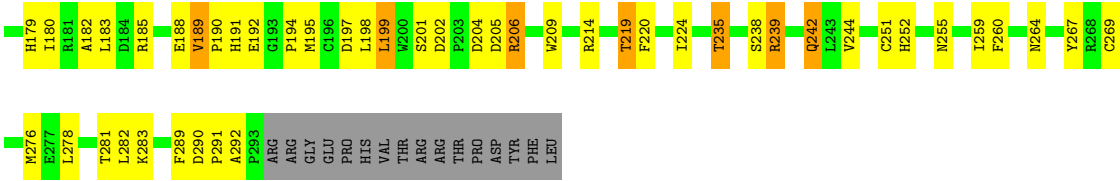
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform



- Molecule 2: Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform





4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	93.41Å 197.24Å 201.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.81 – 2.96 29.81 – 2.96	Depositor EDS
% Data completeness (in resolution range)	99.5 (29.81-2.96) 99.5 (29.81-2.96)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.61 (at 2.96Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.222 , 0.263 0.222 , 0.263	Depositor DCC
R_{free} test set	1921 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	63.0	Xtriage
Anisotropy	0.220	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 44.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6948	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% 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: MN, SO4, XT2

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	0.56	0/4601	1.08	32/6246 (0.5%)
2	C	0.55	0/2379	1.07	17/3227 (0.5%)
All	All	0.56	0/6980	1.08	49/9473 (0.5%)

There are no bond length outliers.

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	417	TRP	N-CA-C	-12.32	94.27	110.53
1	A	520	HIS	N-CA-C	8.50	123.84	112.88
1	A	419	VAL	N-CA-C	-8.41	102.23	110.72
1	A	316	ASP	N-CA-C	7.25	118.97	111.14
1	A	482	ILE	N-CA-C	7.09	117.66	111.56
2	C	141	ASN	N-CA-C	7.09	118.65	111.07
1	A	474	GLY	N-CA-C	6.81	119.92	112.29
2	C	269	CYS	N-CA-C	6.72	119.62	111.82
2	C	127	TYR	N-CA-C	6.45	120.79	112.41
2	C	206	ARG	N-CA-C	-6.42	99.44	109.72
2	C	189	VAL	CA-C-N	6.38	126.74	119.92
2	C	189	VAL	C-N-CA	6.38	126.74	119.92
1	A	340	HIS	N-CA-C	-6.33	103.52	111.11
1	A	20	LEU	N-CA-C	6.32	121.11	113.41
2	C	57	ASP	N-CA-C	6.31	119.18	110.35
1	A	42	LEU	N-CA-C	-6.27	101.66	110.50
1	A	349	ILE	N-CA-C	6.21	116.89	110.36
1	A	326	ILE	N-CA-C	6.18	116.36	110.74
2	C	219	THR	N-CA-C	-6.13	100.20	109.95
1	A	426	TYR	N-CA-C	-6.09	105.89	113.38
2	C	153	LEU	CA-C-N	6.04	126.36	119.83
2	C	153	LEU	C-N-CA	6.04	126.36	119.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	201	VAL	N-CA-C	-6.04	104.62	110.72
2	C	255	ASN	N-CA-C	-5.96	105.84	113.23
1	A	559	GLU	N-CA-C	5.93	120.65	113.41
1	A	473	PHE	N-CA-C	5.92	120.67	113.38
1	A	481	THR	N-CA-C	5.90	120.76	113.50
2	C	19	GLU	N-CA-C	-5.81	106.09	112.72
1	A	157	ARG	N-CA-C	5.80	120.08	112.89
1	A	553	ASN	N-CA-C	5.67	119.01	111.75
1	A	49	SER	N-CA-C	5.51	118.05	111.71
2	C	58	VAL	N-CA-C	-5.50	107.27	111.62
1	A	275	GLY	CA-C-N	5.47	126.68	119.84
1	A	275	GLY	C-N-CA	5.47	126.68	119.84
2	C	75	SER	N-CA-C	-5.44	102.30	110.24
1	A	435	GLY	N-CA-C	5.42	119.03	112.48
1	A	540	VAL	N-CA-C	-5.42	105.09	111.00
1	A	282	ASP	N-CA-C	5.33	119.85	112.45
1	A	63	ASP	N-CA-C	5.21	117.36	111.11
1	A	283	LEU	N-CA-C	5.17	118.05	111.69
2	C	80	TYR	N-CA-C	5.14	117.49	109.52
1	A	442	LYS	N-CA-C	5.13	119.64	113.17
1	A	572	ASP	N-CA-C	5.10	117.61	109.96
1	A	541	ALA	N-CA-C	-5.10	105.61	111.07
2	C	242	GLN	N-CA-C	5.08	117.69	109.40
1	A	436	VAL	N-CA-C	5.05	117.36	111.05
1	A	492	ASP	CA-C-N	5.03	124.52	119.19
1	A	492	ASP	C-N-CA	5.03	124.52	119.19
2	C	201	SER	N-CA-C	5.02	117.01	110.43

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	4527	0	4633	189	0
2	C	2322	0	2224	79	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	5	0	0	0	0
3	C	10	0	0	1	0
4	C	57	0	67	2	0
5	C	2	0	0	0	0
6	A	8	0	0	0	0
6	C	17	0	0	0	0
All	All	6948	0	6924	266	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 19.

