



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:51 PM UTC

PDB ID : 2NCD / pdb_00002ncd
Title : NCD (NON-CLARET DISJUNCTIONAL) DIMER FROM D.
MELANOGASTER
Authors : Sablin, E.P.; Case, R.B.; Dai, S.C.; Hart, C.L.; Ruby, A.; Vale, R.D.; Fletterick, R.J.
Deposited on : 1999-06-04
Resolution : 2.50 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

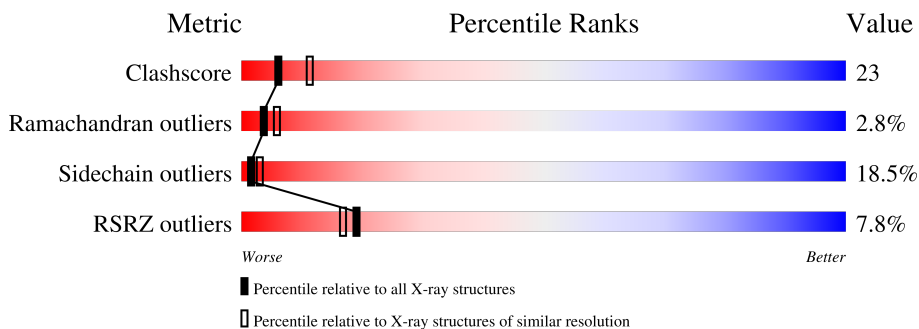
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	420	

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	1110	-	X	-	-
2	SO4	A	1112	-	X	-	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ADP	A	800	-	-	-	X

2 Entry composition [i](#)

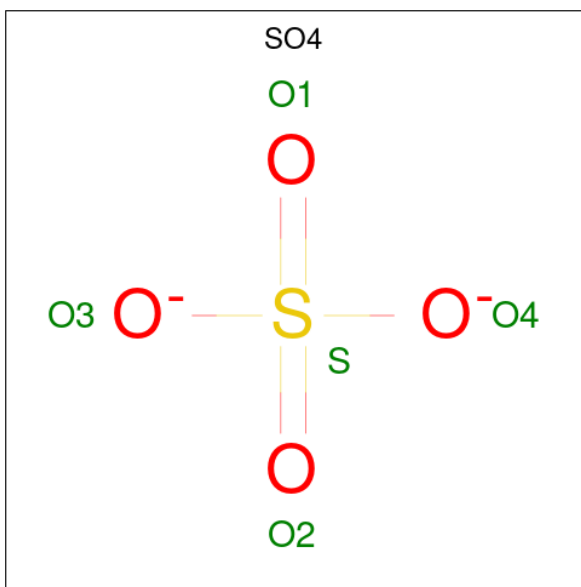
There are 4 unique types of molecules in this entry. The entry contains 2952 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTEIN (Kinesin motor NCD).

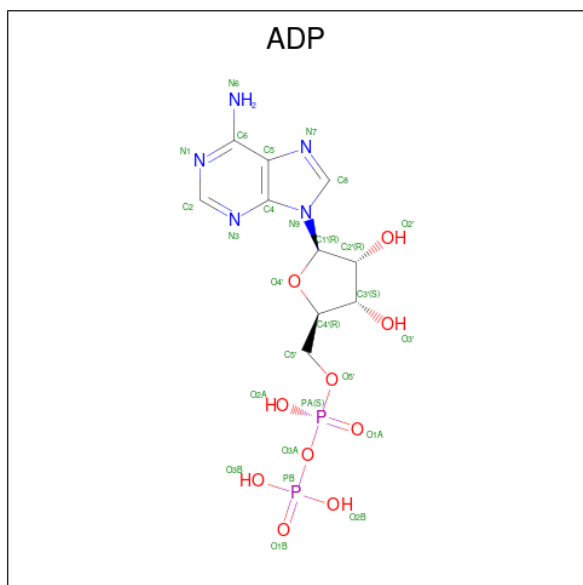
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	358	2851	1772	502	557	20	0	0	0

- 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
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	27	10	5	10	2	0	0

