



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 12:24 AM UTC

PDB ID : 6SN1 / pdb_00006sn1
Title : Crystal structure of the human INTS13-INTS14 complex
Authors : Jonas, S.; Sabath, K.; Staeubli, M.L.
Deposited on : 2019-08-23
Resolution : 2.54 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
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

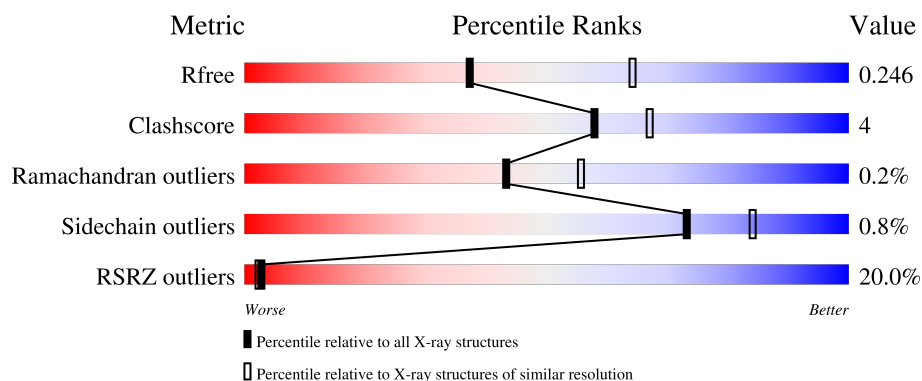
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.54 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	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	763	
2	B	518	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	B	601	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8015 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 Integrator complex subunit 13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	517	4039	2535	705	767	32	0	0	0

There are 57 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-56	MET	-	initiating methionine	UNP Q9NVM9
A	-55	ALA	-	expression tag	UNP Q9NVM9
A	-54	SER	-	expression tag	UNP Q9NVM9
A	-53	ALA	-	expression tag	UNP Q9NVM9
A	-52	TRP	-	expression tag	UNP Q9NVM9
A	-51	SER	-	expression tag	UNP Q9NVM9
A	-50	HIS	-	expression tag	UNP Q9NVM9
A	-49	PRO	-	expression tag	UNP Q9NVM9
A	-48	GLN	-	expression tag	UNP Q9NVM9
A	-47	PHE	-	expression tag	UNP Q9NVM9
A	-46	GLU	-	expression tag	UNP Q9NVM9
A	-45	LYS	-	expression tag	UNP Q9NVM9
A	-44	GLY	-	expression tag	UNP Q9NVM9
A	-43	GLY	-	expression tag	UNP Q9NVM9
A	-42	GLY	-	expression tag	UNP Q9NVM9
A	-41	SER	-	expression tag	UNP Q9NVM9
A	-40	GLY	-	expression tag	UNP Q9NVM9
A	-39	GLY	-	expression tag	UNP Q9NVM9
A	-38	GLY	-	expression tag	UNP Q9NVM9
A	-37	SER	-	expression tag	UNP Q9NVM9
A	-36	GLY	-	expression tag	UNP Q9NVM9
A	-35	GLY	-	expression tag	UNP Q9NVM9
A	-34	SER	-	expression tag	UNP Q9NVM9
A	-33	ALA	-	expression tag	UNP Q9NVM9
A	-32	TRP	-	expression tag	UNP Q9NVM9
A	-31	SER	-	expression tag	UNP Q9NVM9
A	-30	HIS	-	expression tag	UNP Q9NVM9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-29	PRO	-	expression tag	UNP Q9NVM9
A	-28	GLN	-	expression tag	UNP Q9NVM9
A	-27	PHE	-	expression tag	UNP Q9NVM9
A	-26	GLU	-	expression tag	UNP Q9NVM9
A	-25	LYS	-	expression tag	UNP Q9NVM9
A	-24	SER	-	expression tag	UNP Q9NVM9
A	-23	SER	-	expression tag	UNP Q9NVM9
A	-22	GLY	-	expression tag	UNP Q9NVM9
A	-21	SER	-	expression tag	UNP Q9NVM9
A	-20	GLY	-	expression tag	UNP Q9NVM9
A	-19	SER	-	expression tag	UNP Q9NVM9
A	-18	GLY	-	expression tag	UNP Q9NVM9
A	-17	LEU	-	expression tag	UNP Q9NVM9
A	-16	GLU	-	expression tag	UNP Q9NVM9
A	-15	VAL	-	expression tag	UNP Q9NVM9
A	-14	LEU	-	expression tag	UNP Q9NVM9
A	-13	PHE	-	expression tag	UNP Q9NVM9
A	-12	GLN	-	expression tag	UNP Q9NVM9
A	-11	GLY	-	expression tag	UNP Q9NVM9
A	-10	PRO	-	expression tag	UNP Q9NVM9
A	-9	SER	-	expression tag	UNP Q9NVM9
A	-8	ASP	-	expression tag	UNP Q9NVM9
A	-7	PRO	-	expression tag	UNP Q9NVM9
A	-6	GLY	-	expression tag	UNP Q9NVM9
A	-5	PRO	-	expression tag	UNP Q9NVM9
A	-4	LYS	-	expression tag	UNP Q9NVM9
A	-3	ARG	-	expression tag	UNP Q9NVM9
A	-2	ALA	-	expression tag	UNP Q9NVM9
A	-1	GLU	-	expression tag	UNP Q9NVM9
A	0	PHE	-	expression tag	UNP Q9NVM9

