



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 10:28 AM UTC

PDB ID : 1M2V / pdb_00001m2v
Title : Crystal Structure of the yeast Sec23/24 heterodimer
Authors : Bi, X.; Corpina, R.A.; Goldberg, J.
Deposited on : 2002-06-25
Resolution : 2.75 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

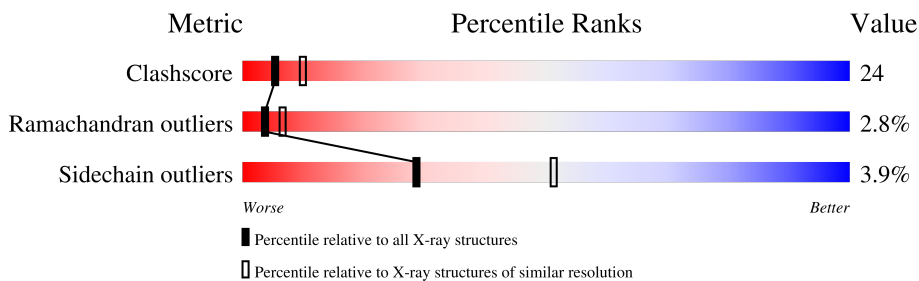
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	768	
2	B	926	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11577 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 transport protein SEC23.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	705	Total	C	N	O	S	0	0	0
			5574	3560	933	1059	22			

- Molecule 2 is a protein called protein transport protein SEC24.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	748	Total	C	N	O	S	0	0	0
			5932	3772	1018	1104	38			

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		

- Molecule 4 is water.

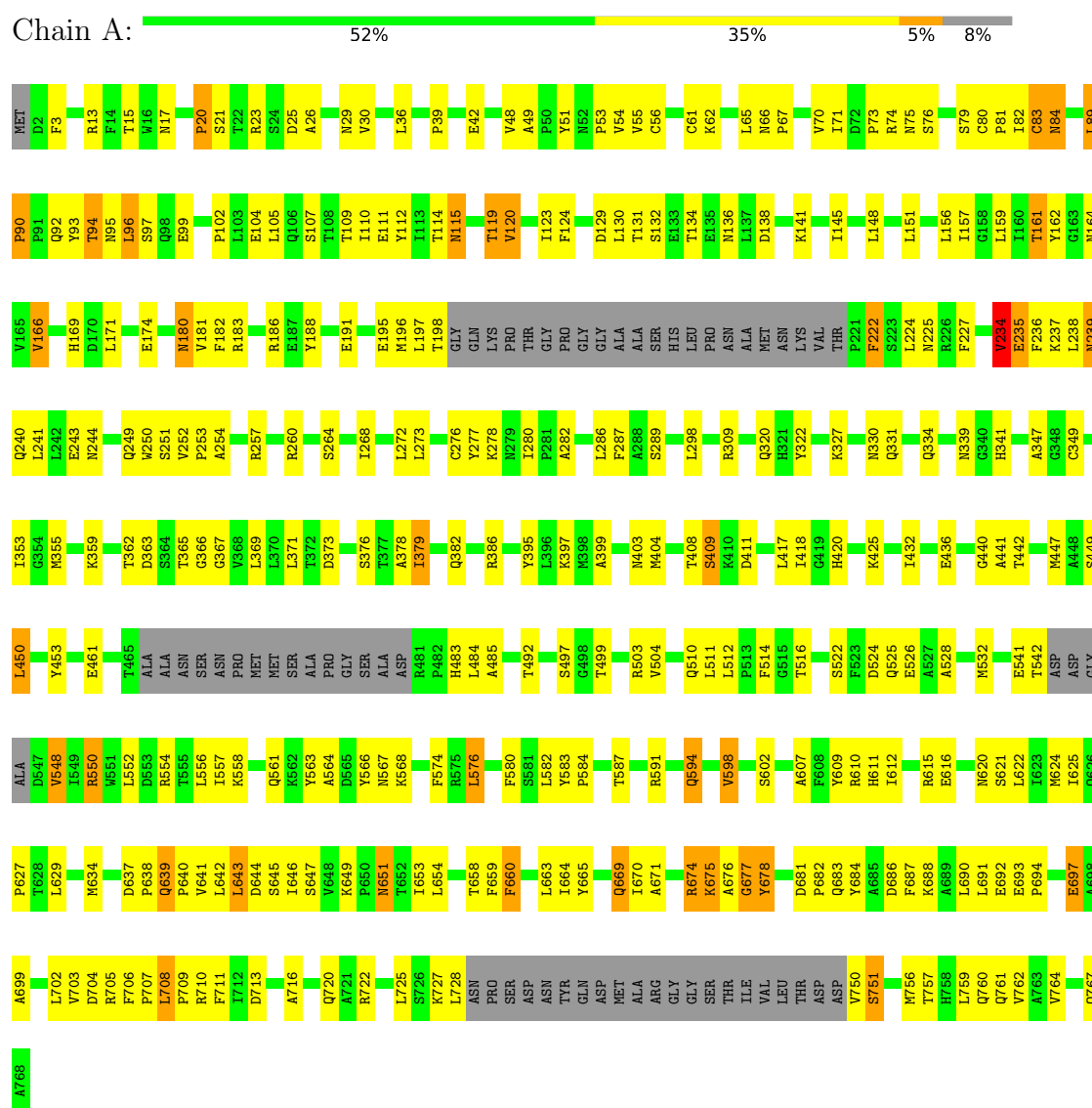
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	34	Total	O	0	0
			34	34		
4	B	35	Total	O	0	0
			35	35		