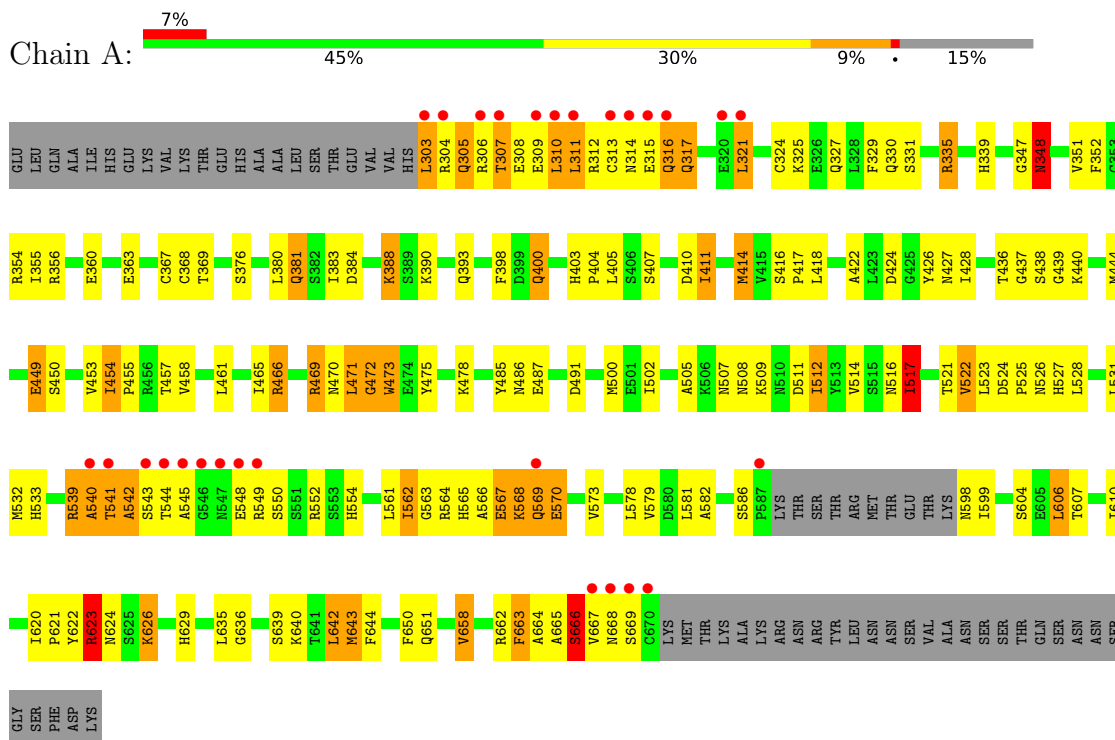
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	54	Total	O	0	0
			54	54		

3 Residue-property plots

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: PROTEIN (Kinesin motor NCD)



4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	123.00Å 123.00Å 121.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.50 20.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.6 (20.00-2.50) 98.5 (20.00-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.01 (at 2.51Å)	Xtrriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.226 , 0.270 0.239 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	25.6	Xtrriage
Anisotropy	0.257	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	2952	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.14% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, ADP

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	0.45	0/2897	0.93	14/3909 (0.4%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	472	GLY	N-CA-C	-7.71	98.20	112.62
1	A	579	VAL	N-CA-C	7.38	118.53	107.75
1	A	543	SER	N-CA-C	-6.97	104.34	112.92
1	A	310	LEU	N-CA-C	-6.32	106.27	112.97
1	A	663	PHE	N-CA-C	-6.19	104.45	111.14
1	A	453	VAL	N-CA-C	6.07	116.19	110.30
1	A	471	LEU	N-CA-C	-5.79	105.10	113.21
1	A	516	ASN	N-CA-C	5.61	119.31	111.74
1	A	666	SER	N-CA-C	-5.34	106.61	113.23
1	A	635	LEU	N-CA-C	-5.28	105.49	112.94
1	A	522	VAL	N-CA-C	5.21	116.41	109.37
1	A	581	LEU	N-CA-C	5.17	116.77	110.41
1	A	517	ILE	CB-CA-C	-5.09	102.75	110.95
1	A	305	GLN	N-CA-C	-5.08	105.34	112.25

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2851	0	2809	129	2
2	A	20	0	0	1	0
3	A	27	0	12	7	0
4	A	54	0	0	2	1
All	All	2952	0	2821	129	3

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 23.