All (266) 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:99:VAL:HG12	1:A:100:GLU:H	1.06	1.09
2:C:103:LEU:HB3	2:C:111:ILE:CD1	1.93	0.98
2:C:67:GLU:HB2	2:C:292:ALA:HB2	1.52	0.88
2:C:81:LEU:HD12	2:C:112:THR:HB	1.52	0.88
1:A:99:VAL:HG12	1:A:100:GLU:N	1.89	0.88
1:A:27:LEU:HD13	1:A:32:ILE:HD11	1.58	0.85
1:A:94:GLU:OE1	1:A:131:LEU:HD13	1.82	0.80
2:C:290:ASP:HB3	2:C:291:PRO:HD2	1.62	0.80
1:A:213:ALA:O	1:A:221:ARG:HD2	1.83	0.79
2:C:281:THR:HG22	2:C:281:THR:O	1.83	0.79
1:A:59:ILE:HG23	1:A:66:LEU:HD21	1.65	0.78
1:A:556:LEU:HD22	1:A:588:LEU:HD11	1.67	0.75
1:A:526:LEU:HD22	1:A:563:ILE:HG13	1.68	0.75
2:C:276:MET:HE3	2:C:278:LEU:HD21	1.69	0.73
1:A:466:LEU:HD22	1:A:482:ILE:HD13	1.71	0.73
2:C:89:ARG:HH21	4:C:401:XT2:H3A	1.53	0.72
1:A:102:THR:HG22	1:A:105:ARG:NH2	2.05	0.71
2:C:103:LEU:HB3	2:C:111:ILE:HD12	1.70	0.70
1:A:102:THR:HG22	1:A:105:ARG:HH22	1.57	0.69
2:C:174:ILE:HD11	2:C:183:LEU:HD11	1.75	0.69
1:A:350:MET:HB3	1:A:391:VAL:CG2	2.24	0.68
1:A:155:TYR:HB3	1:A:156:PRO:HD3	1.76	0.68
1:A:205:ILE:HD13	1:A:208:MET:HE3	1.74	0.68
1:A:356:LEU:O	1:A:360:ASN:HB2	1.93	0.68
1:A:136:ALA:O	1:A:144:ARG:HG3	1.93	0.67
1:A:25:VAL:HG12	1:A:25:VAL:O	1.94	0.67
1:A:205:ILE:HD13	1:A:208:MET:CE	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:339:GLN:NE2	1:A:377:CYS:HB2	2.10	0.66
1:A:407:ALA:O	1:A:411:LEU:HG	1.96	0.66
1:A:99:VAL:CG1	1:A:100:GLU:H	1.89	0.66
1:A:287:PHE:CD2	1:A:291:MET:HE2	2.32	0.65
1:A:24:ASP:O	1:A:25:VAL:HG23	1.98	0.62
1:A:268:THR:HG21	1:A:308:GLU:HB3	1.82	0.62
1:A:90:LEU:HB2	1:A:91:PRO:HD3	1.82	0.61
1:A:205:ILE:HA	1:A:208:MET:HE3	1.81	0.61
1:A:274:VAL:CG1	1:A:278:ILE:HB	2.30	0.61
2:C:103:LEU:HB3	2:C:111:ILE:HD11	1.81	0.61
1:A:271:GLN:HE21	1:A:279:THR:HG21	1.66	0.61
1:A:94:GLU:OE1	1:A:134:ARG:NH2	2.33	0.60
1:A:29:LEU:C	1:A:31:SER:H	2.09	0.59
1:A:535:ASN:HA	1:A:538:PHE:CE2	2.37	0.59
2:C:50:CYS:HB2	2:C:51:PRO:HA	1.85	0.59
1:A:194:LYS:HD2	1:A:194:LYS:O	2.02	0.59
1:A:105:ARG:HH11	1:A:105:ARG:HG3	1.68	0.58
1:A:373:LEU:HD13	1:A:384:ILE:HG21	1.86	0.58
1:A:373:LEU:HD11	1:A:385:ILE:HD11	1.85	0.58
1:A:381:ARG:O	1:A:385:ILE:HG12	2.04	0.58
2:C:174:ILE:HD13	2:C:180:ILE:HG12	1.85	0.57
1:A:70:ALA:HB2	1:A:96:LEU:HD13	1.85	0.57
2:C:156:THR:HG22	2:C:166:LEU:HB3	1.87	0.57
1:A:222:LEU:HD12	1:A:223:LEU:N	2.20	0.57
1:A:317:CYS:O	1:A:321:VAL:HG13	2.05	0.57
1:A:272:LYS:HE2	1:A:312:ASN:HD21	1.69	0.57
1:A:385:ILE:O	1:A:433:GLN:NE2	2.36	0.57
1:A:145:THR:CG2	1:A:146:SER:N	2.68	0.57
1:A:467:LYS:HB2	1:A:507:VAL:HG13	1.86	0.57
2:C:56:GLY:HA3	2:C:259:ILE:O	2.05	0.57
2:C:76:PRO:HB2	2:C:110:ARG:HG3	1.87	0.57
1:A:489:MET:HB2	1:A:501:THR:OG1	2.05	0.56
1:A:171:ARG:O	1:A:174:CYS:N	2.38	0.56
1:A:57:ASP:O	1:A:59:ILE:N	2.37	0.56
1:A:100:GLU:O	1:A:101:GLU:C	2.48	0.56
1:A:139:ASP:O	1:A:140:TRP:O	2.23	0.56
1:A:206:ILE:HB	1:A:207:PRO:HD3	1.86	0.56
1:A:389:ASP:O	1:A:393:GLU:HG3	2.04	0.56
1:A:140:TRP:H	1:A:140:TRP:CD1	2.24	0.56
