



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:34 AM UTC

PDB ID : 1X9P / pdb_00001x9p
Title : The crystal structure of human adenovirus 2 penton base
Authors : Zubieta, C.; Schoehn, G.; Chroboczek, J.; Cusack, S.
Deposited on : 2004-08-24
Resolution : 3.30 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 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

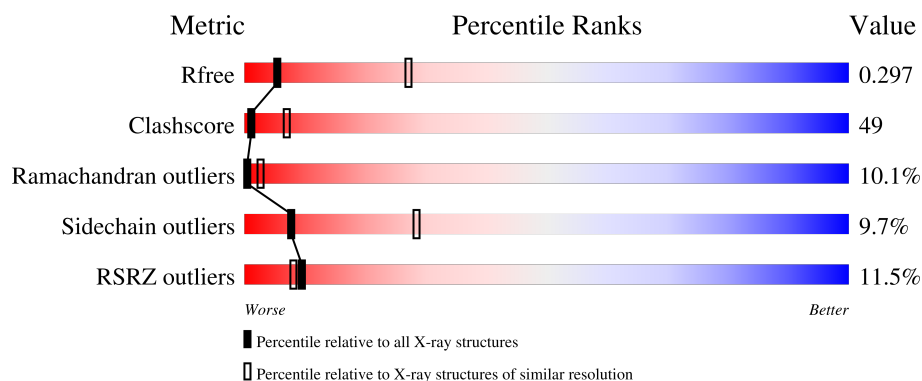
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	523	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	700	-	X	-	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3677 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 Penton protein.

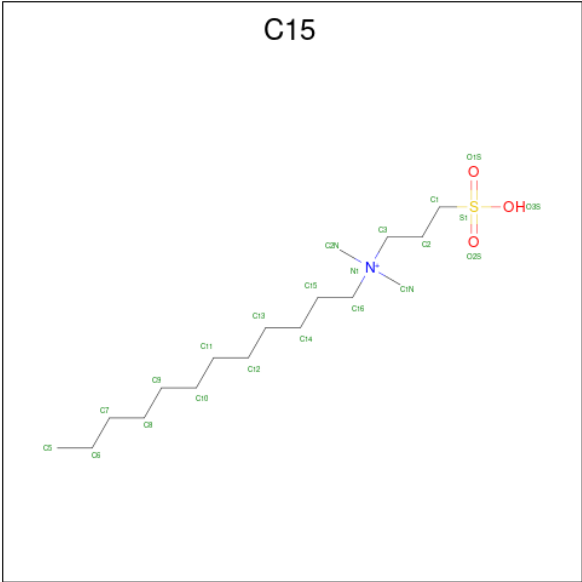
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	460	3632	2294	630	696	12	0	0	0

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 3 is N-DODECYL-N,N-DIMETHYL-3-AMMONIO-1-PROPANESULFONATE (CCD ID: C15) (formula: C₁₇H₃₈NO₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			20	15	1	3	1		
3	A	1	Total	C	N	O	S	0	0
			20	15	1	3	1		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	435.98Å 300.17Å 420.62Å 90.00° 104.36° 90.00°	Depositor
Resolution (Å)	20.00 – 3.30 20.00 – 3.30	Depositor EDS
% Data completeness (in resolution range)	57.1 (20.00-3.30) 56.9 (20.00-3.30)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	0.21	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 3.29Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.307 , 0.307 0.296 , 0.297	Depositor DCC
R_{free} test set	22325 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	80.1	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 20.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.24	EDS
Total number of atoms	3677	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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: C15, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.74	1/3715 (0.0%)	1.27	45/5057 (0.9%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	344	PHE	C-N	7.56	1.42	1.33

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	207	GLY	N-CA-C	11.98	127.11	112.73
1	A	265	GLN	CA-C-N	10.95	133.52	119.84
1	A	265	GLN	C-N-CA	10.95	133.52	119.84
1	A	468	LEU	CA-C-N	9.88	132.19	119.84
1	A	468	LEU	C-N-CA	9.88	132.19	119.84
1	A	441	LEU	CA-C-N	8.74	130.76	119.84
1	A	441	LEU	C-N-CA	8.74	130.76	119.84
1	A	396	ASN	N-CA-C	-8.50	103.07	113.19
1	A	61	ALA	CA-C-N	8.38	128.70	119.90
1	A	61	ALA	C-N-CA	8.38	128.70	119.90
1	A	76	SER	N-CA-C	8.06	120.78	111.11
1	A	376	LYS	CA-C-N	7.69	128.65	120.12
1	A	376	LYS	C-N-CA	7.69	128.65	120.12
1	A	103	PRO	N-CA-C	-7.52	103.32	113.40
1	A	488	GLN	N-CA-C	-7.37	104.09	113.23
1	A	427	THR	CA-C-N	7.33	129.00	119.84
1	A	427	THR	C-N-CA	7.33	129.00	119.84
1	A	447	ASP	CA-C-N	7.12	128.74	119.84
1	A	447	ASP	C-N-CA	7.12	128.74	119.84
1	A	512	THR	N-CA-C	-6.65	100.44	110.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	100	ASP	N-CA-C	6.49	121.20	113.16
1	A	81	SER	N-CA-C	6.37	121.25	112.90
1	A	344	PHE	CA-C-O	6.16	131.28	120.80
1	A	63	LEU	N-CA-C	-6.13	99.41	109.40
1	A	113	LEU	N-CA-C	-6.00	101.39	110.28
1	A	558	LEU	CA-C-N	-5.87	117.66	121.65
1	A	558	LEU	C-N-CA	-5.87	117.66	121.65
1	A	94	THR	N-CA-C	-5.82	99.71	108.96
1	A	175	TYR	N-CA-C	5.82	118.72	109.65
1	A	505	LEU	N-CA-C	-5.78	106.27	113.15
1	A	477	ASN	N-CA-C	5.75	117.67	108.41
1	A	70	TYR	N-CA-C	5.75	118.27	108.90
1	A	282	ASN	N-CA-C	-5.57	100.61	109.96
1	A	55	ILE	N-CA-C	-5.48	99.26	107.37
1	A	137	PHE	N-CA-C	-5.37	99.36	110.80
1	A	411	ASN	N-CA-C	5.36	118.99	112.23
1	A	426	CYS	N-CA-C	5.36	116.43	108.60
1	A	237	HIS	CA-C-N	5.33	125.32	119.89
1	A	237	HIS	C-N-CA	5.33	125.32	119.89
1	A	180	THR	N-CA-C	-5.20	105.26	111.03
1	A	225	LEU	N-CA-C	5.14	117.01	109.24
1	A	449	VAL	N-CA-C	5.13	120.01	109.34
1	A	96	ILE	CB-CA-C	-5.13	105.69	111.23
1	A	499	PHE	CA-C-N	5.10	126.21	119.84
1	A	499	PHE	C-N-CA	5.10	126.21	119.84

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	3632	0	3535	354	0
2	A	5	0	0	0	0
3	A	40	0	64	5	0
All	All	3677	0	3599	356	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 49.