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. 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. 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.

Note EDS was not executed.

- Molecule 1: protein transport protein SEC23



- Molecule 2: protein transport protein SEC24



HIS	ALA	SER	PHE	D761	D681	S563	GLY	M376	T297	V214	SER	L61	MET
ALA	SER	THR	GLY	M762	K687	R567	VAL	D377	L296	D216	ALA	L62	SER
A888	THR	GLN	THR	A763	K687	M568	VAL	I378	R299	D216	ALA	L62	HIS
	ASP	ASP	ASP	E765	V692	M568	N467	F386	Q300	D217	MET	Q66	HIS
	ILE	PHE	ILE	A766	V692	F571	N467	T468	P302	D218	GLY	E87	LYS
	ASP	ASP	ASP	G767	A896	R578	Q479	F387	P303	P219	ASN	Q68	ARG
	ILE	ASP	ASP	L768	G897	S579	I488	R388	L309	N223	MET	Q72	VAL
	PRO	PRO	PRO	P769	G898	S579	I488	P389	L309	E224	R133	I73	TYR
	ILE	ILE	ILE	VAL	A699	S580	V493	M392	V312	D225	P134	ASP	PRO
	GLY	GLY	GLY	THR	P700	D581	V493	V393	S313	G226	M135	GLN	GLN
	LYS	LYS	LYS	THR	R702	L582	Q494	V394	Q314	L227	L138	ALA	ALA
	GLN	GLN	GLN	ASP	L703	T587	I495	A398	T317	V229	D142	THR	LEU
	GLY	GLY	GLY	GLY	C704	M588	T496	C399	K318	R230	L143	SER	GLN
	VAL	VAL	VAL	THR	L707	P589	V497	R400	K318	R235	L144	MET	TYR
	GLY	GLY	GLY	THR	R708	R590	D498	Q401	G320	S236	T145	ASN	GLY
	GLY	GLY	GLY	THR	M709	S593	L499	N402	T325	Y237	E146	MET	ASN
	GLY	GLY	GLY	THR	F710	F596	E504	I403	T325	N238	L147	HIS	ALA
	ASN	ASN	ASN	THR	P711	F596	D505	L406	L329	N239	P148	LEU	THR
	GLY	GLY	GLY	THR	M714	N599	M507	K409	L333	F241	P150	ASN	PRO
	GLY	GLY	GLY	THR	H715	V600	D508	I410	L333	V242	I151	VAL	GLN
	GLY	GLY	GLY	THR	S716	D601	D508	P411	T336	T243	T152	PRO	GLN
	GLY	GLY	GLY	THR	L717	E802	S516	Q412	P337	R257	D153	LEU	PRO
	GLY	GLY	GLY	THR	T718	S603	T519	F414	N338	G248	L154	VAL	ALA
	GLY	GLY	GLY	THR	K719	I604	A520	Q415	N338	R249	L154	VAL	ALA
	GLY	GLY	GLY	THR	A722	Y610	G521	N417	E341	R250	V162	ASP	GLN
	GLY	GLY	GLY	THR	R723	V611	Q522	S416	N251	R259	I163	ASN	PRO
	GLY	GLY	GLY	THR	F724	Q612	T523	N417	R342	C253	P164	ALA	PRO
	GLY	GLY	GLY	THR	S725	L617	H524	L418	R343	C253	P165	TYR	PRO
	GLY	GLY	GLY	THR	V728	S618	F525	I419	T345	N254	E166	MET	GLN
	GLY	GLY	GLY	THR	P729	L619	Y526	T420	S346	C256	M167	GLN	ASP
	GLY	GLY	GLY	THR	S730	N620	P527	N421	S346	R257	L169	GLN	PRO
	GLY	GLY	GLY	THR	D731	Q623	S530	F422	V350	G257	V170	VAL	ALA
	GLY	GLY	GLY	THR	H732	R624	G531	A423	D351	N260	S175	PRO	ALA
	GLY	GLY	GLY	THR	R733	R625	K532	L424	N352	D261	S175	VAL	ALA
	GLY	GLY	GLY	THR	L737	R625	N533	L428	A353	V262	N176	GLY	GLY
	GLY	GLY	GLY	THR	N738	M633	P534	K429	Y356	G270	A177	MET	SER
	GLY	GLY	GLY	THR	L740	P634	N535	S430	G270	P271	I182	THR	GLY
	GLY	GLY	GLY	THR	E741	T635	D536	K441	T359	N272	T185	PRO	GLY
	GLY	GLY	GLY	THR	L743	E641	I537	V445	P360	D273	L186	LEU	MET
	GLY	GLY	GLY	THR	S742	E641	K539	V445	D362	P274	N187	GLN	GLY
	GLY	GLY	GLY	THR	L744	V660	E543	T448	SER	R277	A188	GLN	PRO
	GLY	GLY	GLY	THR	L745	V660	E543	L449	ASN	V278	V189	GLN	PRO
	GLY	GLY	GLY	THR	K750	S667	K546	P450	ASN	D279	P190	GLN	GLY
	GLY	GLY	GLY	THR	N751	L668	K546	N451	ASN	K284	K191	PRO	GLY
	GLY	GLY	GLY	THR	P818	D669	F552	L452	GLU	C285	N192	ALA	ALA
	GLY	GLY	GLY	THR	A819	D670	C553	G453	GLU	L205	L205	ALA	VAL
	GLY	GLY	GLY	THR	P754	A671	V557	I454	ALA	Y290	R208	PRO	SER
	GLY	GLY	GLY	THR	D755	R672	M558	R454	ASP	N291	P209	ALA	MET
	GLY	GLY	GLY	THR	V758	K677	M558	R454	ASP	A292	T208	TYR	GLY
	GLY	GLY	GLY	THR	V758	K677	M558	R454	ASP	P293	P209	GLY	GLY
	GLY	GLY	GLY	THR	V758	K677	M558	R454	ASP	N374	H212	GLN	GLN
	GLY	GLY	GLY	THR	V758	K677	M558	R454	ASP	Y296	L213	PRO	PRO