2:C:61:GLN:HA	3:C:310:SO4:O2	2.04	0.55
1:A:349:ILE:HG23	1:A:350:MET:N	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:ALA:O	1:A:105:ARG:HD2	2.07	0.55
2:C:17:LEU:HD11	2:C:98:THR:HG22	1.88	0.55
1:A:373:LEU:HD13	1:A:384:ILE:CG2	2.38	0.54
1:A:427:MET:HE2	1:A:447:CYS:SG	2.47	0.54
1:A:102:THR:HA	1:A:105:ARG:NH1	2.23	0.54
1:A:141:PHE:C	1:A:141:PHE:CD1	2.85	0.54
1:A:222:LEU:HD12	1:A:223:LEU:HG	1.90	0.54
2:C:188:GLU:HG3	2:C:189:VAL:N	2.21	0.54
2:C:10:LEU:HD11	2:C:105:VAL:HG12	1.89	0.53
2:C:118:HIS:HA	2:C:123:ILE:HG21	1.89	0.53
1:A:417:TRP:O	1:A:418:ARG:CB	2.56	0.53
2:C:81:LEU:CD1	2:C:112:THR:HB	2.32	0.53
2:C:281:THR:O	2:C:281:THR:CG2	2.53	0.53
1:A:373:LEU:HD11	1:A:385:ILE:CD1	2.39	0.53
1:A:417:TRP:O	1:A:418:ARG:CG	2.57	0.53
1:A:130:PRO:O	1:A:134:ARG:HG3	2.09	0.53
2:C:10:LEU:HD13	2:C:106:ARG:HB2	1.89	0.53
1:A:272:LYS:HE2	1:A:312:ASN:ND2	2.24	0.53
1:A:452:VAL:HG22	1:A:497:HIS:CE1	2.44	0.52
2:C:281:THR:HG21	2:C:283:LYS:HE3	1.90	0.52
1:A:564:LEU:O	1:A:568:THR:HG23	2.09	0.52
1:A:183:ARG:HG3	1:A:183:ARG:HH11	1.73	0.52
1:A:136:ALA:O	1:A:144:ARG:CG	2.57	0.52
1:A:67:LEU:CD1	1:A:103:VAL:HG12	2.40	0.52
1:A:136:ALA:O	1:A:144:ARG:HD2	2.10	0.52
1:A:556:LEU:HD13	1:A:588:LEU:HD21	1.91	0.52
1:A:44:VAL:CG1	1:A:45:GLU:N	2.74	0.51
2:C:209:TRP:CE2	2:C:224:ILE:HD13	2.45	0.51
1:A:67:LEU:HD13	1:A:103:VAL:HG12	1.91	0.51
1:A:313:LEU:HD13	1:A:321:VAL:HG21	1.93	0.51
1:A:60:TYR:CG	1:A:61:ASP:N	2.79	0.51
1:A:148:CYS:SG	1:A:173:LEU:HD13	2.50	0.51
2:C:24:SER:OG	2:C:26:SER:HB3	2.11	0.51
1:A:489:MET:HE1	1:A:500:THR:HG22	1.93	0.51
2:C:121:ARG:HG2	2:C:147:THR:HB	1.92	0.51
1:A:272:LYS:CE	1:A:312:ASN:HD21	2.23	0.51
1:A:313:LEU:HD13	1:A:321:VAL:CG2	2.41	0.51
1:A:202:LYS:HE3	1:A:239:ASP:OD2	2.12	0.50
1:A:355:ILE:HG22	1:A:355:ILE:O	2.11	0.50
1:A:102:THR:CG2	1:A:105:ARG:HH22	2.24	0.50
1:A:544:LEU:HD13	1:A:560:VAL:HG13	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:572:ASP:OD2	2:C:110:ARG:NH2	2.43	0.50
1:A:26:GLN:HG2	1:A:27:LEU:N	2.27	0.50
1:A:48:ARG:O	1:A:53:PRO:HD3	2.11	0.50
1:A:414:ASP:CG	1:A:415:ALA:H	2.20	0.50
1:A:38:ILE:N	1:A:38:ILE:HD12	2.26	0.50
1:A:98:THR:O	1:A:98:THR:HG22	2.12	0.49
1:A:568:THR:O	1:A:576:LYS:HG3	2.12	0.49
1:A:372:GLN:OE1	1:A:384:ILE:HD11	2.12	0.49
2:C:171:SER:HB2	2:C:197:ASP:HB2	1.93	0.49
1:A:94:GLU:CD	1:A:134:ARG:HH21	2.19	0.49
1:A:293:ASP:O	1:A:299:ARG:HD3	2.11	0.49
1:A:538:PHE:HB3	1:A:575:VAL:HA	1.94	0.49
2:C:48:VAL:O	2:C:159:VAL:HA	2.12	0.49
2:C:174:ILE:HD11	2:C:194:PRO:HB3	1.95	0.49
1:A:136:ALA:O	1:A:144:ARG:CD	2.60	0.49
1:A:62:GLU:O	1:A:65:VAL:HB	2.11	0.49
1:A:561:LYS:N	1:A:562:PRO:CD	2.76	0.49
1:A:427:MET:HE1	1:A:443:LEU:HB3	1.94	0.49
1:A:546:LYS:O	1:A:549:PRO:HD2	2.12	0.49
1:A:558:SER:O	1:A:562:PRO:HG2	2.13	0.49
2:C:239:ARG:HH22	2:C:242:GLN:HG3	1.77	0.49
2:C:143:TRP:CE2	2:C:147:THR:HG21	2.48	0.48
1:A:405:LEU:HB3	1:A:406:PRO:HD3	1.95	0.48
2:C:244:VAL:HG22	2:C:260:PHE:HB2	1.96	0.48
1:A:139:ASP:O	1:A:140:TRP:C	2.57	0.48
