



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 29, 2026 – 04:57 AM UTC

PDB ID : 2WJV / pdb_00002wjv
Title : Crystal structure of the complex between human nonsense mediated decay factors UPF1 and UPF2
Authors : Clerici, M.; Mourao, A.; Gutsche, I.; Gehring, N.H.; Hentze, M.W.; Kulozik, A.; Kadlec, J.; Sattler, M.; Cusack, S.
Deposited on : 2009-06-01
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	:	FAILED
Mogul	:	2022.3.0, CSD as543be (2022)
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

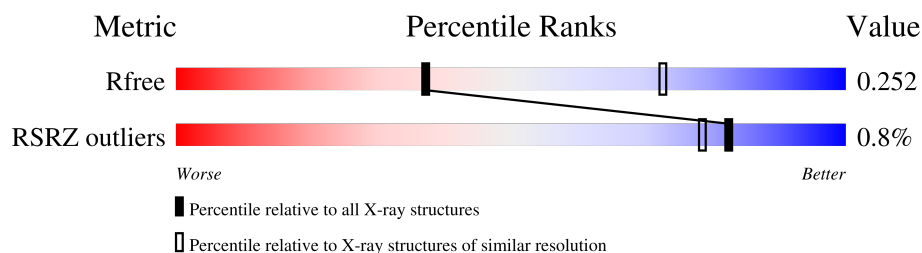
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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))
R_{free}	180053	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13187 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 REGULATOR OF NONSENSE TRANSCRIPTS 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	772	Total	C	N	O	S	0	0	0
			6094	3867	1067	1125	35			
1	B	768	Total	C	N	O	S	0	0	0
			6073	3858	1065	1115	35			

- Molecule 2 is a protein called REGULATOR OF NONSENSE TRANSCRIPTS 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	54	Total	C	N	O	S	0	0	0
			426	268	70	81	7			
2	E	60	Total	C	N	O	S	0	0	0
			473	295	82	89	7			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1102	ALA	-	expression tag	UNP Q9HAU5
D	1103	MET	-	expression tag	UNP Q9HAU5
D	1104	GLY	-	expression tag	UNP Q9HAU5
E	1102	ALA	-	expression tag	UNP Q9HAU5
E	1103	MET	-	expression tag	UNP Q9HAU5
E	1104	GLY	-	expression tag	UNP Q9HAU5

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

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

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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

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3 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	92.41 Å 97.29 Å 124.60 Å 90.00° 102.38° 90.00°	Depositor
Resolution (Å)	48.79 – 2.85 48.79 – 2.85	Depositor EDS
% Data completeness (in resolution range)	96.9 (48.79-2.85) 96.8 (48.79-2.85)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 2.86 Å)	Xtriage
Refinement program	REFMAC 5.5.0038	Depositor
R, R_{free}	0.200 , 0.248 0.206 , 0.252	Depositor DCC
R_{free} test set	2463 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	64.9	Xtriage
Anisotropy	0.265	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 54.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13187	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.78% 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.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

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4.2 Too-close contacts [i](#)

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4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

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4.3.2 Protein sidechains [i](#)

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4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

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

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 29 ligands modelled in this entry, 6 are monoatomic - leaving 23 for Mogul analysis.

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	$\# Z > 2$
4	SO4	A	989	-	4,4,4	0.25	0	6,6,6	0.33	0
4	SO4	B	989	-	4,4,4	0.20	0	6,6,6	0.36	0
4	SO4	A	991	-	4,4,4	0.24	0	6,6,6	0.14	0
4	SO4	B	993	-	4,4,4	0.24	0	6,6,6	0.11	0
4	SO4	B	999	-	4,4,4	0.23	0	6,6,6	0.56	0
4	SO4	A	992	-	4,4,4	0.29	0	6,6,6	0.50	0
4	SO4	B	992	-	4,4,4	0.26	0	6,6,6	0.19	0
4	SO4	B	998	-	4,4,4	0.25	0	6,6,6	0.20	0
4	SO4	B	995	-	4,4,4	0.30	0	6,6,6	0.39	0
4	SO4	A	994	-	4,4,4	0.22	0	6,6,6	0.24	0
4	SO4	A	988	-	4,4,4	0.21	0	6,6,6	0.18	0
4	SO4	A	990	-	4,4,4	0.44	0	6,6,6	0.66	0
4	SO4	A	993	-	4,4,4	0.24	0	6,6,6	0.24	0
4	SO4	B	997	-	4,4,4	0.21	0	6,6,6	0.10	0
4	SO4	A	999	-	4,4,4	0.25	0	6,6,6	0.20	0
4	SO4	A	997	-	4,4,4	0.24	0	6,6,6	0.17	0
4	SO4	A	996	-	4,4,4	0.24	0	6,6,6	0.26	0
4	SO4	B	990	-	4,4,4	0.26	0	6,6,6	0.24	0
4	SO4	B	991	-	4,4,4	0.22	0	6,6,6	0.18	0
4	SO4	A	987	-	4,4,4	0.28	0	6,6,6	0.09	0
4	SO4	A	998	-	4,4,4	0.29	0	6,6,6	0.16	0
4	SO4	A	995	-	4,4,4	0.31	0	6,6,6	0.15	0
4	SO4	B	996	-	4,4,4	0.22	0	6,6,6	0.10	0

