



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:50 AM UTC

PDB ID : 2D2S / pdb_00002d2s
Title : Crystal Structure of the Exo84p C-terminal Domains
Authors : Dong, G.; Hutagalung, A.H.; Fu, C.; Novick, P.; Reinisch, K.M.
Deposited on : 2005-09-16
Resolution : 2.85 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
Xtrriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

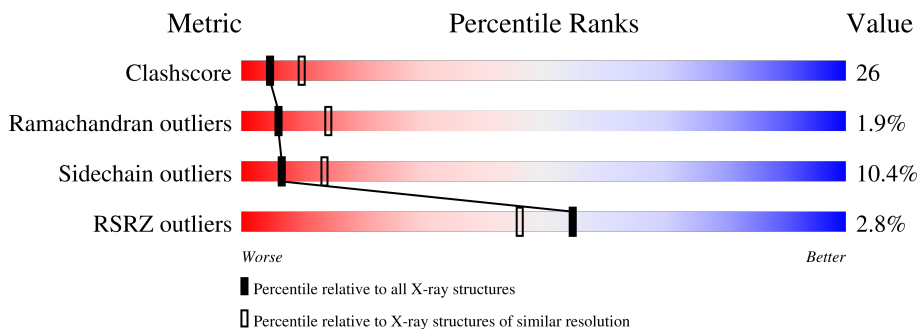
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	235	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1742 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 Exocyst complex component EXO84.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	217	1742	1106	290	342	4	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	519	GLY	-	cloning artifact	UNP P38261
A	520	SER	-	cloning artifact	UNP P38261
A	521	HIS	-	cloning artifact	UNP P38261
A	522	MET	-	cloning artifact	UNP P38261

4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	54.85Å 54.85Å 209.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.85 15.00 – 2.85	Depositor EDS
% Data completeness (in resolution range)	(Not available) (15.00-2.85) 86.3 (15.00-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.51 (at 2.77Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.269 , 0.306 0.285 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	66.5	Xtrriage
Anisotropy	0.738	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 50.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	1742	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.31% 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

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	0.68	3/1757 (0.2%)	1.15	11/2356 (0.5%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	564	SER	C-N	-6.15	1.26	1.33
1	A	603	ILE	CA-CB	5.06	1.59	1.54
1	A	563	GLU	CA-CB	-5.01	1.45	1.53

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	565	GLN	OE1-CD-NE2	-9.95	112.66	122.60
1	A	653	PRO	CA-N-CD	-8.40	100.24	112.00
1	A	565	GLN	CG-CD-NE2	6.23	125.75	116.40
1	A	693	TRP	N-CA-C	-5.98	104.67	111.07
1	A	705	ILE	N-CA-C	-5.55	105.69	111.58
1	A	707	LYS	N-CA-C	-5.52	105.17	111.07
1	A	550	LEU	N-CA-C	5.43	119.19	112.24
1	A	619	MET	N-CA-C	-5.30	105.67	111.82
1	A	563	GLU	CB-CG-CD	-5.14	103.86	112.60
1	A	563	GLU	CA-C-N	-5.04	112.66	120.31
1	A	563	GLU	C-N-CA	-5.04	112.66	120.31

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	1742	0	1796	91	0
All	All	1742	0	1796	91	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 26.