All (356) 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:68:ARG:HH11	1:A:68:ARG:HG2	1.25	0.99
1:A:444:MET:HE1	1:A:561:VAL:HG21	1.47	0.94
1:A:295:SER:HB3	1:A:377:PRO:HG3	1.51	0.91
1:A:278:LEU:HD23	1:A:419:ILE:HD12	1.53	0.91
1:A:292:TYR:HA	1:A:377:PRO:CG	2.01	0.90
1:A:68:ARG:HH12	1:A:562:SER:HB3	1.38	0.89
1:A:451:PHE:HD2	1:A:461:PRO:HA	1.38	0.89
1:A:376:LYS:HB3	1:A:377:PRO:HD2	1.54	0.88
1:A:83:ASN:HD22	1:A:91:PHE:HB2	1.40	0.86
1:A:504:ILE:HG22	1:A:505:LEU:HD23	1.57	0.86
1:A:211:ASP:HA	1:A:508:PRO:CG	2.05	0.86
1:A:52:ARG:HB3	1:A:117:SER:OG	1.75	0.86
1:A:193:LEU:HD11	1:A:498:ARG:HH12	1.41	0.85
1:A:58:SER:O	1:A:60:LEU:N	2.09	0.84
1:A:178:THR:HG21	1:A:511:PRO:HD2	1.60	0.84
1:A:49:THR:HG23	1:A:53:ASN:OD1	1.79	0.83
1:A:156:ASP:O	1:A:157:LYS:HG3	1.78	0.83
1:A:214:ASN:HD22	1:A:214:ASN:C	1.86	0.83
1:A:468:LEU:HD12	1:A:469:PRO:HD2	1.59	0.82
1:A:544:THR:CG2	1:A:548:ARG:HA	2.10	0.81
1:A:384:GLU:HG2	1:A:390:SER:HA	1.62	0.80
1:A:237:HIS:CD2	1:A:425:LEU:HD11	2.18	0.78
1:A:249:ASP:C	1:A:249:ASP:OD1	2.26	0.78
1:A:154:THR:OG1	1:A:160:GLU:HB2	1.84	0.77
1:A:389:ARG:HD3	1:A:502:ASN:HD22	1.47	0.77
1:A:379:ILE:O	1:A:381:PRO:HD3	1.85	0.76
1:A:211:ASP:HA	1:A:508:PRO:HG3	1.67	0.76
1:A:403:TYR:CE1	1:A:504:ILE:HG21	2.21	0.76
1:A:292:TYR:HA	1:A:377:PRO:HG2	1.67	0.76
1:A:68:ARG:NH1	1:A:562:SER:HB3	2.01	0.75
1:A:475:PHE:O	1:A:513:ILE:HA	1.87	0.74
1:A:295:SER:O	1:A:296:LEU:HB2	1.88	0.74
1:A:451:PHE:CD2	1:A:461:PRO:HA	2.22	0.73
1:A:544:THR:HG22	1:A:548:ARG:HA	1.70	0.73
1:A:441:LEU:HD12	1:A:445:MET:HE2	1.71	0.73
1:A:145:ALA:HB3	1:A:168:PHE:HE1	1.53	0.72
1:A:148:MET:HA	1:A:163:TYR:HD2	1.54	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:LYS:HG2	1:A:169:THR:HG22	1.70	0.72
1:A:244:PRO:HA	1:A:275:TYR:CD2	2.24	0.72
1:A:197:ARG:HG3	1:A:198:GLN:N	2.05	0.72
1:A:243:LEU:HD21	1:A:403:TYR:CE2	2.23	0.72
1:A:403:TYR:HD1	1:A:504:ILE:HD13	1.52	0.72
1:A:468:LEU:CD1	1:A:469:PRO:HD2	2.19	0.72
1:A:419:ILE:HG22	1:A:423:THR:CG2	2.21	0.71
1:A:160:GLU:OE2	1:A:162:LYS:HE3	1.91	0.70
1:A:243:LEU:HD21	1:A:403:TYR:CD2	2.26	0.70
1:A:249:ASP:HB2	1:A:272:ARG:HG2	1.73	0.70
1:A:68:ARG:HG2	1:A:68:ARG:NH1	1.92	0.69
1:A:215:PHE:CE1	1:A:241:ILE:HD11	2.27	0.69
1:A:444:MET:O	1:A:444:MET:HG2	1.92	0.69
1:A:122:ASP:OD1	1:A:528:THR:HB	1.91	0.69
1:A:142:LYS:HD3	1:A:167:GLU:OE2	1.93	0.69
1:A:217:LEU:HB2	1:A:232:THR:HG21	1.73	0.69
1:A:419:ILE:HG22	1:A:423:THR:HG21	1.75	0.68
1:A:146:ARG:O	1:A:246:CYS:HB2	1.94	0.68
1:A:149:VAL:HG23	1:A:195:VAL:HG11	1.76	0.68
1:A:278:LEU:HD22	1:A:406:TRP:HA	1.76	0.68
1:A:512:THR:O	1:A:513:ILE:HB	1.93	0.67
1:A:217:LEU:HB2	1:A:232:THR:CG2	2.25	0.66
1:A:227:MET:HB2	1:A:228:PRO:HD3	1.76	0.66
1:A:430:VAL:HG21	1:A:517:SER:N	2.10	0.66
1:A:468:LEU:HD12	1:A:469:PRO:CD	2.26	0.66
1:A:386:SER:O	1:A:387:LYS:HB2	1.94	0.66
1:A:393:LEU:HD12	1:A:393:LEU:N	2.12	0.65
1:A:60:LEU:O	1:A:61:ALA:HB3	1.97	0.65
1:A:193:LEU:HD11	1:A:498:ARG:NH1	2.12	0.65
1:A:83:ASN:OD1	1:A:83:ASN:N	2.26	0.64
1:A:211:ASP:O	1:A:212:THR:HG22	1.97	0.64
1:A:513:ILE:HG22	1:A:513:ILE:O	1.97	0.64
1:A:133:ASN:HB2	1:A:174:ASN:OD1	1.97	0.64
1:A:278:LEU:O	1:A:404:ARG:HD3	1.98	0.63
1:A:422:TRP:CZ3	3:A:999:C15:H1C2	2.34	0.63
1:A:544:THR:HG21	1:A:548:ARG:HD2	1.81	0.63
1:A:287:LEU:HD23	1:A:287:LEU:C	2.24	0.62
1:A:493:THR:HG21	1:A:497:ASN:O	1.99	0.62
1:A:499:PHE:N	1:A:500:PRO:HD3	2.13	0.62
1:A:134:VAL:HA	1:A:140:THR:OG1	1.99	0.62
1:A:148:MET:HA	1:A:163:TYR:CD2	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:THR:CG2	1:A:511:PRO:HD2	2.30	0.62
1:A:394:ILE:HG23	1:A:398:SER:HB2	1.82	0.62
1:A:125:THR:HG23	1:A:524:THR:CG2	2.29	0.61
1:A:125:THR:CG2	1:A:526:HIS:NE2	2.63	0.61
1:A:220:ASP:OD1	1:A:222:VAL:HG12	2.00	0.61
1:A:233:ASN:CG	1:A:233:ASN:O	2.43	0.61
1:A:444:MET:HB2	1:A:539:GLN:OE1	2.01	0.61
1:A:278:LEU:HD23	1:A:419:ILE:CD1	2.30	0.60
1:A:394:ILE:HG23	1:A:395:SER:H	1.67	0.60