All (129) 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:347:GLY:O	1:A:348:ASN:HB2	1.69	0.92
1:A:552:ARG:HD2	1:A:599:ILE:CG2	2.09	0.83
1:A:418:LEU:HD11	1:A:642:LEU:HD13	1.60	0.82
1:A:308:GLU:HA	1:A:311:LEU:HD23	1.68	0.75
1:A:542:ALA:N	1:A:550:SER:HB2	2.00	0.75
1:A:418:LEU:HD12	1:A:642:LEU:HD22	1.71	0.72
1:A:569:GLN:O	1:A:570:GLU:HG2	1.92	0.70
1:A:461:LEU:O	1:A:465:ILE:HG13	1.91	0.69
1:A:539:ARG:HG3	1:A:541:THR:HG23	1.73	0.69
1:A:458:VAL:CG2	1:A:532:MET:HE1	2.24	0.67
1:A:554:HIS:CD2	1:A:582:ALA:H	2.13	0.67
1:A:524:ASP:HB2	1:A:525:PRO:HD2	1.76	0.66
1:A:541:THR:HB	1:A:550:SER:OG	1.95	0.66
1:A:440:LYS:HZ3	3:A:800:ADP:PB	2.18	0.65
1:A:568:LYS:O	1:A:569:GLN:HG3	1.95	0.65
1:A:449:GLU:H	1:A:449:GLU:CD	2.04	0.64
1:A:552:ARG:HD2	1:A:599:ILE:HG21	1.77	0.64
1:A:524:ASP:HB2	1:A:525:PRO:CD	2.27	0.64
1:A:303:LEU:HA	1:A:306:ARG:NH2	2.12	0.64
1:A:454:ILE:HB	1:A:455:PRO:HD3	1.80	0.64
1:A:542:ALA:HB1	1:A:545:ALA:O	1.98	0.63
1:A:352:PHE:CD1	1:A:400:GLN:HB3	2.35	0.62
1:A:554:HIS:HD2	1:A:582:ALA:H	1.48	0.62
1:A:568:LYS:C	1:A:569:GLN:HG3	2.26	0.61
1:A:383:ILE:HG12	1:A:651:GLN:OE1	1.99	0.61
1:A:335:ARG:NH2	1:A:424:ASP:OD2	2.34	0.60
1:A:437:GLY:H	3:A:800:ADP:PB	2.25	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:SER:HB2	1:A:398:PHE:O	2.01	0.59
1:A:620:ILE:HB	1:A:622:TYR:CE1	2.37	0.59
1:A:565:HIS:CD2	1:A:568:LYS:HB3	2.38	0.58
1:A:539:ARG:CG	1:A:541:THR:HG23	2.34	0.58
1:A:665:ALA:O	1:A:669:SER:HB3	2.04	0.58
1:A:383:ILE:HG12	1:A:651:GLN:CD	2.30	0.57
1:A:440:LYS:HB2	3:A:800:ADP:O3B	2.04	0.57
1:A:335:ARG:HH22	1:A:424:ASP:CG	2.12	0.56
1:A:514:VAL:HB	1:A:517:ILE:HG12	1.86	0.56
1:A:461:LEU:HD21	1:A:561:LEU:HD21	1.87	0.56
1:A:667:VAL:HG12	1:A:668:ASN:N	2.20	0.56
1:A:321:LEU:HD22	1:A:325:LYS:HE3	1.87	0.56
1:A:473:TRP:HA	1:A:564:ARG:O	2.05	0.56
1:A:500:MET:CE	1:A:517:ILE:HG23	2.35	0.56
1:A:355:ILE:O	1:A:404:PRO:HA	2.06	0.56
1:A:541:THR:C	1:A:550:SER:HB2	2.30	0.56
1:A:356:ARG:HG2	1:A:438:SER:O	2.05	0.55
1:A:416:SER:OG	1:A:417:PRO:HD3	2.07	0.55
1:A:458:VAL:HG23	1:A:532:MET:HE1	1.87	0.55
1:A:352:PHE:HD1	1:A:400:GLN:HB3	1.71	0.55
1:A:623:ARG:HB2	2:A:1110:SO4:O1	2.04	0.55
1:A:491:ASP:HB2	1:A:500:MET:CE	2.37	0.55
1:A:308:GLU:O	1:A:311:LEU:HB2	2.07	0.54
1:A:485:TYR:CE1	1:A:549:ARG:HA	2.42	0.54
1:A:514:VAL:O	1:A:517:ILE:HD11	2.07	0.54
1:A:539:ARG:O	1:A:541:THR:N	2.40	0.54
1:A:306:ARG:CZ	1:A:306:ARG:HB3	2.37	0.54
1:A:486:ASN:ND2	1:A:599:ILE:HD13	2.22	0.54
1:A:472:GLY:O	1:A:473:TRP:HB2	2.06	0.53
1:A:487:GLU:O	1:A:626:LYS:HD3	2.07	0.53
1:A:303:LEU:HG	1:A:306:ARG:NH2	2.24	0.52
1:A:351:VAL:HG21	1:A:667:VAL:HG21	1.92	0.52
1:A:352:PHE:CZ	1:A:414:MET:HG2	2.45	0.52
1:A:329:PHE:CE2	1:A:568:LYS:HG2	2.45	0.52
1:A:367:CYS:HA	1:A:650:PHE:HA	1.90	0.52
1:A:478:LYS:HD2	1:A:562:ILE:HD11	1.93	0.51
1:A:473:TRP:CE3	1:A:565:HIS:HB2	2.46	0.51
1:A:398:PHE:CE2	1:A:664:ALA:CB	2.94	0.51
1:A:457:THR:O	1:A:461:LEU:HB2	2.11	0.51