All (91) 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:715:LEU:HD22	1:A:716:SER:H	1.31	0.93
1:A:657:LEU:HD11	1:A:705:ILE:HG12	1.60	0.83
1:A:707:LYS:O	1:A:710:LEU:HB2	1.85	0.77
1:A:535:PHE:HA	1:A:538:GLU:HG3	1.66	0.76
1:A:566:LEU:HD22	1:A:588:ILE:HD12	1.68	0.75
1:A:623:GLY:C	1:A:624:LEU:HD12	2.12	0.74
1:A:657:LEU:HD23	1:A:719:SER:HB3	1.70	0.74
1:A:660:LEU:HD21	1:A:704:LEU:HD23	1.71	0.72
1:A:559:LEU:HD22	1:A:595:ILE:HD12	1.70	0.72
1:A:715:LEU:HD12	1:A:752:ILE:HG12	1.72	0.71
1:A:619:MET:HE3	1:A:627:GLN:HG2	1.72	0.70
1:A:603:ILE:HD11	1:A:616:THR:HA	1.75	0.69
1:A:629:LEU:HD22	1:A:686:ILE:HG23	1.74	0.69
1:A:741:LEU:O	1:A:745:ILE:HG13	1.94	0.68
1:A:533:LEU:HD22	1:A:584:ILE:HD12	1.74	0.67
1:A:636:ARG:HH22	1:A:670:LYS:HD2	1.59	0.66
1:A:599:LEU:HD23	1:A:619:MET:HA	1.78	0.66
1:A:741:LEU:CD2	1:A:745:ILE:HD11	2.26	0.65
1:A:709:LEU:HD11	1:A:715:LEU:HB2	1.77	0.65
1:A:715:LEU:HD22	1:A:716:SER:N	2.09	0.64
1:A:620:ILE:O	1:A:623:GLY:N	2.27	0.63
1:A:623:GLY:O	1:A:624:LEU:HD12	1.99	0.63
1:A:546:GLU:OE2	1:A:551:ARG:HG3	1.99	0.62
1:A:724:ARG:HA	1:A:741:LEU:CD1	2.29	0.62
1:A:619:MET:CG	1:A:628:ALA:HB2	2.29	0.62
1:A:570:SER:HB3	1:A:581:LEU:HD21	1.81	0.61
1:A:545:ILE:N	1:A:545:ILE:HD13	2.16	0.61
1:A:600:SER:HA	1:A:631:LEU:HD13	1.84	0.59
1:A:705:ILE:HG22	1:A:709:LEU:HD13	1.84	0.59
1:A:669:LYS:O	1:A:673:GLU:HG3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:652:ASN:HD22	1:A:655:ASN:HD22	1.52	0.57
1:A:724:ARG:HA	1:A:741:LEU:HD11	1.86	0.57
1:A:636:ARG:HG3	1:A:671:THR:OG1	2.03	0.57
1:A:545:ILE:O	1:A:548:ALA:HB3	2.05	0.56
1:A:672:VAL:O	1:A:676:GLN:HG3	2.06	0.56
1:A:613:LYS:O	1:A:617:GLU:HG3	2.06	0.55
1:A:745:ILE:HG23	1:A:752:ILE:HD13	1.87	0.55
1:A:662:VAL:O	1:A:663:ILE:C	2.50	0.54
1:A:717:PRO:HD3	1:A:752:ILE:O	2.07	0.54
1:A:664:ARG:HG3	1:A:668:ILE:HD11	1.90	0.54
1:A:619:MET:HG3	1:A:628:ALA:HB2	1.88	0.54
1:A:664:ARG:NH1	1:A:697:GLU:OE1	2.42	0.52
1:A:644:ILE:HG13	1:A:663:ILE:HG21	1.90	0.52
1:A:584:ILE:O	1:A:588:ILE:HG13	2.10	0.52
1:A:578:LEU:HG	1:A:582:ASN:ND2	2.25	0.52
1:A:661:ALA:O	1:A:662:VAL:C	2.52	0.52
1:A:556:VAL:HG22	1:A:622:LEU:HG	1.92	0.51
1:A:675:PHE:CD2	1:A:690:LEU:HD22	2.46	0.51
1:A:629:LEU:HB2	1:A:679:PHE:CE2	2.46	0.51
1:A:562:ILE:O	1:A:566:LEU:HB2	2.10	0.51
1:A:736:ASP:OD1	1:A:738:VAL:HG23	2.11	0.50
1:A:745:ILE:HG23	1:A:752:ILE:CD1	2.41	0.50
1:A:672:VAL:HG11	1:A:733:VAL:HB	1.94	0.50
1:A:741:LEU:HD21	1:A:745:ILE:HD11	1.93	0.50
1:A:694:CYS:SG	1:A:735:LEU:HD21	2.52	0.49
1:A:699:ASP:OD1	1:A:740:LYS:HE2	2.13	0.48
1:A:663:ILE:HG22	1:A:664:ARG:N	2.28	0.48
1:A:643:LEU:HD12	1:A:663:ILE:HD11	1.95	0.48
1:A:704:LEU:O	1:A:708:GLN:HG2	2.14	0.48
1:A:528:SER:O	1:A:531:GLN:HB3	2.13	0.47
1:A:637:SER:O	1:A:640:ILE:HB	2.14	0.47
1:A:540:VAL:HG12	1:A:541:GLU:N	2.30	0.46
1:A:734:GLY:C	1:A:735:LEU:HD12	2.41	0.46
1:A:566:LEU:HD22	1:A:588:ILE:CD1	2.43	0.45
1:A:592:ARG:NH2	1:A:622:LEU:O	2.50	0.45
1:A:626:GLU:HG3	1:A:686:ILE:HD11	1.98	0.45
1:A:672:VAL:CG1	1:A:733:VAL:HB	2.47	0.45
1:A:559:LEU:O	1:A:563:GLU:HG3	2.17	0.45
1:A:734:GLY:O	1:A:735:LEU:HD12	2.16	0.45
1:A:724:ARG:CA	1:A:741:LEU:HD11	2.47	0.45
1:A:617:GLU:O	1:A:620:ILE:HB	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:640:ILE:HD11	1:A:667:THR:HB	1.98	0.44
1:A:644:ILE:HA	1:A:647:ILE:HD11	2.00	0.43
1:A:680:LYS:O	1:A:682:LEU:HD23	2.19	0.43
1:A:614:SER:O	1:A:615:GLY:C	2.62	0.42
1:A:724:ARG:HA	1:A:741:LEU:HD12	1.99	0.42
1:A:533:LEU:HD21	1:A:581:LEU:HD12	2.02	0.42
1:A:613:LYS:HD2	1:A:678:ILE:CD1	2.50	0.41
1:A:562:ILE:HG22	1:A:588:ILE:CD1	2.50	0.41
1:A:561:ASP:O	1:A:565:GLN:HB2	2.20	0.41
1:A:679:PHE:O	1:A:682:LEU:HB2	2.20	0.41
1:A:643:LEU:HB3	1:A:663:ILE:HD12	2.03	0.41
1:A:641:GLN:CA	1:A:641:GLN:HE21	2.33	0.41
1:A:613:LYS:HD2	1:A:678:ILE:HG12	2.03	0.40
1:A:629:LEU:HA	1:A:679:PHE:CZ	2.56	0.40
1:A:662:VAL:O	1:A:666:GLN:HB2	2.21	0.40
1:A:547:LEU:HD23	1:A:547:LEU:HA	1.86	0.40
1:A:650:VAL:HA	1:A:656:TYR:CD1	2.57	0.40
1:A:708:GLN:NE2	1:A:708:GLN:HA	2.37	0.40
1:A:679:PHE:C	1:A:682:LEU:HD23	2.47	0.40
1:A:604:LEU:HD12	1:A:604:LEU:HA	1.90	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	209/235 (89%)	188 (90%)	17 (8%)	4 (2%)	6 14