1:A:258:LEU:HD12	1:A:258:LEU:O	2.00	0.60
1:A:60:LEU:O	1:A:60:LEU:HG	2.00	0.60
1:A:263:LYS:NZ	1:A:268:GLN:HB2	2.16	0.60
1:A:383:THR:HG22	1:A:384:GLU:HG3	1.83	0.60
1:A:440:SER:HB3	1:A:461:PRO:O	2.02	0.60
1:A:125:THR:HG21	1:A:526:HIS:NE2	2.17	0.60
1:A:410:TYR:CD1	1:A:420:ARG:HA	2.37	0.60
1:A:378:VAL:HG12	1:A:379:ILE:N	2.15	0.60
1:A:278:LEU:CD2	1:A:406:TRP:HA	2.32	0.59
1:A:282:ASN:HD21	1:A:404:ARG:HE	1.50	0.59
1:A:378:VAL:O	1:A:380:LYS:N	2.35	0.59
1:A:494:HIS:C	1:A:496:PHE:H	2.07	0.59
1:A:243:LEU:HD11	1:A:403:TYR:HE2	1.67	0.59
1:A:501:GLU:H	1:A:501:GLU:CD	2.10	0.59
1:A:75:LYS:HZ2	1:A:94:THR:HG23	1.68	0.59
1:A:224:GLY:O	1:A:399:THR:HB	2.03	0.59
1:A:211:ASP:CG	1:A:212:THR:H	2.10	0.59
1:A:525:ASP:C	1:A:525:ASP:OD1	2.45	0.59
1:A:243:LEU:CD2	1:A:403:TYR:CD2	2.86	0.59
1:A:389:ARG:NH1	1:A:389:ARG:HG2	2.17	0.59
1:A:440:SER:C	1:A:442:PRO:HD3	2.27	0.59
1:A:220:ASP:HB2	1:A:227:MET:HG2	1.84	0.58
1:A:520:VAL:CG2	1:A:521:PRO:HD2	2.33	0.58
1:A:385:ASP:O	1:A:386:SER:C	2.45	0.58
1:A:154:THR:HG22	1:A:155:LYS:N	2.18	0.58
1:A:197:ARG:HG3	1:A:198:GLN:CG	2.33	0.58
1:A:203:GLU:C	1:A:205:ASP:H	2.11	0.58
1:A:478:ASP:C	1:A:480:ALA:H	2.12	0.58
1:A:211:ASP:O	1:A:212:THR:CG2	2.52	0.58
1:A:282:ASN:ND2	1:A:404:ARG:HE	2.03	0.57
1:A:482:TYR:CE1	1:A:486:ILE:HD12	2.40	0.57
1:A:53:ASN:O	1:A:54:SER:C	2.48	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:THR:CG2	1:A:524:THR:HG23	2.35	0.56
1:A:134:VAL:HG22	1:A:173:GLY:O	2.05	0.56
1:A:263:LYS:HZ3	1:A:268:GLN:HB2	1.70	0.56
1:A:67:THR:O	1:A:68:ARG:HG2	2.06	0.56
1:A:392:ASN:HB3	1:A:402:GLN:NE2	2.21	0.56
1:A:479:GLN:HG2	1:A:479:GLN:O	2.05	0.56
1:A:494:HIS:C	1:A:496:PHE:N	2.64	0.56
1:A:239:ASP:C	1:A:239:ASP:OD1	2.46	0.56
1:A:419:ILE:O	1:A:423:THR:HG22	2.06	0.56
1:A:428:PRO:O	1:A:429:ASP:HB3	2.06	0.55
1:A:273:ILE:O	1:A:273:ILE:HG23	2.05	0.55
1:A:395:SER:C	1:A:397:ASP:H	2.14	0.55
1:A:214:ASN:C	1:A:214:ASN:ND2	2.55	0.55
1:A:68:ARG:NH1	1:A:68:ARG:CG	2.66	0.55
1:A:544:THR:HG21	1:A:548:ARG:HA	1.89	0.55
1:A:283:ILE:O	1:A:401:THR:HG23	2.07	0.54
1:A:493:THR:HG22	1:A:494:HIS:N	2.21	0.54
1:A:505:LEU:O	1:A:506:ALA:O	2.26	0.54
1:A:197:ARG:HG3	1:A:198:GLN:H	1.71	0.54
1:A:389:ARG:HG2	1:A:389:ARG:HH11	1.73	0.54
1:A:192:TYR:CZ	1:A:197:ARG:HB3	2.43	0.54
1:A:136:GLU:O	1:A:137:PHE:HB2	2.07	0.54
1:A:266:PRO:C	1:A:268:GLN:H	2.15	0.54
1:A:463:VAL:HB	1:A:529:LEU:CD1	2.38	0.53
1:A:215:PHE:HE1	1:A:241:ILE:HD11	1.71	0.53
1:A:154:THR:CG2	1:A:155:LYS:N	2.72	0.53
1:A:69:VAL:CG2	1:A:561:VAL:HB	2.39	0.53
1:A:208:VAL:O	1:A:208:VAL:HG23	2.08	0.53
1:A:236:PHE:O	1:A:237:HIS:HB3	2.09	0.53
1:A:151:ARG:HG3	1:A:161:LEU:CD2	2.39	0.53
1:A:151:ARG:HG3	1:A:161:LEU:HD21	1.91	0.53
1:A:197:ARG:C	1:A:199:ASN:H	2.17	0.53
1:A:222:VAL:HG13	1:A:223:THR:N	2.24	0.53
1:A:386:SER:O	1:A:387:LYS:CB	2.57	0.52
1:A:441:LEU:N	1:A:442:PRO:HD3	2.24	0.52
1:A:449:VAL:HG12	1:A:450:THR:N	2.23	0.52
1:A:211:ASP:HA	1:A:508:PRO:HG2	1.89	0.52
1:A:93:THR:HG22	1:A:94:THR:N	2.23	0.52
1:A:413:GLY:O	1:A:414:ASP:C	2.53	0.52
1:A:120:GLY:O	1:A:563:PRO:HA	2.10	0.52
1:A:403:TYR:CD1	1:A:504:ILE:HG21	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:ARG:HB3	1:A:200:GLY:O	2.10	0.52
1:A:125:THR:HG22	1:A:524:THR:HG23	1.92	0.51
1:A:138:MET:HB3	1:A:254:ARG:NH1	2.26	0.51
1:A:180:THR:HG21	1:A:258:LEU:CD2	2.40	0.51
1:A:520:VAL:HG23	1:A:521:PRO:HD2	1.92	0.51
1:A:125:THR:CG2	1:A:524:THR:CG2	2.88	0.51
1:A:211:ASP:C	1:A:212:THR:CG2	2.84	0.51
1:A:403:TYR:CD1	1:A:504:ILE:HD13	2.39	0.51
1:A:425:LEU:HD12	1:A:426:CYS:N	2.26	0.51
1:A:403:TYR:HD1	1:A:504:ILE:CD1	2.19	0.51
1:A:430:VAL:HG23	1:A:517:SER:HB2	1.93	0.51
1:A:547:ARG:O	1:A:548:ARG:HB2	2.11	0.51
1:A:266:PRO:O	1:A:268:GLN:N	2.43	0.50
1:A:130:ASN:HA	1:A:519:ASN:CG	2.36	0.50
1:A:233:ASN:O	1:A:233:ASN:OD1	2.30	0.50
1:A:233:ASN:OD1	1:A:233:ASN:C	2.54	0.50
1:A:295:SER:OG	1:A:377:PRO:HD3	2.10	0.50