1:A:354:ARG:CZ	1:A:411:ILE:HD13	2.41	0.51
1:A:512:ILE:HD11	1:A:629:HIS:NE2	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:622:TYR:C	1:A:624:ASN:H	2.18	0.50
1:A:428:ILE:HD12	1:A:640:LYS:HB2	1.93	0.50
1:A:473:TRP:CD1	1:A:565:HIS:HD1	2.30	0.49
1:A:548:GLU:HG2	1:A:548:GLU:O	2.11	0.49
1:A:562:ILE:HG23	1:A:573:VAL:HG22	1.93	0.49
1:A:439:GLY:C	3:A:800:ADP:O2A	2.56	0.49
1:A:502:ILE:CG2	1:A:512:ILE:HG12	2.42	0.49
1:A:407:SER:O	1:A:410:ASP:HB2	2.13	0.48
1:A:458:VAL:HG22	1:A:528:LEU:HD23	1.94	0.48
1:A:458:VAL:HG22	1:A:528:LEU:CD2	2.42	0.48
1:A:312:ARG:O	1:A:315:GLU:HB2	2.13	0.48
1:A:381:GLN:NE2	1:A:388:LYS:HE3	2.28	0.48
1:A:539:ARG:O	1:A:540:ALA:C	2.56	0.48
1:A:486:ASN:O	1:A:487:GLU:HB2	2.12	0.47
1:A:526:ASN:HB2	4:A:954:HOH:O	2.13	0.47
1:A:663:PHE:O	1:A:666:SER:OG	2.32	0.47
1:A:311:LEU:C	1:A:313:CYS:H	2.21	0.47
1:A:439:GLY:N	3:A:800:ADP:O1A	2.47	0.47
1:A:486:ASN:HD22	1:A:599:ILE:HA	1.79	0.47
1:A:522:VAL:HG11	1:A:528:LEU:HB2	1.96	0.47
1:A:428:ILE:CD1	1:A:640:LYS:HB2	2.45	0.47
1:A:511:ASP:OD1	1:A:512:ILE:N	2.43	0.46
1:A:566:ALA:O	1:A:567:GLU:CB	2.63	0.46
1:A:422:ALA:HA	1:A:426:TYR:O	2.16	0.46
1:A:311:LEU:C	1:A:313:CYS:N	2.73	0.45
1:A:339:HIS:HD2	4:A:942:HOH:O	1.99	0.45
1:A:466:ARG:O	1:A:469:ARG:HB2	2.17	0.45
1:A:475:TYR:CE1	1:A:563:GLY:HA3	2.52	0.45
1:A:427:ASN:O	1:A:428:ILE:HD13	2.16	0.45
1:A:403:HIS:CG	1:A:404:PRO:HD2	2.52	0.45
1:A:411:ILE:HG23	1:A:644:PHE:CE2	2.53	0.44
1:A:436:THR:HA	3:A:800:ADP:O1B	2.18	0.44
1:A:542:ALA:H	1:A:550:SER:HB2	1.82	0.44
1:A:643:MET:HE2	1:A:643:MET:HB2	1.71	0.44
1:A:541:THR:CA	1:A:550:SER:HB2	2.47	0.44
1:A:324:CYS:O	1:A:327:GLN:HB2	2.18	0.44
1:A:552:ARG:HD2	1:A:599:ILE:HG22	1.97	0.43
1:A:440:LYS:NZ	3:A:800:ADP:O3B	2.49	0.43
1:A:491:ASP:HB2	1:A:500:MET:HE3	2.00	0.43
1:A:303:LEU:CG	1:A:306:ARG:HH21	2.32	0.43
1:A:312:ARG:HA	1:A:315:GLU:HG3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:313:CYS:HA	1:A:316:GLN:OE1	2.18	0.43
1:A:384:ASP:OD1	1:A:384:ASP:C	2.61	0.42
1:A:312:ARG:O	1:A:316:GLN:HG3	2.19	0.42
1:A:444:MET:O	1:A:454:ILE:HG13	2.18	0.42
1:A:307:THR:O	1:A:307:THR:HG23	2.19	0.42
1:A:539:ARG:HG3	1:A:539:ARG:O	2.19	0.42
1:A:541:THR:HG22	1:A:550:SER:HA	2.02	0.42
1:A:527:HIS:O	1:A:531:LEU:HG	2.19	0.42
1:A:502:ILE:HG22	1:A:512:ILE:HG12	2.02	0.42
1:A:622:TYR:C	1:A:624:ASN:N	2.78	0.42
1:A:356:ARG:NH1	1:A:437:GLY:O	2.42	0.42
1:A:606:LEU:HD22	1:A:606:LEU:O	2.20	0.41
1:A:658:VAL:O	1:A:662:ARG:HB2	2.20	0.41
1:A:621:PRO:O	1:A:624:ASN:HB2	2.19	0.41
1:A:662:ARG:O	1:A:665:ALA:HB3	2.21	0.41
1:A:511:ASP:CG	1:A:512:ILE:H	2.28	0.40
1:A:314:ASN:HA	1:A:317:GLN:HB2	2.03	0.40
1:A:303:LEU:HA	1:A:306:ARG:HH21	1.84	0.40
1:A:505:ALA:CB	1:A:511:ASP:HB3	2.52	0.40
1:A:500:MET:HE1	1:A:517:ILE:HG23	2.03	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:314:ASN:ND2	1:A:314:ASN:ND2[9_555]	1.74	0.46
1:A:303:LEU:CD2	1:A:303:LEU:CD2[9_555]	1.91	0.29
4:A:943:HOH:O	4:A:944:HOH:O[12_566]	2.15	0.05