1:A:509:SER:O	1:A:550:ILE:HD13	2.13	0.48
1:A:24:ASP:O	1:A:25:VAL:CG2	2.62	0.48
1:A:427:MET:HE1	1:A:443:LEU:HD13	1.96	0.48
1:A:60:TYR:CD1	1:A:61:ASP:N	2.81	0.47
1:A:183:ARG:HG3	1:A:183:ARG:NH1	2.29	0.47
2:C:158:LEU:HD21	2:C:161:GLY:HA2	1.96	0.47
1:A:86:VAL:HG21	1:A:118:GLU:HB2	1.97	0.47
2:C:251:CYS:O	2:C:252:HIS:HB2	2.13	0.47
1:A:102:THR:O	1:A:103:VAL:C	2.57	0.47
1:A:279:THR:HA	1:A:283:LEU:HB2	1.95	0.47
2:C:179:HIS:O	2:C:182:ALA:HB3	2.13	0.47
1:A:24:ASP:O	1:A:25:VAL:CB	2.62	0.47
1:A:463:THR:HG23	1:A:504:CYS:SG	2.55	0.47
2:C:28:VAL:HG11	2:C:142:VAL:HG13	1.95	0.47
2:C:61:GLN:HB3	2:C:64:ASP:OD2	2.14	0.47
2:C:71:ILE:HD13	2:C:289:PHE:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:106:ARG:HD2	2:C:106:ARG:O	2.15	0.47
2:C:191:HIS:CD2	2:C:192:GLU:HG3	2.49	0.47
1:A:133:LYS:HE2	1:A:169:TYR:CE1	2.49	0.47
1:A:366:LEU:N	1:A:367:PRO:CD	2.78	0.47
2:C:204:ASP:HB2	2:C:219:THR:HB	1.97	0.47
2:C:204:ASP:OD2	2:C:206:ARG:HG3	2.15	0.47
1:A:131:LEU:HD12	1:A:131:LEU:O	2.16	0.46
2:C:44:ASN:OD1	2:C:185:ARG:NH1	2.45	0.46
2:C:165:CYS:HA	2:C:238:SER:O	2.14	0.46
1:A:120:SER:HB2	1:A:121:PRO:HD2	1.96	0.46
2:C:204:ASP:OD1	2:C:205:ASP:N	2.47	0.46
1:A:229:VAL:HG22	1:A:270:LEU:HD23	1.98	0.46
1:A:24:ASP:C	1:A:25:VAL:HG23	2.41	0.46
1:A:29:LEU:C	1:A:31:SER:N	2.73	0.46
1:A:23:GLU:HG3	1:A:26:GLN:OE1	2.16	0.46
1:A:99:VAL:CG1	1:A:100:GLU:N	2.61	0.46
1:A:45:GLU:H	1:A:45:GLU:CD	2.24	0.46
1:A:165:GLU:O	1:A:169:TYR:HD1	1.99	0.46
1:A:222:LEU:HD12	1:A:222:LEU:C	2.41	0.46
1:A:100:GLU:O	1:A:105:ARG:NH1	2.49	0.46
1:A:83:PRO:O	1:A:85:TYR:N	2.50	0.45
1:A:17:ILE:HG22	1:A:18:ASP:N	2.32	0.45
2:C:264:ASN:ND2	2:C:267:TYR:HA	2.32	0.45
2:C:29:LYS:HB2	2:C:145:TYR:CE1	2.51	0.45
1:A:349:ILE:CG2	1:A:350:MET:N	2.80	0.45
1:A:339:GLN:CD	1:A:377:CYS:HB2	2.42	0.45
1:A:155:TYR:CE2	1:A:196:LEU:HD23	2.52	0.44
1:A:248:LEU:O	1:A:248:LEU:HD12	2.17	0.44
1:A:56:THR:HG22	1:A:57:ASP:N	2.31	0.44
2:C:84:GLY:O	2:C:85:ASP:HB2	2.17	0.44
2:C:169:GLY:O	2:C:198:LEU:HA	2.17	0.44
1:A:306:VAL:HG12	1:A:307:LYS:N	2.32	0.44
1:A:561:LYS:HB3	1:A:562:PRO:HD3	2.00	0.44
1:A:145:THR:HG23	1:A:146:SER:N	2.33	0.44
1:A:570:ASP:O	1:A:576:LYS:CE	2.66	0.44
1:A:21:ARG:HD2	1:A:26:GLN:OE1	2.18	0.44
1:A:58:THR:O	1:A:58:THR:HG22	2.18	0.44
1:A:59:ILE:O	1:A:59:ILE:HG22	2.18	0.44
1:A:538:PHE:CB	1:A:575:VAL:HA	2.48	0.44
1:A:222:LEU:CD1	1:A:223:LEU:HG	2.48	0.44
1:A:373:LEU:HA	1:A:373:LEU:HD12	1.76	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:470:VAL:HG22	1:A:478:ALA:HB2	1.99	0.44
1:A:307:LYS:O	1:A:311:GLU:HB2	2.18	0.43
2:C:22:GLN:HE22	2:C:136:LYS:HB3	1.82	0.43
1:A:44:VAL:HG12	1:A:45:GLU:OE2	2.19	0.43
1:A:522:LEU:N	1:A:523:PRO:CD	2.81	0.43
2:C:29:LYS:HG3	2:C:145:TYR:CZ	2.54	0.43
2:C:189:VAL:HA	2:C:195:MET:HE2	2.00	0.43
1:A:21:ARG:NH1	1:A:26:GLN:HE22	2.16	0.43
1:A:271:GLN:NE2	1:A:309:PHE:CE1	2.87	0.43
1:A:509:SER:HB2	1:A:550:ILE:HD12	2.00	0.43
2:C:163:ILE:HD12	2:C:282:LEU:HD22	2.00	0.43