1:A:60:LEU:O	1:A:61:ALA:CB	2.59	0.50
1:A:422:TRP:CD1	1:A:422:TRP:H	2.29	0.50
1:A:135:ASN:HA	1:A:172:GLU:HG2	1.94	0.50
1:A:192:TYR:CD2	1:A:193:LEU:HD23	2.47	0.50
1:A:243:LEU:CD2	1:A:244:PRO:HD3	2.42	0.50
1:A:243:LEU:CD2	1:A:403:TYR:HD2	2.24	0.50
1:A:292:TYR:HA	1:A:377:PRO:HG3	1.90	0.50
1:A:132:PRO:HD3	1:A:553:TYR:CE2	2.46	0.50
1:A:197:ARG:HG3	1:A:198:GLN:HG2	1.93	0.50
1:A:178:THR:O	1:A:181:ILE:N	2.45	0.50
1:A:237:HIS:ND1	1:A:238:PRO:O	2.45	0.50
1:A:264:ARG:NH1	1:A:424:LEU:HD13	2.26	0.50
1:A:61:ALA:HB1	1:A:62:PRO:CD	2.42	0.49
1:A:67:THR:OG1	1:A:68:ARG:N	2.45	0.49
1:A:126:ILE:HG23	1:A:523:LEU:HD23	1.94	0.49
1:A:394:ILE:HG22	1:A:400:PHE:O	2.13	0.49
1:A:544:THR:HG22	1:A:545:ASP:N	2.27	0.49
1:A:114:ASP:OD1	1:A:115:ASP:N	2.45	0.49
1:A:258:LEU:HD12	1:A:258:LEU:C	2.38	0.49
1:A:427:THR:HG23	1:A:428:PRO:HD2	1.94	0.49
1:A:171:PRO:O	1:A:175:TYR:OH	2.25	0.49
1:A:212:THR:HG23	1:A:508:PRO:HB3	1.94	0.49
1:A:491:SER:O	1:A:492:LEU:O	2.29	0.49
1:A:346:THR:C	1:A:348:ALA:H	2.21	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:ARG:HG3	1:A:198:GLN:HG3	1.94	0.49
1:A:211:ASP:OD1	1:A:213:ARG:HG2	2.13	0.49
1:A:468:LEU:HD12	1:A:468:LEU:C	2.38	0.49
1:A:203:GLU:O	1:A:205:ASP:N	2.46	0.48
3:A:999:C15:H131	3:A:999:C15:H2C1	1.95	0.48
1:A:125:THR:HG22	1:A:526:HIS:NE2	2.28	0.48
1:A:214:ASN:HD21	1:A:216:ARG:HG2	1.78	0.48
1:A:129:THR:HG22	1:A:553:TYR:O	2.13	0.48
1:A:202:LEU:O	1:A:203:GLU:C	2.55	0.48
1:A:243:LEU:HD22	1:A:244:PRO:CD	2.43	0.48
1:A:476:TYR:HD1	1:A:513:ILE:HD12	1.79	0.48
1:A:391:TYR:O	1:A:392:ASN:C	2.57	0.48
1:A:449:VAL:HG12	1:A:450:THR:HG23	1.95	0.48
1:A:98:ASN:HD22	1:A:99:ASN:N	2.11	0.48
1:A:69:VAL:HG22	1:A:561:VAL:HB	1.95	0.48
1:A:106:ALA:C	1:A:108:THR:H	2.22	0.48
1:A:66:THR:HA	1:A:563:PRO:O	2.13	0.48
1:A:203:GLU:C	1:A:205:ASP:N	2.70	0.48
1:A:243:LEU:HD22	1:A:244:PRO:HD2	1.96	0.48
1:A:451:PHE:HE2	1:A:462:VAL:HG23	1.78	0.48
1:A:545:ASP:OD1	1:A:549:ARG:HG2	2.13	0.48
1:A:444:MET:HB2	1:A:539:GLN:CD	2.39	0.47
1:A:410:TYR:O	1:A:420:ARG:HD3	2.14	0.47
1:A:430:VAL:CG2	1:A:431:THR:N	2.77	0.47
1:A:91:PHE:N	1:A:91:PHE:CD2	2.81	0.47
1:A:203:GLU:HA	1:A:206:ILE:HG13	1.96	0.47
1:A:431:THR:O	1:A:432:CYS:HB2	2.14	0.47
1:A:78:ASP:OD1	1:A:94:THR:HG22	2.15	0.47
1:A:106:ALA:C	1:A:108:THR:N	2.71	0.47
1:A:216:ARG:O	1:A:216:ARG:HG3	2.15	0.47
1:A:499:PHE:N	1:A:500:PRO:CD	2.77	0.47
1:A:445:MET:HE3	1:A:463:VAL:HG11	1.97	0.47
1:A:131:MET:HA	1:A:553:TYR:CD2	2.50	0.47
1:A:149:VAL:CG2	1:A:195:VAL:HG11	2.45	0.47
1:A:405:SER:HB3	1:A:408:LEU:HB2	1.97	0.47
1:A:502:ASN:C	1:A:504:ILE:H	2.23	0.47
1:A:178:THR:C	1:A:180:THR:N	2.73	0.46
1:A:180:THR:O	1:A:181:ILE:C	2.58	0.46
1:A:65:ASP:O	1:A:66:THR:C	2.57	0.46
1:A:146:ARG:NH1	3:A:998:C15:H1C1	2.30	0.46
1:A:395:SER:C	1:A:397:ASP:N	2.71	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:478:ASP:C	1:A:480:ALA:N	2.73	0.46
1:A:538:VAL:HG23	1:A:538:VAL:O	2.14	0.46
1:A:202:LEU:O	1:A:205:ASP:OD1	2.34	0.46
1:A:261:ILE:HD12	1:A:406:TRP:CE3	2.50	0.46
1:A:468:LEU:HA	1:A:469:PRO:HD3	1.76	0.46
1:A:244:PRO:HA	1:A:275:TYR:CE2	2.51	0.46
1:A:513:ILE:HD12	1:A:513:ILE:N	2.31	0.46
1:A:146:ARG:HE	1:A:246:CYS:HA	1.80	0.46
1:A:197:ARG:CG	1:A:198:GLN:N	2.72	0.46
3:A:999:C15:H151	3:A:999:C15:H1C1	1.98	0.46
1:A:138:MET:HE3	1:A:254:ARG:NH1	2.31	0.46
1:A:178:THR:O	1:A:180:THR:N	2.49	0.46
1:A:481:VAL:O	1:A:482:TYR:C	2.57	0.46
1:A:51:GLY:HA3	1:A:116:ARG:HH12	1.81	0.45
1:A:151:ARG:NH1	1:A:205:ASP:OD2	2.49	0.45
1:A:287:LEU:HD23	1:A:288:ASP:C	2.41	0.45
1:A:493:THR:HG22	1:A:494:HIS:O	2.16	0.45
1:A:225:LEU:HD22	1:A:285:ALA:O	2.16	0.45
1:A:93:THR:HG22	1:A:94:THR:O	2.17	0.45
1:A:135:ASN:HA	1:A:172:GLU:CG	2.47	0.45
1:A:138:MET:HB3	1:A:254:ARG:HH11	1.80	0.45
1:A:383:THR:C	1:A:384:GLU:HG3	2.41	0.45
1:A:146:ARG:HB2	1:A:165:TRP:CD2	2.52	0.45
1:A:544:THR:HG23	1:A:549:ARG:N	2.31	0.45
1:A:211:ASP:C	1:A:212:THR:HG23	2.41	0.45