- Molecule 2 is a protein called Integrator complex subunit 14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	503	Total	C	N	O	S	0	0	0
			3856	2466	637	728	25			

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

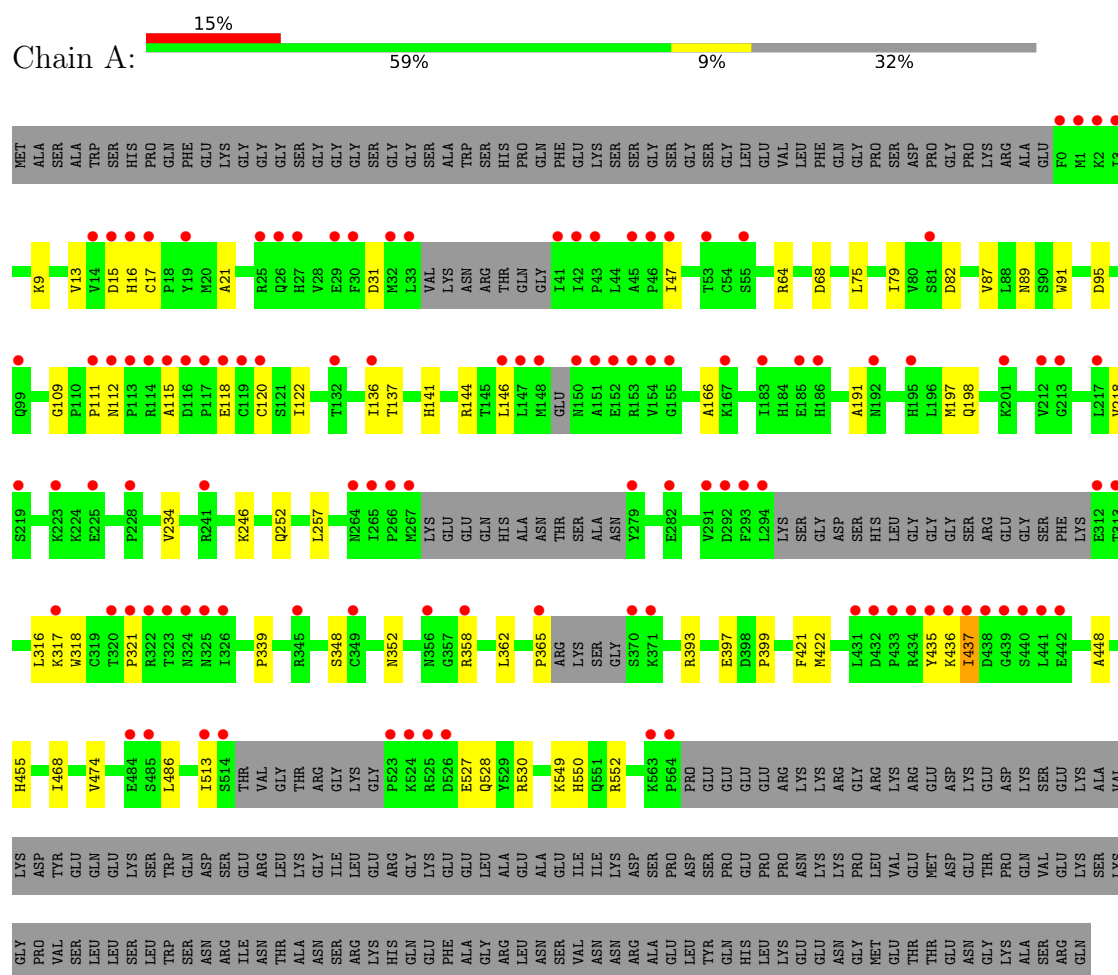
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	37	Total	O	0	0
			37	37		
4	B	53	Total	O	0	0
			53	53		