1:A:116:SER:O	1:A:119:HIS:HB2	2.19	0.43
1:A:121:PRO:O	1:A:124:LEU:HB2	2.19	0.43
1:A:576:LYS:HE3	1:A:576:LYS:HB2	1.87	0.43
2:C:89:ARG:HH21	4:C:401:XT2:C3	2.26	0.43
1:A:129:VAL:N	1:A:130:PRO:CD	2.83	0.42
1:A:133:LYS:O	1:A:134:ARG:C	2.61	0.42
1:A:353:SER:N	1:A:354:PRO:HD2	2.33	0.42
1:A:429:LEU:HD23	1:A:429:LEU:HA	1.84	0.42
1:A:470:VAL:HG11	1:A:511:VAL:HG23	2.00	0.42
1:A:566:LYS:HB3	1:A:566:LYS:HE2	1.86	0.42
2:C:174:ILE:HG13	2:C:194:PRO:HB3	2.00	0.42
1:A:561:LYS:HE3	1:A:588:LEU:O	2.19	0.42
1:A:129:VAL:HB	1:A:130:PRO:HD3	2.00	0.42
1:A:467:LYS:HB2	1:A:507:VAL:CG1	2.48	0.42
2:C:48:VAL:HB	2:C:159:VAL:HG22	2.01	0.42
2:C:115:ARG:HB2	2:C:153:LEU:HB2	2.01	0.42
2:C:199:LEU:HA	2:C:199:LEU:HD12	1.81	0.42
1:A:255:LYS:HD3	1:A:255:LYS:HA	1.75	0.42
1:A:498:ARG:NE	1:A:531:ASP:OD2	2.44	0.42
1:A:35:LEU:C	1:A:37:THR:H	2.27	0.42
2:C:114:LEU:HD21	2:C:157:ALA:HB2	2.02	0.42
1:A:155:TYR:CE1	1:A:163:LYS:HB3	2.55	0.42
2:C:13:TRP:CZ2	2:C:27:GLN:HB3	2.55	0.42
1:A:112:LEU:HD23	1:A:112:LEU:HA	1.90	0.41
1:A:268:THR:CG2	1:A:308:GLU:HB3	2.49	0.41
1:A:427:MET:HE3	1:A:439:PHE:HE1	1.85	0.41
2:C:10:LEU:HD23	2:C:10:LEU:HA	1.77	0.41
2:C:189:VAL:HA	2:C:190:PRO:HD3	1.90	0.41
1:A:59:ILE:HD12	1:A:95:SER:OG	2.20	0.41
1:A:419:VAL:O	1:A:423:ILE:HG12	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:456:TYR:CG	2:C:73:GLY:HA2	2.55	0.41
2:C:24:SER:O	2:C:25:GLU:C	2.62	0.41
1:A:80:VAL:O	1:A:80:VAL:HG12	2.19	0.41
1:A:140:TRP:CD1	1:A:140:TRP:N	2.84	0.41
2:C:134:LEU:HD12	2:C:134:LEU:HA	1.93	0.41
1:A:135:LEU:O	1:A:143:SER:O	2.37	0.41
2:C:17:LEU:HD13	2:C:99:LEU:HA	2.02	0.41
1:A:311:GLU:HG3	1:A:355:ILE:HD11	2.02	0.41
1:A:192:PHE:CZ	1:A:196:LEU:HD21	2.54	0.41
1:A:405:LEU:HD12	1:A:405:LEU:HA	1.91	0.41
1:A:586:LEU:O	1:A:587:SER:HB2	2.20	0.41
1:A:358:LYS:HE2	1:A:358:LYS:HB3	1.89	0.41
2:C:103:LEU:CB	2:C:111:ILE:HD12	2.44	0.41
1:A:35:LEU:C	1:A:37:THR:N	2.78	0.41
2:C:95:GLU:OE1	2:C:95:GLU:N	2.49	0.41
2:C:170:LEU:HD12	2:C:220:PHE:CE1	2.55	0.41
1:A:18:ASP:O	1:A:20:LEU:N	2.54	0.41
1:A:171:ARG:O	1:A:172:ASN:C	2.63	0.41
1:A:206:ILE:CB	1:A:207:PRO:HD3	2.51	0.41
2:C:174:ILE:CD1	2:C:194:PRO:HB3	2.51	0.41
2:C:282:LEU:HD23	2:C:282:LEU:HA	1.82	0.41
1:A:142:THR:C	1:A:144:ARG:N	2.78	0.41
1:A:436:VAL:HB	1:A:473:PHE:CD1	2.56	0.41
1:A:133:LYS:O	1:A:137:GLY:N	2.52	0.40
1:A:240:LEU:HD13	1:A:274:VAL:HG22	2.03	0.40
2:C:170:LEU:HD12	2:C:220:PHE:CD1	2.56	0.40
2:C:214:ARG:HH21	2:C:242:GLN:HG2	1.86	0.40
1:A:59:ILE:HG23	1:A:66:LEU:CD2	2.42	0.40
2:C:31:LEU:HD11	2:C:102:ALA:HA	2.02	0.40
2:C:202:ASP:O	2:C:219:THR:HA	2.22	0.40
1:A:102:THR:HG22	1:A:105:ARG:CZ	2.50	0.40
1:A:44:VAL:HG12	1:A:45:GLU:N	2.37	0.40
2:C:162:GLN:HB3	2:C:235:THR:OG1	2.21	0.40
2:C:281:THR:HG21	2:C:283:LYS:CE	2.52	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	579/589 (98%)	515 (89%)	45 (8%)	19 (3%)	3	7
2	C	286/309 (93%)	262 (92%)	23 (8%)	1 (0%)	36	59
All	All	865/898 (96%)	777 (90%)	68 (8%)	20 (2%)	5	14