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.

4.7 Other polymers ⓘ

There are no such residues in this entry.

4.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

5 Fit of model and data [i](#)

5.1 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	772/800 (96%)	-0.13	5 (0%) 85 82	9, 20, 33, 44	0
1	B	768/800 (96%)	-0.26	3 (0%) 88 87	8, 20, 34, 46	0
2	D	54/97 (55%)	0.01	1 (1%) 66 59	9, 29, 45, 47	0
2	E	60/97 (61%)	0.35	4 (6%) 24 17	9, 34, 49, 52	0
All	All	1654/1794 (92%)	-0.17	13 (0%) 82 78	8, 20, 38, 52	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	1102	ALA	3.5
2	E	1105	VAL	2.8
2	E	1104	GLY	2.8
1	A	356	LEU	2.8
1	A	278	GLU	2.6
1	B	592	GLU	2.6
2	E	1180	LYS	2.5
1	A	337	LEU	2.5
2	D	1105	VAL	2.4
1	A	403	VAL	2.3
1	B	734	GLY	2.3
1	B	220	LYS	2.1
1	A	217	SER	2.0

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

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

5.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.4 Ligands ⓘ

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(Å ²)	Q<0.9
4	SO4	B	991	5/5	0.63	0.09	151,151,152,152	0
4	SO4	A	993	5/5	0.65	0.16	113,113,113,113	0
4	SO4	B	992	5/5	0.65	0.13	129,129,129,129	0
4	SO4	A	997	5/5	0.67	0.12	133,133,133,133	0
4	SO4	A	996	5/5	0.72	0.15	138,138,138,138	0
4	SO4	A	988	5/5	0.77	0.11	141,141,142,142	0
4	SO4	A	989	5/5	0.78	0.16	113,114,114,114	0
4	SO4	A	992	5/5	0.79	0.17	96,97,97,97	0
4	SO4	B	997	5/5	0.79	0.09	131,131,131,131	0
4	SO4	A	991	5/5	0.80	0.07	117,118,118,118	0
4	SO4	A	998	5/5	0.81	0.14	119,120,120,120	0
4	SO4	A	990	5/5	0.82	0.13	71,72,73,73	0
4	SO4	B	990	5/5	0.83	0.11	110,111,111,112	0
4	SO4	B	993	5/5	0.83	0.11	106,107,107,108	0
4	SO4	A	987	5/5	0.83	0.12	127,127,127,128	0
4	SO4	B	999	5/5	0.83	0.12	73,75,76,76	0
4	SO4	A	994	5/5	0.85	0.09	126,126,126,127	0
4	SO4	B	989	5/5	0.86	0.13	118,118,119,119	0
4	SO4	B	996	5/5	0.87	0.12	152,152,153,153	0
4	SO4	B	998	5/5	0.88	0.14	104,104,105,105	0
4	SO4	A	999	5/5	0.88	0.12	135,135,135,136	0
4	SO4	A	995	5/5	0.90	0.15	96,96,97,97	0
4	SO4	B	995	5/5	0.91	0.09	79,80,81,82	0
3	ZN	A	2	1/1	0.96	0.04	20,20,20,20	1
3	ZN	A	3	1/1	0.98	0.05	19,19,19,19	0
3	ZN	B	3	1/1	0.99	0.04	13,13,13,13	0
3	ZN	A	1	1/1	0.99	0.03	11,11,11,11	0
3	ZN	B	2	1/1	0.99	0.02	24,24,24,24	1
3	ZN	B	1	1/1	1.00	0.01	10,10,10,10	0

5.5 Other polymers [i](#)

There are no such residues in this entry.