



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:27 AM UTC

PDB ID : 4BSN / pdb_00004bsn
Title : Crystal structure of the Nuclear Export Receptor CRM1 (exportin-1) lacking the C-terminal helical extension at 4.1Å
Authors : Dian, C.; Bernaudat, F.; Langer, K.; Oliva, M.F.; Fornerod, M.; Schoehn, G.; Muller, C.W.; Petosa, C.
Deposited on : 2013-06-11
Resolution : 4.10 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
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

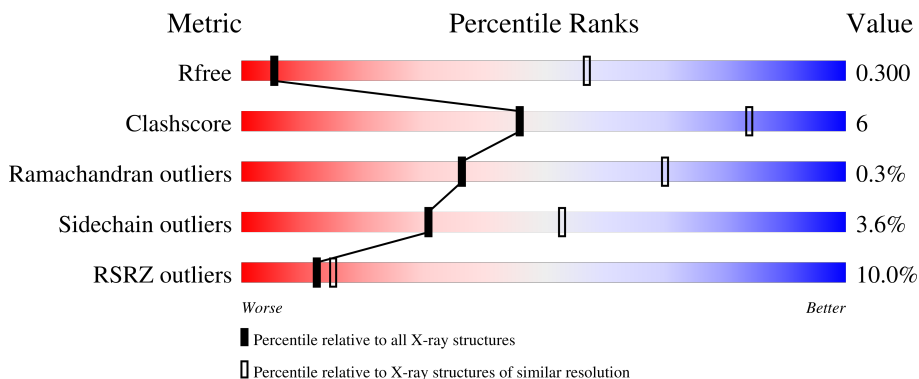
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.10 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	1243 (4.40-3.80)
Clashscore	190562	1293 (4.40-3.80)
Ramachandran outliers	187476	1206 (4.40-3.80)
Sidechain outliers	187428	1193 (4.40-3.80)
RSRZ outliers	180081	1240 (4.40-3.80)

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	1032	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5481 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 EXPORTIN-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	707	Total	C	N	O	S	0	0	0
			5481	3520	916	1004	41			

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	146.96Å 246.75Å 106.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.05 – 4.10 48.05 – 4.10	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.05-4.10) 99.5 (48.05-4.10)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 3.88Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.8_1056)	Depositor
R, R_{free}	0.275 , 0.298 0.275 , 0.300	Depositor DCC
R_{free} test set	904 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	135.0	Xtriage
Anisotropy	0.585	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 154.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.076 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.064 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	5481	wwPDB-VP
Average B, all atoms (Å ²)	130.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.41% 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	0.28	0/5587	0.73	1/7602 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	778	PRO	N-CA-C	5.06	116.88	110.70

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	5481	0	5282	62	0
All	All	5481	0	5282	62	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 6.