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	25	VAL
1	A	58	THR
1	A	99	VAL
1	A	140	TRP
1	A	318	ARG
1	A	415	ALA
1	A	418	ARG
1	A	19	GLU
1	A	21	ARG
1	A	22	ASN
1	A	84	GLU
1	A	96	LEU
1	A	101	GLU
1	A	30	ASN
1	A	102	THR
1	A	139	ASP
1	A	41	ALA
1	A	95	SER
2	C	129	PHE
1	A	306	VAL

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	508/512 (99%)	477 (94%)	31 (6%)	17	40
2	C	254/274 (93%)	242 (95%)	12 (5%)	23	49
All	All	762/786 (97%)	719 (94%)	43 (6%)	19	43

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	LEU
1	A	22	ASN
1	A	42	LEU
1	A	44	VAL
1	A	76	PHE
1	A	78	THR
1	A	123	ASP
1	A	131	LEU
1	A	141	PHE
1	A	144	ARG
1	A	145	THR
1	A	160	SER
1	A	178	THR
1	A	179	PRO
1	A	204	GLU
1	A	211	ASN
1	A	238	GLU
1	A	274	VAL
1	A	321	VAL
1	A	376	GLU
1	A	379	GLU
1	A	389	ASP
1	A	397	ILE
1	A	452	VAL
1	A	482	ILE
1	A	500	THR
1	A	501	THR
1	A	507	VAL
1	A	540	VAL
1	A	556	LEU
1	A	573	VAL