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	646	GLN

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Mol	Chain	Res	Type
1	A	662	VAL
1	A	663	ILE
1	A	664	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	202/218 (93%)	181 (90%)	21 (10%)	7 14

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	532	ARG
1	A	538	GLU
1	A	540	VAL
1	A	541	GLU
1	A	545	ILE
1	A	549	ARG
1	A	564	SER
1	A	579	MET
1	A	583	LEU
1	A	590	GLN
1	A	599	LEU
1	A	604	LEU
1	A	641	GLN
1	A	652	ASN
1	A	653	PRO
1	A	654	THR
1	A	715	LEU
1	A	733	VAL
1	A	738	VAL
1	A	741	LEU
1	A	745	ILE

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	582	ASN
1	A	601	GLN
1	A	611	HIS
1	A	627	GLN
1	A	641	GLN
1	A	655	ASN
1	A	659	GLN
1	A	676	GLN
1	A	700	ASN
1	A	701	HIS
1	A	708	GLN
1	A	748	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](#)

There are no ligands in this entry.

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	217/235 (92%)	0.42	6 (2%) 55 46	56, 83, 100, 100	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	525	ASP	5.7
1	A	708	GLN	2.9
1	A	749	SER	2.6
1	A	652	ASN	2.2
1	A	655	ASN	2.2
1	A	677	ASP	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.