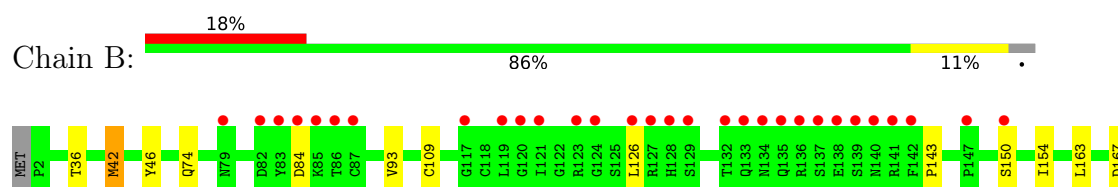
3 Residue-property plots

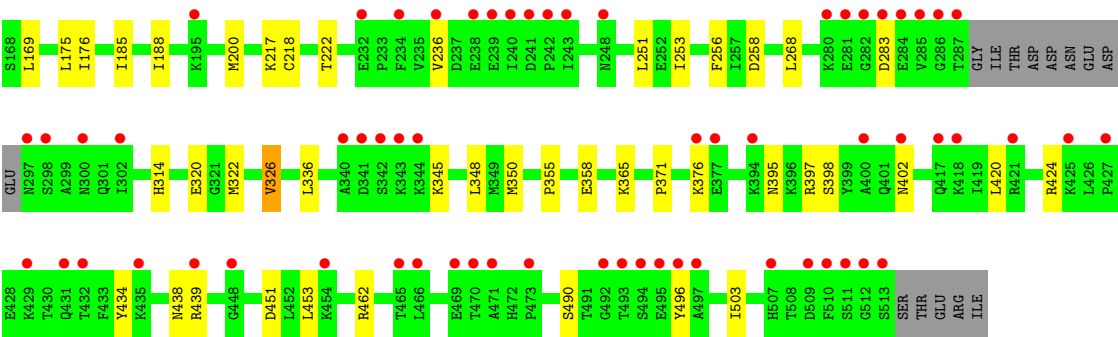
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

• Molecule 1: Integrator complex subunit 13



• Molecule 2: Integrator complex subunit 14





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	190.99Å 115.35Å 147.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.47 – 2.54 45.47 – 2.54	Depositor EDS
% Data completeness (in resolution range)	99.5 (45.47-2.54) 88.4 (45.47-2.54)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.51 (at 2.54Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.224 , 0.244 0.228 , 0.246	Depositor DCC
R_{free} test set	5463 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	55.2	Xtriage
Anisotropy	0.539	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 50.1	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	0.94	EDS
Total number of atoms	8015	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.56% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.09	0/4118	0.28	0/5588
2	B	0.10	0/3943	0.30	0/5365
All	All	0.09	0/8061	0.29	0/10953

There are no bond length outliers.

There are no bond angle outliers.

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	4039	0	3931	39	0
2	B	3856	0	3813	37	0
3	A	20	0	0	0	0
3	B	10	0	0	3	0
4	A	37	0	0	0	0
4	B	53	0	0	0	0
All	All	8015	0	7744	70	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 4.

