



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 02:59 PM UTC

PDB ID : 3SR2 / pdb_00003sr2
Title : Crystal Structure of Human XLF-XRCC4 Complex
Authors : Hammel, M.; Classen, S.; Tainer, J.A.
Deposited on : 2011-07-06
Resolution : 3.97 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) : 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

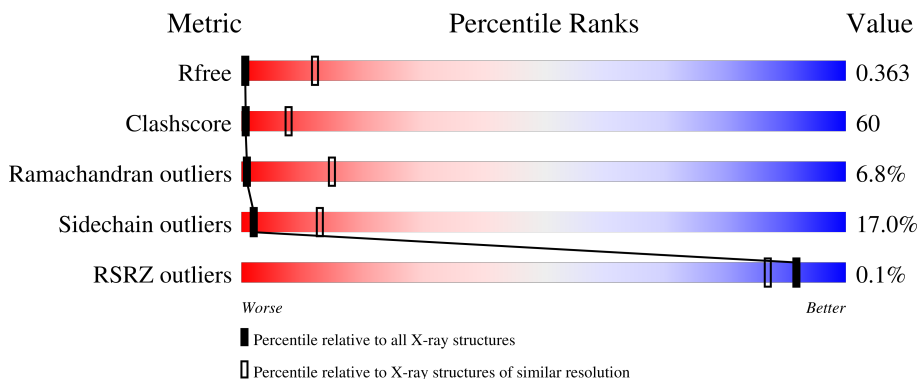
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.97 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	1016 (4.18-3.78)
Clashscore	190562	1007 (4.16-3.80)
Ramachandran outliers	187476	1000 (4.18-3.78)
Sidechain outliers	187428	1131 (4.20-3.76)
RSRZ outliers	180081	1016 (4.18-3.78)

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	145	
1	B	145	
1	E	145	
1	F	145	
2	C	229	

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Mol	Chain	Length	Quality of chain
2	D	229	
2	G	229	
2	H	229	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11363 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 DNA repair protein XRCC4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	139	1103	701	179	217	6	0	0	0
1	B	140	1112	707	181	218	6	0	0	0
1	E	140	1112	707	181	218	6	0	0	0
1	F	140	1112	707	181	218	6	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

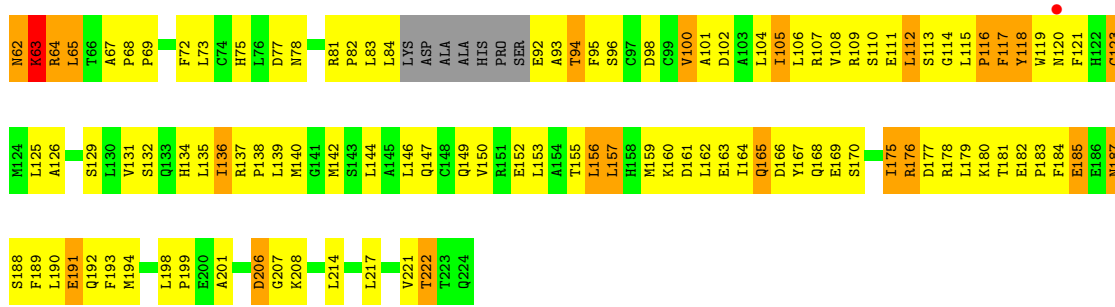
Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP Q13426
A	-3	PRO	-	expression tag	UNP Q13426
A	-2	LEU	-	expression tag	UNP Q13426
A	-1	GLY	-	expression tag	UNP Q13426
A	0	SER	-	expression tag	UNP Q13426
B	-4	GLY	-	expression tag	UNP Q13426
B	-3	PRO	-	expression tag	UNP Q13426
B	-2	LEU	-	expression tag	UNP Q13426
B	-1	GLY	-	expression tag	UNP Q13426
B	0	SER	-	expression tag	UNP Q13426
E	-4	GLY	-	expression tag	UNP Q13426
E	-3	PRO	-	expression tag	UNP Q13426
E	-2	LEU	-	expression tag	UNP Q13426
E	-1	GLY	-	expression tag	UNP Q13426
E	0	SER	-	expression tag	UNP Q13426
F	-4	GLY	-	expression tag	UNP Q13426
F	-3	PRO	-	expression tag	UNP Q13426
F	-2	LEU	-	expression tag	UNP Q13426
F	-1	GLY	-	expression tag	UNP Q13426
F	0	SER	-	expression tag	UNP Q13426

- Molecule 2 is a protein called Non-homologous end-joining factor 1.