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Mol	Chain	Res	Type
2	C	30	SER
2	C	40	THR
2	C	47	GLU
2	C	58	VAL
2	C	110	ARG
2	C	111	ILE
2	C	134	LEU
2	C	160	ASP
2	C	166	LEU
2	C	199	LEU
2	C	235	THR
2	C	239	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	127	HIS
1	A	230	ASN
1	A	233	GLN
1	A	271	GLN
1	A	288	GLN
1	A	312	ASN
1	A	339	GLN
1	A	392	ASN
1	A	399	GLN
1	A	444	ASN
1	A	514	GLN
2	C	22	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	XT2	C	401	-	60,63,63	1.48	4 (6%)	68,97,97	1.63	14 (20%)
3	SO4	A	590	-	4,4,4	0.39	0	6,6,6	0.26	0
3	SO4	C	310	-	4,4,4	0.27	0	6,6,6	0.20	0
3	SO4	C	311	-	4,4,4	0.37	0	6,6,6	0.10	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
4	XT2	C	401	-	-	8/32/130/130	0/7/7/7

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	401	XT2	C8-C9	-9.06	1.39	1.50
4	C	401	XT2	C41-C25	4.11	1.39	1.32
4	C	401	XT2	C15-C14	2.35	1.39	1.32
4	C	401	XT2	C16-C15	-2.19	1.39	1.50

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	401	XT2	C7-C8-C9	-6.27	107.33	114.00
4	C	401	XT2	C11-C12-C13	-4.33	106.46	116.21
4	C	401	XT2	C38-O13-C34	-3.37	111.46	114.00
4	C	401	XT2	O7-C19-C18	-2.95	101.24	104.47
4	C	401	XT2	C23-C24-C25	-2.94	107.16	112.08
4	C	401	XT2	C21-C20-C19	-2.81	108.39	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	401	XT2	C31-C30-C29	-2.70	109.97	115.12
4	C	401	XT2	C37-C36-C35	-2.55	108.83	112.68
4	C	401	XT2	C43-C10-C11	2.53	120.18	116.14
4	C	401	XT2	O6-C8-O4	2.49	111.50	106.17
4	C	401	XT2	C22-C23-C24	-2.46	106.43	110.31
4	C	401	XT2	O8-C23-C22	2.44	112.77	109.36
4	C	401	XT2	C32-C33-C34	-2.28	109.38	111.50
4	C	401	XT2	C13-C14-C15	-2.22	119.11	125.81

There are no chirality outliers.