1:A:215:PHE:O	1:A:216:ARG:HB3	2.15	0.45
1:A:504:ILE:C	1:A:506:ALA:H	2.25	0.45
1:A:243:LEU:CD2	1:A:403:TYR:CE2	2.96	0.45
1:A:135:ASN:HB2	1:A:172:GLU:OE2	2.16	0.45
1:A:419:ILE:C	1:A:421:SER:N	2.72	0.45
1:A:132:PRO:HD3	1:A:553:TYR:CD2	2.51	0.45
1:A:180:THR:HG21	1:A:258:LEU:HD23	1.97	0.45
1:A:243:LEU:HD23	1:A:244:PRO:HD3	1.99	0.44
1:A:446:GLN:O	1:A:448:PRO:HD3	2.17	0.44
1:A:389:ARG:HH11	1:A:389:ARG:CG	2.28	0.44
1:A:558:LEU:HA	1:A:558:LEU:HD23	1.62	0.44
1:A:49:THR:O	1:A:50:GLY:C	2.60	0.44
1:A:154:THR:HG1	1:A:160:GLU:HB2	1.80	0.44
1:A:170:LEU:HB3	1:A:171:PRO:HD2	1.99	0.44
1:A:202:LEU:C	1:A:204:SER:N	2.75	0.44
1:A:229:GLY:O	1:A:286:LEU:HD13	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:420:ARG:O	1:A:420:ARG:HG3	2.17	0.44
1:A:493:THR:CG2	1:A:494:HIS:N	2.80	0.44
1:A:533:ASN:OD1	1:A:533:ASN:N	2.50	0.44
1:A:250:PHE:O	1:A:252:HIS:N	2.50	0.44
1:A:74:ASN:ND2	1:A:556:LYS:NZ	2.66	0.44
1:A:261:ILE:HD12	1:A:406:TRP:CZ3	2.53	0.44
1:A:272:ARG:HH12	3:A:998:C15:H3C1	1.82	0.44
1:A:195:VAL:HG12	1:A:196:GLY:N	2.32	0.44
1:A:476:TYR:HD1	1:A:513:ILE:CD1	2.30	0.44
1:A:83:ASN:ND2	1:A:92:LEU:O	2.51	0.43
1:A:225:LEU:HD13	1:A:287:LEU:HA	1.99	0.43
1:A:525:ASP:OD1	1:A:525:ASP:O	2.35	0.43
1:A:113:LEU:HD23	1:A:113:LEU:HA	1.71	0.43
1:A:230:VAL:HG13	1:A:503:GLN:CD	2.43	0.43
1:A:524:THR:OG1	1:A:525:ASP:N	2.52	0.43
1:A:290:ASP:O	1:A:291:ALA:C	2.60	0.43
1:A:197:ARG:CG	1:A:198:GLN:H	2.30	0.43
1:A:254:ARG:HH21	1:A:432:CYS:C	2.26	0.43
1:A:429:ASP:OD1	1:A:432:CYS:N	2.51	0.43
1:A:128:HIS:HD2	1:A:555:TYR:HD2	1.66	0.43
1:A:436:GLN:OE1	1:A:436:GLN:N	2.39	0.43
1:A:470:VAL:C	1:A:471:HIS:HD2	2.27	0.43
1:A:145:ALA:HB3	1:A:168:PHE:CE1	2.44	0.43
1:A:264:ARG:O	1:A:264:ARG:HG3	2.18	0.43
1:A:63:LEU:HD12	1:A:63:LEU:HA	1.82	0.43
1:A:295:SER:HB3	1:A:377:PRO:CG	2.33	0.43
1:A:389:ARG:CD	1:A:502:ASN:HD22	2.23	0.43
1:A:419:ILE:O	1:A:421:SER:N	2.52	0.43
1:A:463:VAL:HB	1:A:529:LEU:HD13	1.99	0.43
1:A:195:VAL:O	1:A:196:GLY:C	2.62	0.42
1:A:429:ASP:OD1	1:A:429:ASP:C	2.62	0.42
1:A:430:VAL:O	1:A:432:CYS:N	2.53	0.42
1:A:75:LYS:NZ	1:A:94:THR:HG23	2.32	0.42
1:A:217:LEU:CB	1:A:232:THR:HG21	2.46	0.42
1:A:275:TYR:CE1	1:A:404:ARG:HD2	2.54	0.42
1:A:393:LEU:N	1:A:393:LEU:CD1	2.81	0.42
1:A:427:THR:HA	1:A:428:PRO:HD3	1.75	0.42
1:A:497:ASN:O	1:A:500:PRO:HD3	2.19	0.42
1:A:135:ASN:N	1:A:140:THR:OG1	2.47	0.42
1:A:381:PRO:O	1:A:382:LEU:C	2.63	0.42
1:A:406:TRP:O	1:A:407:TYR:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:237:HIS:CD2	1:A:425:LEU:CD1	2.97	0.42
1:A:194:LYS:O	1:A:194:LYS:HG2	2.19	0.42
1:A:237:HIS:NE2	1:A:425:LEU:CD1	2.83	0.42
1:A:227:MET:C	1:A:229:GLY:H	2.27	0.42
1:A:68:ARG:NH1	1:A:562:SER:CB	2.79	0.41
1:A:93:THR:CG2	1:A:94:THR:N	2.83	0.41
1:A:266:PRO:C	1:A:268:GLN:N	2.78	0.41
1:A:149:VAL:HG22	1:A:149:VAL:O	2.21	0.41
1:A:230:VAL:HG13	1:A:503:GLN:NE2	2.35	0.41
1:A:406:TRP:HE1	1:A:419:ILE:HG21	1.85	0.41
1:A:382:LEU:HD12	1:A:382:LEU:HA	1.75	0.41
1:A:475:PHE:CD1	1:A:475:PHE:N	2.88	0.41
1:A:88:HIS:CD2	1:A:555:TYR:O	2.74	0.41
1:A:279:GLU:O	1:A:280:GLY:O	2.38	0.41
1:A:501:GLU:O	1:A:501:GLU:HG2	2.20	0.41
1:A:507:ARG:O	1:A:508:PRO:C	2.63	0.41
1:A:265:GLN:NE2	1:A:268:GLN:NE2	2.68	0.41
1:A:381:PRO:O	1:A:381:PRO:HG2	2.21	0.41
1:A:53:ASN:O	1:A:54:SER:O	2.38	0.41
1:A:98:ASN:C	1:A:98:ASN:ND2	2.78	0.41
1:A:134:VAL:HG21	1:A:175:TYR:CE2	2.56	0.41
1:A:467:LEU:HA	1:A:467:LEU:HD12	1.83	0.41
1:A:96:ILE:HG22	1:A:98:ASN:H	1.86	0.40
1:A:502:ASN:C	1:A:504:ILE:N	2.79	0.40
1:A:98:ASN:HD22	1:A:98:ASN:C	2.29	0.40
1:A:129:THR:HB	1:A:130:ASN:H	1.65	0.40
1:A:153:LEU:HD23	1:A:159:VAL:HG12	2.03	0.40
1:A:542:THR:O	1:A:542:THR:HG22	2.21	0.40
1:A:153:LEU:O	1:A:154:THR:C	2.62	0.40
1:A:268:GLN:O	1:A:269:GLU:C	2.61	0.40
1:A:481:VAL:HG13	1:A:482:TYR:N	2.37	0.40
1:A:78:ASP:OD1	1:A:94:THR:CG2	2.70	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries