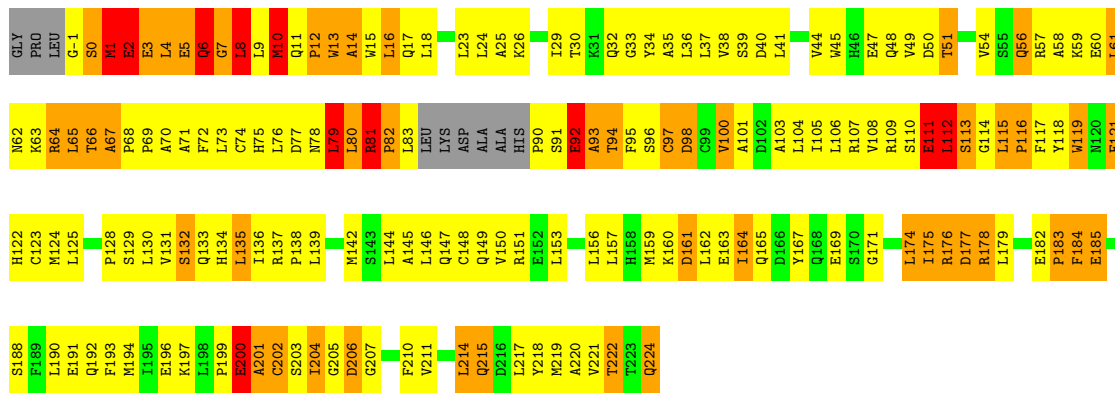
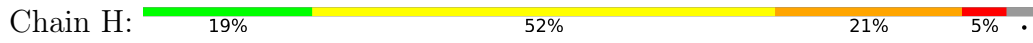
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	218	Total 1736	C 1112	N 290	O 319	S 15	0	0	0
2	D	218	Total 1720	C 1100	N 286	O 319	S 15	0	0	0
2	G	217	Total 1731	C 1108	N 288	O 320	S 15	0	0	0
2	H	220	Total 1737	C 1109	N 288	O 325	S 15	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	GLY	-	expression tag	UNP Q9H9Q4
C	-3	PRO	-	expression tag	UNP Q9H9Q4
C	-2	LEU	-	expression tag	UNP Q9H9Q4
C	-1	GLY	-	expression tag	UNP Q9H9Q4
C	0	SER	-	expression tag	UNP Q9H9Q4
D	-4	GLY	-	expression tag	UNP Q9H9Q4
D	-3	PRO	-	expression tag	UNP Q9H9Q4
D	-2	LEU	-	expression tag	UNP Q9H9Q4
D	-1	GLY	-	expression tag	UNP Q9H9Q4
D	0	SER	-	expression tag	UNP Q9H9Q4
G	-4	GLY	-	expression tag	UNP Q9H9Q4
G	-3	PRO	-	expression tag	UNP Q9H9Q4
G	-2	LEU	-	expression tag	UNP Q9H9Q4
G	-1	GLY	-	expression tag	UNP Q9H9Q4
G	0	SER	-	expression tag	UNP Q9H9Q4
H	-4	GLY	-	expression tag	UNP Q9H9Q4
H	-3	PRO	-	expression tag	UNP Q9H9Q4
H	-2	LEU	-	expression tag	UNP Q9H9Q4
H	-1	GLY	-	expression tag	UNP Q9H9Q4
H	0	SER	-	expression tag	UNP Q9H9Q4



• Molecule 2: Non-homologous end-joining factor 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	110.02Å 110.02Å 763.68Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	67.44 – 3.97 67.44 – 3.97	Depositor EDS
% Data completeness (in resolution range)	86.5 (67.44-3.97) 86.8 (67.44-3.97)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.83 (at 4.01Å)	Xtrriage
Refinement program	PHENIX 1.6.1_357	Depositor
R, R_{free}	0.358 , 0.369 0.348 , 0.363	Depositor DCC
R_{free} test set	2000 reflections (7.96%)	wwPDB-VP
Wilson B-factor (Å ²)	150.2	Xtrriage
Anisotropy	0.669	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 52.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11363	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.76% 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	1.02	1/1125 (0.1%)	1.38	13/1517 (0.9%)
1	B	0.79	0/1134	1.08	3/1528 (0.2%)
1	E	0.41	0/1134	0.85	4/1528 (0.3%)
1	F	0.40	0/1134	0.79	0/1528
2	C	0.36	0/1770	0.82	2/2398 (0.1%)
2	D	0.39	0/1754	0.87	4/2379 (0.2%)
2	G	0.48	0/1765	0.87	4/2392 (0.2%)
2	H	0.54	0/1772	0.86	3/2402 (0.1%)
All	All	0.56	1/11588 (0.0%)	0.94	33/15672 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	83	VAL	CA-CB	6.24	1.61	1.53