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	354/420 (84%)	312 (88%)	32 (9%)	10 (3%)	4 6

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	540	ALA
1	A	542	ALA
1	A	568	LYS
1	A	348	ASN
1	A	570	GLU
1	A	636	GLY
1	A	508	ASN
1	A	569	GLN
1	A	473	TRP
1	A	623	ARG

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	324/380 (85%)	264 (82%)	60 (18%)	1 3

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	303	LEU
1	A	304	ARG
1	A	305	GLN
1	A	307	THR
1	A	309	GLU
1	A	310	LEU
1	A	311	LEU
1	A	316	GLN
1	A	317	GLN
1	A	321	LEU
1	A	330	GLN

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Mol	Chain	Res	Type
1	A	331	SER
1	A	335	ARG
1	A	348	ASN
1	A	360	GLU
1	A	363	GLU
1	A	368	CYS
1	A	369	THR
1	A	380	LEU
1	A	381	GLN
1	A	388	LYS
1	A	390	LYS
1	A	393	GLN
1	A	400	GLN
1	A	405	LEU
1	A	411	ILE
1	A	414	MET
1	A	449	GLU
1	A	450	SER
1	A	454	ILE
1	A	466	ARG
1	A	469	ARG
1	A	470	ASN
1	A	471	LEU
1	A	507	ASN
1	A	509	LYS
1	A	512	ILE
1	A	517	ILE
1	A	521	THR
1	A	523	LEU
1	A	533	HIS
1	A	539	ARG
1	A	541	THR
1	A	544	THR
1	A	562	ILE
1	A	567	GLU
1	A	578	LEU
1	A	586	SER
1	A	598	ASN
1	A	604	SER
1	A	606	LEU
1	A	607	THR
1	A	610	ILE