of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	454/523 (87%)	332 (73%)	76 (17%)	46 (10%)	0 3

All (46) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	54	SER
1	A	59	GLU
1	A	130	ASN
1	A	137	PHE
1	A	296	LEU
1	A	375	LYS
1	A	378	VAL
1	A	379	ILE
1	A	449	VAL
1	A	469	PRO
1	A	492	LEU
1	A	506	ALA
1	A	50	GLY
1	A	79	VAL
1	A	157	LYS
1	A	196	GLY
1	A	204	SER
1	A	212	THR
1	A	216	ARG
1	A	251	THR
1	A	267	PHE
1	A	280	GLY
1	A	386	SER
1	A	527	GLY
1	A	66	THR
1	A	74	ASN
1	A	198	GLN
1	A	199	ASN
1	A	215	PHE
1	A	233	ASN
1	A	392	ASN
1	A	414	ASP
1	A	428	PRO
1	A	431	THR

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Mol	Chain	Res	Type
1	A	479	GLN
1	A	388	LYS
1	A	155	LYS
1	A	179	MET
1	A	232	THR
1	A	490	THR
1	A	513	ILE
1	A	61	ALA
1	A	237	HIS
1	A	266	PRO
1	A	486	ILE
1	A	195	VAL

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	404/451 (90%)	365 (90%)	39 (10%)	8 28

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	SER
1	A	68	ARG
1	A	72	VAL
1	A	76	SER
1	A	83	ASN
1	A	100	ASP
1	A	102	SER
1	A	153	LEU
1	A	166	VAL
1	A	183	LEU
1	A	203	GLU
1	A	214	ASN
1	A	223	THR
1	A	232	THR

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Mol	Chain	Res	Type
1	A	233	ASN
1	A	238	PRO
1	A	249	ASP
1	A	256	SER
1	A	258	LEU
1	A	262	ARG
1	A	287	LEU
1	A	389	ARG
1	A	401	THR
1	A	429	ASP
1	A	430	VAL
1	A	440	SER
1	A	446	GLN
1	A	468	LEU
1	A	473	LYS
1	A	482	TYR
1	A	512	THR
1	A	519	ASN
1	A	525	ASP
1	A	528	THR
1	A	531	LEU
1	A	533	ASN
1	A	534	SER
1	A	542	THR
1	A	562	SER

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	74	ASN
1	A	86	ASN
1	A	88	HIS
1	A	98	ASN
1	A	128	HIS
1	A	199	ASN
1	A	214	ASN
1	A	265	GLN
1	A	282	ASN
1	A	402	GLN
1	A	459	ASN
1	A	471	HIS