The worst 5 of 33 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	D	115	LEU	CA-C-N	8.82	130.87	119.84
2	D	115	LEU	C-N-CA	8.82	130.87	119.84
1	A	71	ARG	N-CA-C	-7.56	103.05	111.82
1	A	34	ILE	N-CA-C	6.58	118.26	108.46
1	A	109	GLY	N-CA-C	6.58	122.39	110.95

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	1103	0	1075	186	0
1	B	1112	0	1088	216	0
1	E	1112	0	1088	110	0
1	F	1112	0	1088	110	0
2	C	1736	0	1752	238	0
2	D	1720	0	1712	192	0
2	G	1731	0	1743	214	0
2	H	1737	0	1733	286	0
All	All	11363	0	11279	1367	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 60.

The worst 5 of 1367 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:134:ILE:HG22	1:B:134:ILE:CG1	1.37	1.50
2:H:8:LEU:CD1	2:H:26:LYS:HD2	1.39	1.49
1:B:107:ARG:NH1	2:C:64:ARG:HD2	1.31	1.43
1:E:134:ILE:HG22	1:F:134:ILE:CG1	1.48	1.42
1:A:134:ILE:CG2	1:B:134:ILE:HD11	1.51	1.40

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	137/145 (94%)	95 (69%)	30 (22%)	12 (9%)	0 10
1	B	138/145 (95%)	95 (69%)	32 (23%)	11 (8%)	1 12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	138/145 (95%)	121 (88%)	13 (9%)	4 (3%)	3	27
1	F	138/145 (95%)	113 (82%)	19 (14%)	6 (4%)	2	21
2	C	214/229 (93%)	175 (82%)	30 (14%)	9 (4%)	2	21
2	D	214/229 (93%)	166 (78%)	36 (17%)	12 (6%)	1	18
2	G	213/229 (93%)	170 (80%)	34 (16%)	9 (4%)	2	21
2	H	216/229 (94%)	151 (70%)	32 (15%)	33 (15%)	0	3
All	All	1408/1496 (94%)	1086 (77%)	226 (16%)	96 (7%)	1	15

5 of 96 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	ALA
1	A	81	ALA
1	A	102	LYS
1	A	107	ARG
1	B	76	SER

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	122/126 (97%)	99 (81%)	23 (19%)	1	10
1	B	123/126 (98%)	102 (83%)	21 (17%)	2	13
1	E	123/126 (98%)	102 (83%)	21 (17%)	2	13
1	F	123/126 (98%)	104 (85%)	19 (15%)	2	15
2	C	193/201 (96%)	166 (86%)	27 (14%)	3	17
2	D	189/201 (94%)	161 (85%)	28 (15%)	3	16
2	G	193/201 (96%)	161 (83%)	32 (17%)	2	13
2	H	193/201 (96%)	150 (78%)	43 (22%)	1	6
All	All	1259/1308 (96%)	1045 (83%)	214 (17%)	2	13

5 of 214 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	108	LEU
2	G	43	GLN
2	H	164	ILE
1	E	131	LEU
1	F	104	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	224	GLN
2	H	149	GLN
1	F	118	ASN
2	H	75	HIS
1	F	112	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

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	139/145 (95%)	-0.67	0 100 100	80, 80, 80, 80	0
1	B	140/145 (96%)	-0.65	0 100 100	80, 80, 80, 80	0
1	E	140/145 (96%)	-0.50	1 (0%) 84 68	80, 80, 80, 80	0
1	F	140/145 (96%)	-0.50	0 100 100	80, 80, 80, 80	0
2	C	218/229 (95%)	-0.54	0 100 100	80, 80, 80, 80	0
2	D	218/229 (95%)	-0.43	0 100 100	80, 80, 80, 80	0
2	G	217/229 (94%)	-0.53	1 (0%) 87 73	80, 80, 80, 80	0
2	H	220/229 (96%)	-0.40	0 100 100	80, 80, 80, 80	0
All	All	1432/1496 (95%)	-0.52	2 (0%) 92 87	80, 80, 80, 80	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	120	ASN	2.2
1	E	137	ASN	2.2

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.