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Mol	Chain	Res	Type
1	A	623	ARG
1	A	626	LYS
1	A	639	SER
1	A	642	LEU
1	A	643	MET
1	A	658	VAL
1	A	666	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	314	ASN
1	A	317	GLN
1	A	348	ASN
1	A	364	ASN
1	A	381	GLN
1	A	486	ASN
1	A	507	ASN
1	A	533	HIS
1	A	668	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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	1110	-	4,4,4	0.39	0	6,6,6	3.19	5 (83%)
2	SO4	A	1113	-	4,4,4	0.35	0	6,6,6	2.58	3 (50%)
3	ADP	A	800	-	28,29,29	2.52	7 (25%)	43,45,45	2.72	14 (32%)
2	SO4	A	1111	-	4,4,4	0.46	0	6,6,6	3.07	3 (50%)
2	SO4	A	1112	-	4,4,4	0.41	0	6,6,6	4.14	4 (66%)

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	ADP	A	800	-	-	6/16/32/32	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	800	ADP	PA-O3A	10.75	1.71	1.59
3	A	800	ADP	C5-N7	-4.05	1.31	1.39
3	A	800	ADP	O4'-C1'	3.03	1.49	1.42
3	A	800	ADP	C1'-N9	2.74	1.53	1.46
3	A	800	ADP	C5'-C4'	2.20	1.58	1.51
3	A	800	ADP	C4-N9	-2.06	1.33	1.37
3	A	800	ADP	O4'-C4'	2.02	1.49	1.45

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	800	ADP	O4'-C1'-N9	8.60	124.61	108.09
3	A	800	ADP	N3-C2-N1	-6.36	118.95	128.58
2	A	1112	SO4	O4-S-O3	-6.35	73.53	108.54
2	A	1111	SO4	O3-S-O2	6.28	142.40	109.56
3	A	800	ADP	C5-C4-N3	-6.22	118.16	126.72
3	A	800	ADP	N3-C4-N9	5.68	136.83	127.17
3	A	800	ADP	O5'-C5'-C4'	4.92	125.74	108.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1112	SO4	O4-S-O2	4.84	134.88	109.56
2	A	1112	SO4	O4-S-O1	4.71	134.17	109.56
2	A	1110	SO4	O2-S-O1	-4.51	77.31	109.06
2	A	1113	SO4	O3-S-O1	-4.34	86.88	109.56
3	A	800	ADP	C2-N3-C4	4.30	122.33	111.83
2	A	1110	SO4	O4-S-O1	-3.89	89.20	109.56
2	A	1112	SO4	O2-S-O1	-3.67	83.24	109.06
3	A	800	ADP	C6-C5-N7	-3.38	125.57	132.09
2	A	1110	SO4	O4-S-O3	3.30	126.72	108.54
2	A	1113	SO4	O3-S-O2	3.08	125.68	109.56
2	A	1113	SO4	O4-S-O3	2.96	124.85	108.54
3	A	800	ADP	C3'-C2'-C1'	2.93	107.00	101.46
2	A	1110	SO4	O4-S-O2	2.89	124.69	109.56
3	A	800	ADP	C4-C5-N7	2.88	113.87	110.58
2	A	1111	SO4	O4-S-O1	-2.82	94.83	109.56
2	A	1110	SO4	O3-S-O1	-2.52	96.38	109.56
3	A	800	ADP	C6-C5-C4	2.46	120.54	117.18
3	A	800	ADP	O4'-C4'-C5'	2.25	116.53	109.33
3	A	800	ADP	C2-N1-C6	2.21	122.36	118.73
3	A	800	ADP	O2A-PA-O1A	2.20	122.66	112.44
3	A	800	ADP	C2'-C3'-C4'	2.18	106.81	102.61
2	A	1111	SO4	O4-S-O3	-2.12	96.86	108.54

There are no chirality outliers.