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 ⓘ

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	SO4	A	700	-	4,4,4	1.85	1 (25%)	6,6,6	3.67	3 (50%)
3	C15	A	998	-	19,19,21	2.09	2 (10%)	21,21,26	1.45	4 (19%)
3	C15	A	999	-	19,19,21	1.99	2 (10%)	21,21,26	1.42	4 (19%)

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
3	C15	A	998	-	-	8/17/17/21	-
3	C15	A	999	-	-	11/17/17/21	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	998	C15	O3S-S1	8.03	1.77	1.47
3	A	999	C15	O3S-S1	7.73	1.76	1.47
3	A	998	C15	C1-S1	3.83	1.83	1.77
3	A	999	C15	C1-S1	3.12	1.82	1.77
2	A	700	SO4	O1-S	3.12	1.63	1.44

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	700	SO4	O4-S-O1	-6.10	77.68	109.56
2	A	700	SO4	O4-S-O2	-4.99	83.46	109.56
3	A	998	C15	O2S-S1-C1	3.61	112.19	106.73
2	A	700	SO4	O4-S-O3	-3.23	90.73	108.54
3	A	999	C15	O2S-S1-C1	3.15	111.49	106.73
3	A	999	C15	O3S-S1-C1	2.62	111.13	106.00
3	A	998	C15	C2-C1-S1	2.27	116.73	113.25
3	A	998	C15	O3S-S1-O1S	-2.25	105.76	111.40
3	A	999	C15	C2-C1-S1	2.25	116.69	113.25
3	A	999	C15	O3S-S1-O1S	-2.15	106.02	111.40
3	A	998	C15	C9-C8-C7	-2.09	103.80	114.37

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	999	C15	C2-C1-S1-O3S
3	A	999	C15	C14-C15-C16-N1
3	A	998	C15	C2-C1-S1-O3S
3	A	998	C15	C12-C13-C14-C15
3	A	999	C15	C7-C8-C9-C10
3	A	999	C15	C9-C10-C11-C12
3	A	999	C15	C12-C13-C14-C15
3	A	999	C15	C1-C2-C3-N1
3	A	998	C15	C11-C10-C9-C8
3	A	998	C15	C2-C1-S1-O1S
3	A	998	C15	C2-C1-S1-O2S
3	A	999	C15	C2-C1-S1-O1S
3	A	999	C15	C2-C1-S1-O2S
3	A	998	C15	C9-C10-C11-C12
3	A	998	C15	C10-C11-C12-C13
3	A	998	C15	C5-C6-C7-C8
3	A	999	C15	C15-C16-N1-C3

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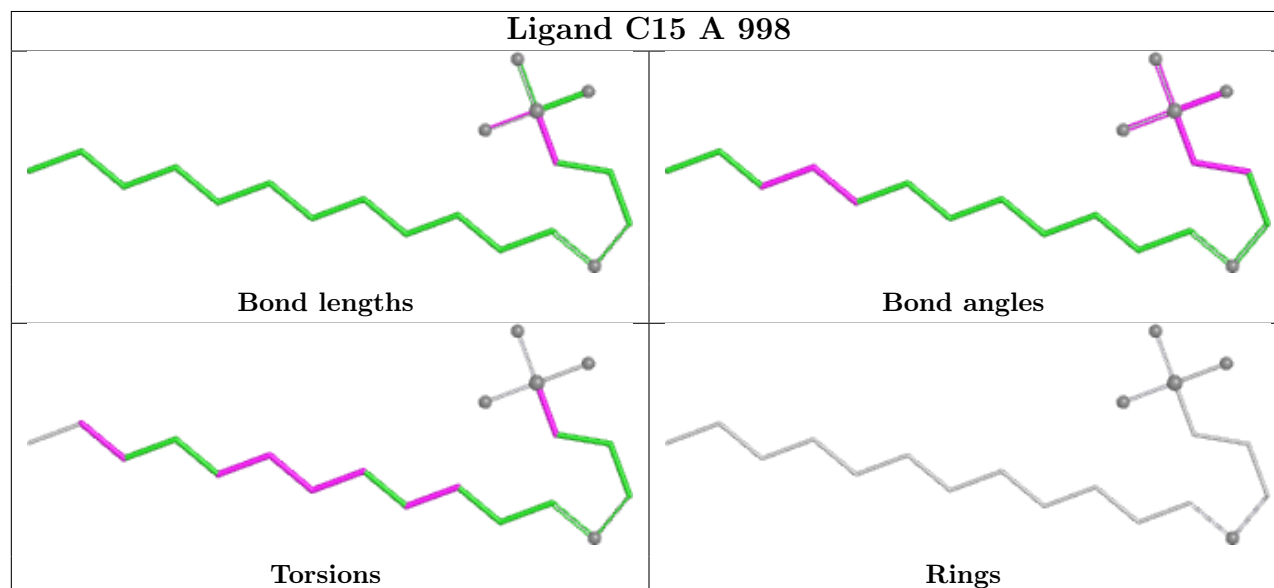
Mol	Chain	Res	Type	Atoms
3	A	999	C15	C2-C3-N1-C16
3	A	999	C15	C10-C11-C12-C13

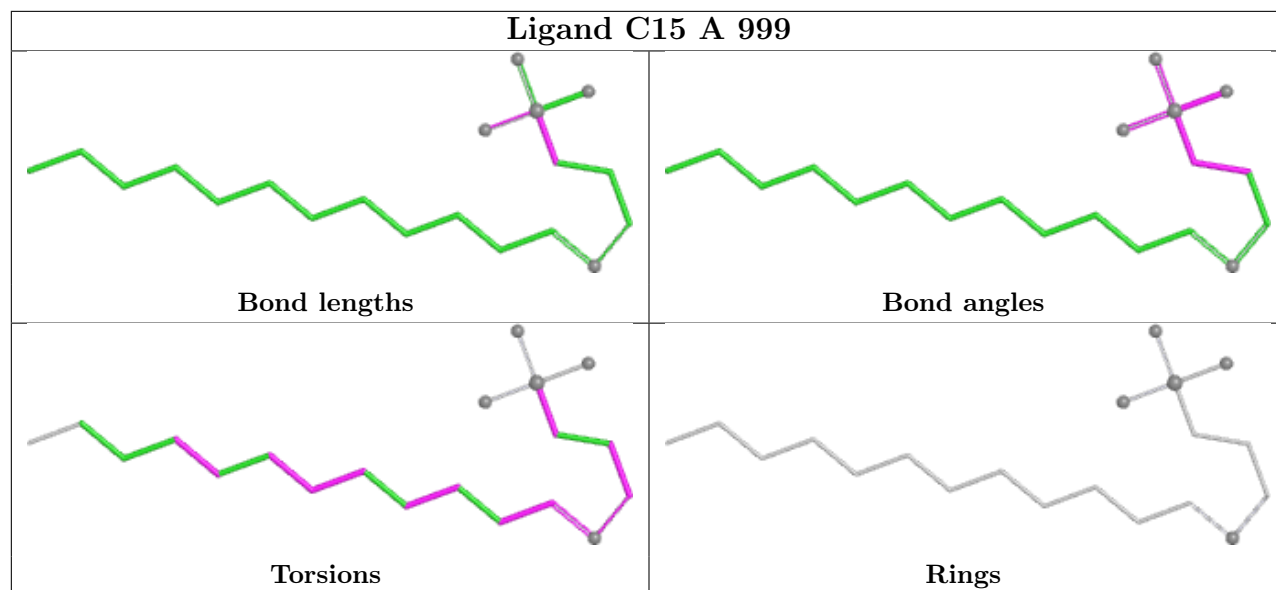
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	998	C15	2	0
3	A	999	C15	3	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 ⓘ