All (62) 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:370:LEU:HD11	1:A:457:MET:HG2	1.66	0.77
1:A:233:LEU:HD23	1:A:270:GLU:HB3	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:GLU:HB3	1:A:57:PRO:HD2	1.77	0.66
1:A:454:TYR:OH	1:A:546:TYR:OH	2.12	0.65
1:A:483:GLN:HG2	1:A:494:LEU:HD13	1.78	0.64
1:A:362:GLU:HB3	1:A:365:ILE:HG22	1.79	0.64
1:A:298:LEU:O	1:A:353:TYR:OH	2.19	0.60
1:A:627:PRO:O	1:A:631:HIS:ND1	2.27	0.60
1:A:524:LEU:HD13	1:A:544:ILE:HG12	1.84	0.60
1:A:251:ILE:HG21	1:A:289:LEU:HB3	1.84	0.59
1:A:616:ASN:ND2	1:A:617:ASN:OD1	2.35	0.59
1:A:715:LEU:O	1:A:719:ASN:ND2	2.34	0.57
1:A:559:TRP:HH2	1:A:610:PHE:HB2	1.69	0.57
1:A:495:ASN:ND2	1:A:543:ASN:OD1	2.39	0.56
1:A:429:GLU:OE1	1:A:590:LYS:NZ	2.39	0.55
1:A:491:TRP:NE1	1:A:536:ASN:OD1	2.38	0.54
1:A:555:LEU:HB3	1:A:562:LEU:HD13	1.90	0.54
1:A:338:GLU:HG2	1:A:408:LEU:HD13	1.91	0.53
1:A:325:PHE:HD2	1:A:326:LEU:HD22	1.73	0.53
1:A:131:ASN:HD21	1:A:166:ASN:HD21	1.57	0.53
1:A:113:THR:HG21	1:A:126:TYR:HE2	1.74	0.53
1:A:403:PRO:HB2	1:A:406:ARG:HB2	1.91	0.53
1:A:329:PHE:HD2	1:A:330:LEU:HD12	1.73	0.53
1:A:600:VAL:HG11	1:A:644:GLN:HB2	1.91	0.53
1:A:62:ARG:NH1	1:A:75:THR:O	2.41	0.52
1:A:781:LEU:HG	1:A:785:LEU:HD12	1.91	0.52
1:A:500:ALA:O	1:A:504:ILE:HG12	2.10	0.51
1:A:284:VAL:HG21	1:A:340:ARG:HH21	1.76	0.50
1:A:116:ASP:OD2	1:A:118:THR:OG1	2.28	0.50
1:A:429:GLU:OE2	1:A:550:GLN:NE2	2.45	0.49
1:A:559:TRP:CD2	1:A:603:GLN:HG3	2.47	0.49
1:A:154:VAL:HG13	1:A:208:LEU:HD12	1.94	0.48
1:A:563:LYS:HG3	1:A:610:PHE:HE1	1.78	0.48
1:A:497:LEU:O	1:A:501:ILE:HG12	2.14	0.48
1:A:637:VAL:HA	1:A:640:MET:HE2	1.96	0.47
1:A:417:ARG:NH1	1:A:471:ASP:OD2	2.48	0.47
1:A:87:ILE:O	1:A:91:TRP:HB2	2.15	0.47
1:A:580:VAL:HA	1:A:583:MET:HE3	1.97	0.47
1:A:476:MET:HE1	1:A:504:ILE:HG13	1.97	0.46
1:A:556:ARG:O	1:A:598:HIS:NE2	2.48	0.46
1:A:388:THR:HA	1:A:389:SER:HA	1.64	0.46
1:A:56:HIS:N	1:A:57:PRO:HD2	2.31	0.46
1:A:536:ASN:O	1:A:540:ILE:HG12	2.17	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:387:SER:HB3	1:A:468:ASP:HA	1.99	0.45
1:A:384:SER:OG	1:A:406:ARG:NE	2.50	0.45
1:A:206:PHE:HB2	1:A:236:ILE:HD13	1.98	0.45
1:A:491:TRP:CD1	1:A:539:ILE:HG13	2.52	0.45
1:A:157:SER:HB2	1:A:208:LEU:HD11	2.01	0.43
1:A:570:PHE:HA	1:A:573:MET:HE3	1.99	0.43
1:A:178:VAL:HG11	1:A:235:TRP:HH2	1.83	0.43
1:A:573:MET:HG2	1:A:625:LEU:HD21	2.02	0.42
1:A:157:SER:OG	1:A:167:ASN:ND2	2.46	0.42
1:A:418:LEU:HD13	1:A:475:ILE:HD12	2.01	0.42
1:A:206:PHE:CE2	1:A:240:TYR:HB3	2.55	0.41
1:A:257:VAL:HA	1:A:258:PRO:HD3	1.84	0.41
1:A:62:ARG:HH12	1:A:76:LYS:HA	1.86	0.41
1:A:299:PRO:O	1:A:302:THR:OG1	2.39	0.41
1:A:258:PRO:HA	1:A:261:ARG:HD2	2.01	0.41
1:A:406:ARG:NH2	1:A:467:LEU:HA	2.36	0.41
1:A:453:LEU:O	1:A:457:MET:HG3	2.20	0.41
1:A:323:SER:HB2	1:A:357:VAL:HG11	2.03	0.40
1:A:614:ILE:O	1:A:618:ILE:HG23	2.21	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	693/1032 (67%)	676 (98%)	15 (2%)	2 (0%)	36 70