All (6) torsion outliers are listed below:

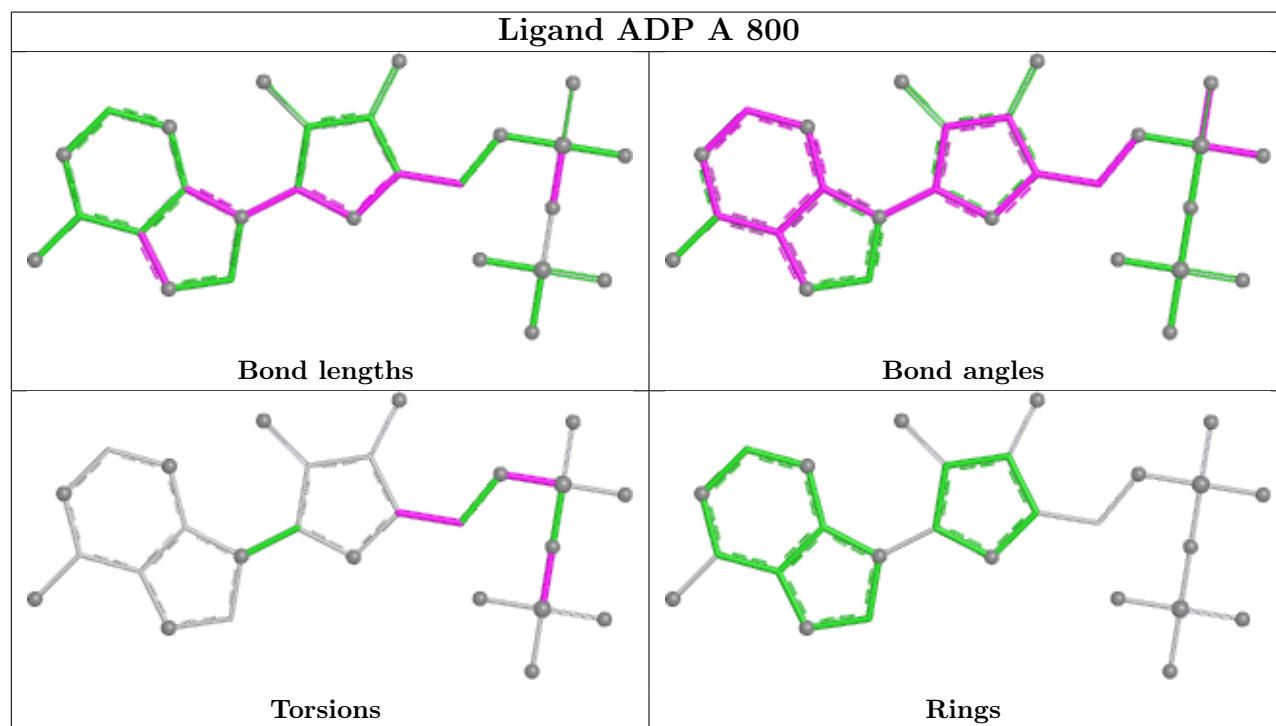
Mol	Chain	Res	Type	Atoms
3	A	800	ADP	PA-O3A-PB-O2B
3	A	800	ADP	C3'-C4'-C5'-O5'
3	A	800	ADP	O4'-C4'-C5'-O5'
3	A	800	ADP	C5'-O5'-PA-O1A
3	A	800	ADP	PA-O3A-PB-O1B
3	A	800	ADP	PA-O3A-PB-O3B

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1110	SO4	1	0
3	A	800	ADP	7	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	358/420 (85%)	-0.01	28 (7%) 19 17	3, 17, 81, 99	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	310	LEU	6.4
1	A	546	GLY	5.4
1	A	545	ALA	5.1
1	A	307	THR	4.6
1	A	543	SER	4.6
1	A	303	LEU	4.6
1	A	541	THR	4.2
1	A	544	THR	4.2
1	A	540	ALA	4.1
1	A	304	ARG	4.0
1	A	315	GLU	3.7
1	A	548	GLU	3.5
1	A	311	LEU	3.5
1	A	668	ASN	3.2
1	A	670	CYS	3.1
1	A	309	GLU	3.1
1	A	306	ARG	2.9
1	A	587	PRO	2.7
1	A	314	ASN	2.7
1	A	316	GLN	2.6
1	A	669	SER	2.6
1	A	547	ASN	2.4
1	A	569	GLN	2.3
1	A	667	VAL	2.3
1	A	321	LEU	2.3
1	A	313	CYS	2.2
1	A	549	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	320	GLU	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](#)