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	460/523 (87%)	0.73	53 (11%) 9 8	30, 54, 150, 186	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	298	ASP	7.5
1	A	156	ASP	5.7
1	A	297	LYS	4.9
1	A	350	GLU	4.6
1	A	247	GLY	4.3
1	A	376	LYS	4.3
1	A	344	PHE	4.2
1	A	488	GLN	4.2
1	A	356	GLU	4.0
1	A	517	SER	3.8
1	A	253	SER	3.6
1	A	355	ALA	3.5
1	A	200	GLY	3.4
1	A	379	ILE	3.4
1	A	201	VAL	3.3
1	A	152	SER	3.3
1	A	375	LYS	3.3
1	A	377	PRO	3.2
1	A	482	TYR	3.2
1	A	158	GLN	3.1
1	A	346	THR	3.1
1	A	492	LEU	3.0
1	A	177	GLU	2.9
1	A	169	THR	2.9
1	A	203	GLU	2.6
1	A	419	ILE	2.5
1	A	494	HIS	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	49	THR	2.5
1	A	157	LYS	2.4
1	A	510	ALA	2.4
1	A	151	ARG	2.4
1	A	153	LEU	2.4
1	A	282	ASN	2.3
1	A	479	GLN	2.3
1	A	493	THR	2.3
1	A	501	GLU	2.3
1	A	489	PHE	2.3
1	A	149	VAL	2.3
1	A	155	LYS	2.3
1	A	176	SER	2.2
1	A	447	ASP	2.2
1	A	420	ARG	2.2
1	A	398	SER	2.2
1	A	394	ILE	2.1
1	A	430	VAL	2.1
1	A	51	GLY	2.1
1	A	245	GLY	2.1
1	A	518	GLU	2.1
1	A	395	SER	2.1
1	A	497	ASN	2.1
1	A	345	ALA	2.1
1	A	80	ALA	2.0
1	A	96	ILE	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](#)

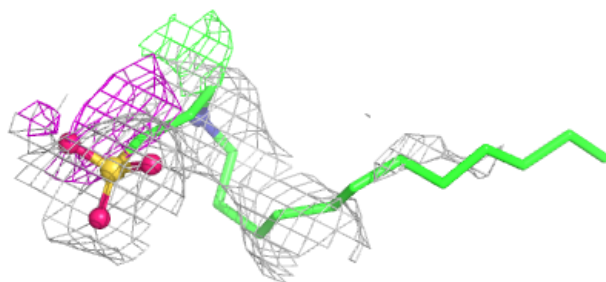
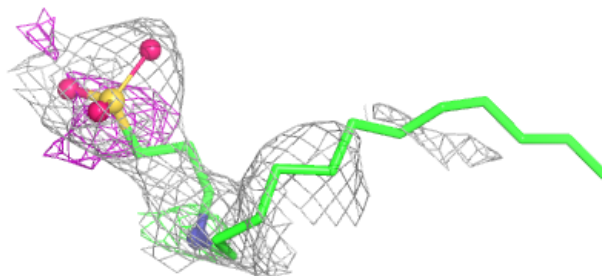
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
2	SO4	A	700	5/5	0.80	0.21	166,166,166,166	0
3	C15	A	999	20/22	0.87	0.29	70,83,94,94	0
3	C15	A	998	20/22	0.88	0.23	91,95,113,114	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.

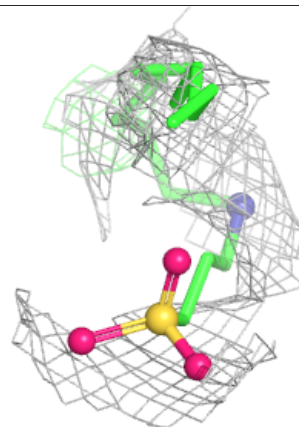
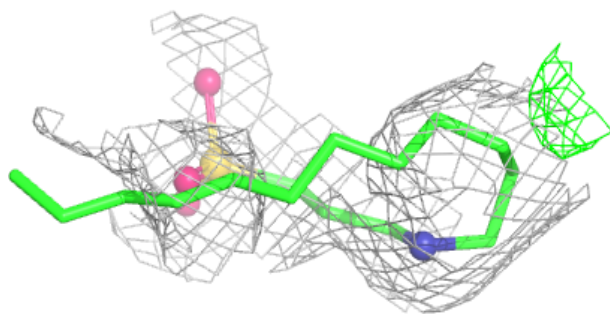
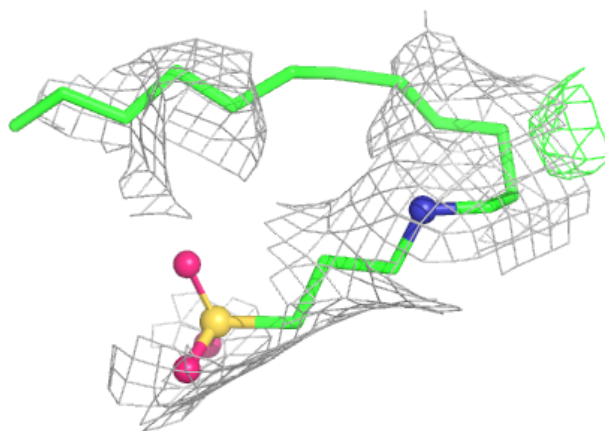
Electron density around C15 A 999:

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



Electron density around C15 A 998:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.