All (8) torsion outliers are listed below:

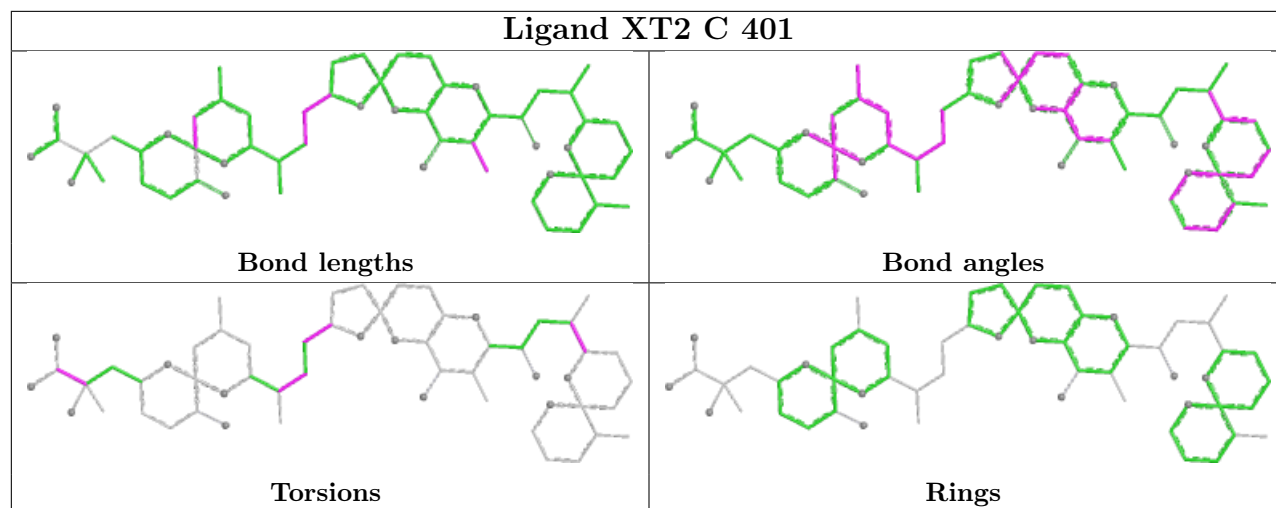
Mol	Chain	Res	Type	Atoms
4	C	401	XT2	C14-C15-C16-O7
4	C	401	XT2	C42-C13-C14-C15
4	C	401	XT2	O2-C1-C2-C44
4	C	401	XT2	O1-C1-C2-C44
4	C	401	XT2	C14-C15-C16-C17
4	C	401	XT2	C40-C29-C30-C31
4	C	401	XT2	O1-C1-C2-C3
4	C	401	XT2	O2-C1-C2-C3

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	401	XT2	2	0
3	C	310	SO4	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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 [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	581/589 (98%)	0.14	19 (3%) 49 42	44, 68, 102, 141	0
2	C	288/309 (93%)	-0.31	1 (0%) 90 88	38, 53, 70, 90	0
All	All	869/898 (96%)	-0.01	20 (2%) 61 53	38, 62, 95, 141	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	140	TRP	5.4
1	A	22	ASN	4.7
1	A	24	ASP	3.5
1	A	60	TYR	3.2
1	A	25	VAL	3.2
1	A	23	GLU	3.0
1	A	64	GLU	2.9
1	A	369	PHE	2.8
1	A	415	ALA	2.7
1	A	379	GLU	2.6
1	A	84	GLU	2.5
1	A	411	LEU	2.4
1	A	26	GLN	2.4
1	A	100	GLU	2.4
1	A	589	ALA	2.3
1	A	390	CYS	2.3
2	C	6	PHE	2.2
1	A	61	ASP	2.1
1	A	98	THR	2.1
1	A	34	LYS	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](#)

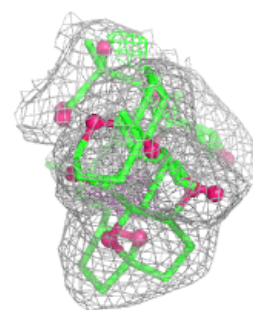
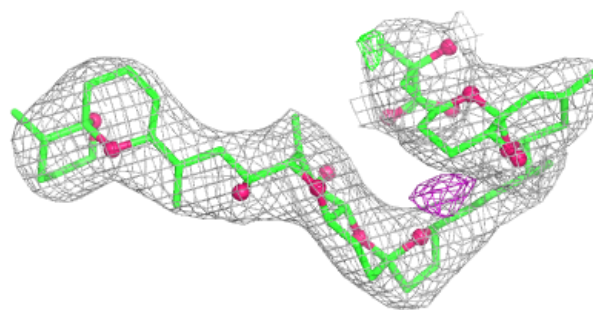
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	C	311	5/5	0.70	0.26	66,67,67,70	5
3	SO4	C	310	5/5	0.90	0.18	61,62,62,63	5
3	SO4	A	590	5/5	0.93	0.12	47,48,51,51	5
4	XT2	C	401	57/57	0.95	0.10	52,59,69,70	0
5	MN	C	502	1/1	0.96	0.06	59,59,59,59	0
5	MN	C	501	1/1	0.99	0.02	41,41,41,41	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around XT2 C 401:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.