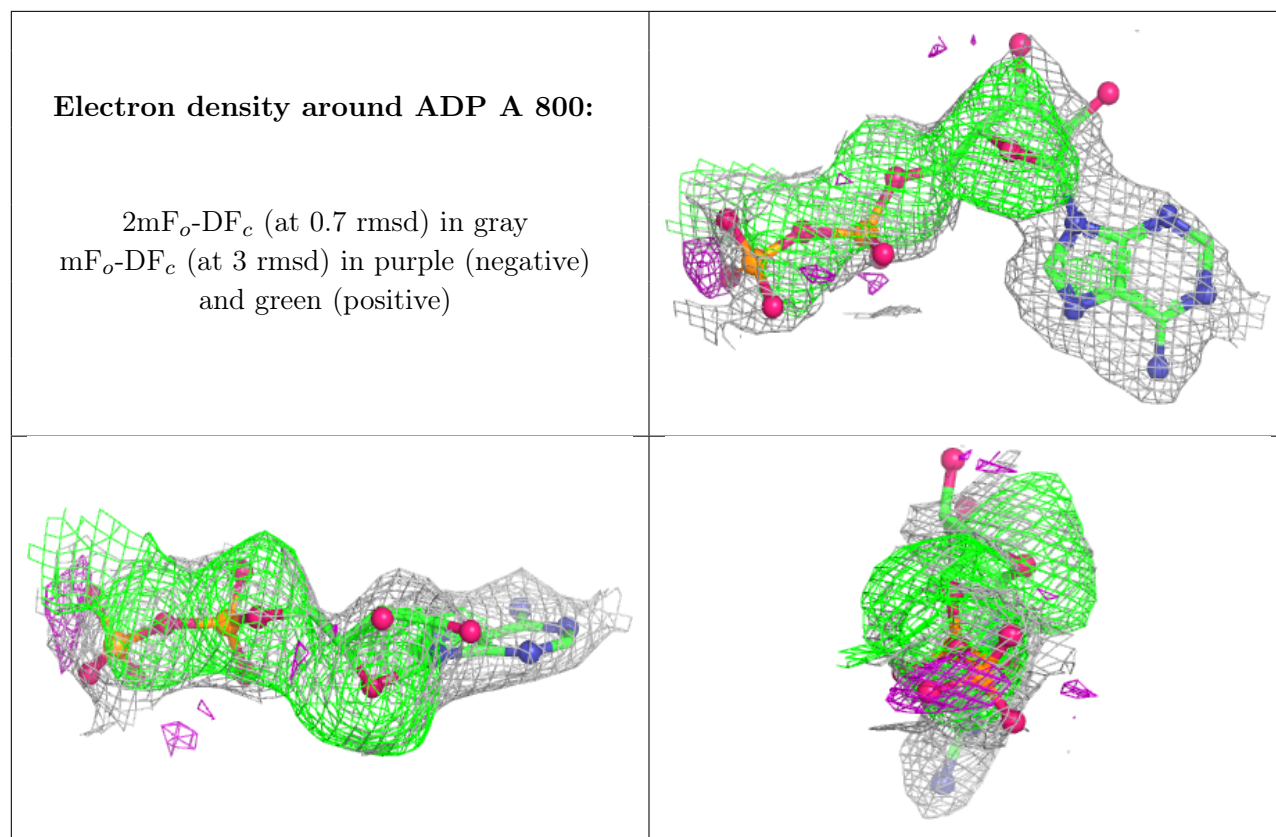
There are no oligosaccharides in this entry.

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(\AA^2)	Q<0.9
2	SO4	A	1113	5/5	0.67	0.29	90,92,100,100	0
3	ADP	A	800	27/27	0.74	0.44	39,85,100,100	0
2	SO4	A	1111	5/5	0.84	0.20	83,90,91,96	0
2	SO4	A	1110	5/5	0.86	0.14	74,75,81,87	0
2	SO4	A	1112	5/5	0.86	0.12	60,65,70,74	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.