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	90.31Å 126.37Å 180.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.96 – 2.75	Depositor
% Data completeness (in resolution range)	91.2 (19.96-2.75)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.210 , 0.257	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11577	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.46	0/5706	1.00	29/7765 (0.4%)
2	B	0.48	0/6054	1.04	44/8214 (0.5%)
All	All	0.47	0/11760	1.02	73/15979 (0.5%)

There are no bond length outliers.

The worst 5 of 73 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	189	VAL	N-CA-C	9.15	116.50	108.63
1	A	649	LYS	CA-C-N	8.38	127.96	119.24
1	A	649	LYS	C-N-CA	8.38	127.96	119.24
1	A	320	GLN	N-CA-C	8.30	121.25	111.71
2	B	394	VAL	N-CA-C	7.50	120.72	109.17

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	5574	0	5475	244	0
2	B	5932	0	5958	311	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	34	0	0	5	0
4	B	35	0	0	3	0
All	All	11577	0	11433	553	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 24.

The worst 5 of 553 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)
2:B:907:ILE:HG22	2:B:908:LEU:HG	1.35	1.08
2:B:147:LEU:HB3	2:B:148:PRO:HD2	1.16	1.08
2:B:147:LEU:CB	2:B:148:PRO:HD2	1.97	0.95
1:A:651:ASN:H	1:A:651:ASN:HD22	0.96	0.94
1:A:359:LYS:HD2	1:A:607:ALA:HB1	1.49	0.92

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	695/768 (90%)	631 (91%)	52 (8%)	12 (2%)	7	14
2	B	734/926 (79%)	651 (89%)	55 (8%)	28 (4%)	2	4
All	All	1429/1694 (84%)	1282 (90%)	107 (8%)	40 (3%)	4	6

5 of 40 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	115	ASN
1	A	120	VAL

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Mol	Chain	Res	Type
1	A	234	VAL
1	A	254	ALA
1	A	678	TYR

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	621/668 (93%)	596 (96%)	25 (4%)	28	50
2	B	672/819 (82%)	647 (96%)	25 (4%)	30	54
All	All	1293/1487 (87%)	1243 (96%)	50 (4%)	28	51

5 of 50 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	152	THR
2	B	352	ASN
2	B	874	VAL
2	B	166	GLU
2	B	270	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	599	ASN
2	B	676	ASN
2	B	918	GLN
1	A	382	GLN
1	A	360	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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.