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	54	LYS
1	A	447	ASP

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	579/940 (62%)	558 (96%)	21 (4%)	31 53

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

Mol	Chain	Res	Type
1	A	48	GLU
1	A	62	ARG
1	A	102	ILE
1	A	109	LEU
1	A	145	HIS
1	A	173	LEU
1	A	192	LYS
1	A	198	MET
1	A	255	LEU
1	A	265	LEU
1	A	379	GLU
1	A	380	LEU
1	A	386	PHE
1	A	483	GLN
1	A	524	LEU
1	A	527	LEU
1	A	544	ILE
1	A	548	VAL
1	A	574	HIS
1	A	589	ILE
1	A	602	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	GLN
1	A	145	HIS
1	A	166	ASN
1	A	217	GLN

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Mol	Chain	Res	Type
1	A	223	HIS
1	A	321	ASN
1	A	342	ASN
1	A	374	ASN
1	A	375	HIS
1	A	452	ASN
1	A	456	ASN
1	A	466	HIS
1	A	483	GLN
1	A	493	ASN
1	A	495	ASN
1	A	543	ASN
1	A	616	ASN
1	A	709	GLN

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

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	707/1032 (68%)	0.80	71 (10%) 12 15	30, 119, 248, 290	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	72	ASN	6.5
1	A	607	VAL	5.4
1	A	390	ALA	5.4
1	A	26	ASN	4.0
1	A	3	ALA	4.0
1	A	545	MET	3.9
1	A	634	TYR	3.7
1	A	610	PHE	3.6
1	A	758	LEU	3.6
1	A	641	ILE	3.5
1	A	544	ILE	3.2
1	A	711	GLY	3.2
1	A	660	LEU	3.2
1	A	33	ASN	3.1
1	A	78	TYR	3.0
1	A	469	TYR	3.0
1	A	759	ILE	3.0
1	A	774	GLU	3.0
1	A	708	ILE	2.9
1	A	763	VAL	2.8
1	A	640	MET	2.8
1	A	585	CYS	2.7
1	A	702	VAL	2.7
1	A	216	SER	2.6
1	A	767	ASN	2.6
1	A	782	ASP	2.5
1	A	58	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	659	LEU	2.5
1	A	74	ASN	2.5
1	A	707	VAL	2.5
1	A	75	THR	2.5
1	A	289	LEU	2.5
1	A	450	SER	2.4
1	A	65	THR	2.4
1	A	17	LEU	2.4
1	A	586	ASP	2.4
1	A	137	ILE	2.4
1	A	790	ARG	2.4
1	A	488	GLU	2.4
1	A	251	ILE	2.4
1	A	276	VAL	2.4
1	A	4	ILE	2.3
1	A	22	LYS	2.3
1	A	199	CYS	2.3
1	A	126	TYR	2.3
1	A	34	CYS	2.3
1	A	170	ILE	2.3
1	A	343	LEU	2.3
1	A	52	HIS	2.3
1	A	578	ASP	2.3
1	A	541	ALA	2.3
1	A	143	PRO	2.2
1	A	620	THR	2.2
1	A	233	LEU	2.2
1	A	493	ASN	2.2
1	A	29	ASP	2.2
1	A	267	CYS	2.2
1	A	18	ASP	2.1
1	A	342	ASN	2.1
1	A	275	SER	2.1
1	A	174	LEU	2.1
1	A	781	LEU	2.1
1	A	245	LYS	2.1
1	A	638	GLY	2.1
1	A	664	VAL	2.1
1	A	498	CYS	2.1
1	A	609	PRO	2.0
1	A	212	VAL	2.0
1	A	19	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	247	ILE	2.0
1	A	760	SER	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.