All (70) 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:513:ILE:HD13	1:A:528:GLN:HG2	1.74	0.69
1:A:348:SER:O	1:A:352:ASN:ND2	2.33	0.62
1:A:317:LYS:HE3	1:A:365:PRO:HB3	1.80	0.62
2:B:217:LYS:HG2	2:B:222:THR:HG22	1.81	0.62
1:A:435:TYR:HD1	1:A:436:LYS:H	1.47	0.62
1:A:64:ARG:NH1	1:A:339:PRO:O	2.33	0.61
1:A:9:LYS:HE2	1:A:137:THR:HG23	1.81	0.60
1:A:435:TYR:HD1	1:A:437:ILE:H	1.49	0.60
1:A:47:ILE:HG12	2:B:451:ASP:HB3	1.84	0.59
2:B:320:GLU:HB3	2:B:322:MET:HE3	1.84	0.59
1:A:15:ASP:HB3	1:A:122:ILE:HD13	1.85	0.57
1:A:112:ASN:HB3	1:A:115:ALA:HB2	1.88	0.56
2:B:439:ARG:NH2	3:B:602:SO4:O2	2.37	0.56
2:B:176:ILE:HD12	2:B:185:ILE:HG12	1.89	0.54
2:B:163:LEU:HB3	2:B:169:LEU:HB2	1.89	0.54
2:B:126:LEU:HD11	2:B:175:LEU:HD21	1.90	0.53
2:B:251:LEU:HD13	2:B:350:MET:HE1	1.90	0.53
2:B:268:LEU:HD11	2:B:355:PRO:HD3	1.91	0.52
1:A:79:ILE:HG12	1:A:87:VAL:HG12	1.92	0.51
2:B:154:ILE:HB	2:B:185:ILE:HD13	1.93	0.51
2:B:283:ASP:N	2:B:283:ASP:OD1	2.41	0.51
2:B:188:ILE:HG13	2:B:200:MET:HE3	1.92	0.50
1:A:527:GLU:OE1	1:A:530:ARG:NH2	2.44	0.50
1:A:252:GLN:HA	1:A:257:LEU:HB2	1.93	0.50
1:A:144:ARG:HH11	1:A:197:MET:HE3	1.77	0.50
1:A:144:ARG:HD2	1:A:197:MET:HE3	1.95	0.49
1:A:316:LEU:HB3	1:A:362:LEU:HB3	1.96	0.48
1:A:421:PHE:HE1	1:A:455:HIS:HB3	1.77	0.48
1:A:136:ILE:HD13	1:A:141:HIS:HB2	1.95	0.48
2:B:109:CYS:O	2:B:150:SER:HA	2.15	0.47
2:B:42:MET:HG3	2:B:46:TYR:HB3	1.96	0.46
2:B:453:LEU:HB2	2:B:490:SER:HB3	1.98	0.46
1:A:191:ALA:HB2	1:A:198:GLN:NE2	2.31	0.46
1:A:549:LYS:HG2	1:A:552:ARG:NH2	2.31	0.46
2:B:376:LYS:HB2	2:B:376:LYS:HE2	1.80	0.45
2:B:93:VAL:HG23	2:B:143:PRO:HG3	1.99	0.45
2:B:314:HIS:HB2	2:B:348:LEU:HB2	1.99	0.45
1:A:21:ALA:HB2	1:A:111:PRO:HG2	1.98	0.45
1:A:31:ASP:OD2	2:B:462:ARG:NH2	2.49	0.45
2:B:395:ASN:N	3:B:601:SO4:O1	2.33	0.45
1:A:13:VAL:HG12	1:A:122:ILE:HD11	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:CYS:SG	1:A:120:CYS:HB3	2.57	0.44
1:A:166:ALA:HB3	1:A:218:VAL:HG21	1.99	0.44
2:B:336:LEU:HD23	2:B:350:MET:HB2	2.00	0.44
2:B:258:ASP:HA	2:B:322:MET:HG3	1.99	0.44
1:A:321:PRO:HB2	1:A:358:ARG:HH21	1.82	0.43
2:B:326:VAL:HG21	2:B:350:MET:HE2	2.00	0.43
1:A:89:ASN:HB2	1:A:95:ASP:HB3	2.00	0.42
2:B:336:LEU:HD21	2:B:350:MET:HE3	2.01	0.42
2:B:36:THR:HA	2:B:74:GLN:HE22	1.85	0.42
1:A:448:ALA:HA	2:B:371:PRO:HG3	2.01	0.42
1:A:468:ILE:HB	1:A:474:VAL:HG11	2.01	0.42
2:B:218:CYS:HB2	2:B:253:ILE:HD12	2.02	0.42
2:B:496:TYR:CD2	2:B:503:ILE:HG12	2.55	0.42
1:A:399:PRO:HD2	2:B:345:LYS:HB3	2.02	0.42
2:B:397:ARG:NH2	3:B:601:SO4:O3	2.41	0.42
1:A:16:HIS:NE2	1:A:109:GLY:O	2.50	0.41
1:A:393:ARG:NH2	1:A:397:GLU:OE1	2.50	0.41
1:A:68:ASP:OD2	2:B:398:SER:OG	2.29	0.41
2:B:402:ASN:OD1	2:B:439:ARG:HD3	2.21	0.41
2:B:434:TYR:O	2:B:438:ASN:ND2	2.43	0.41
1:A:118:GLU:C	1:A:120:CYS:H	2.28	0.41
1:A:318:TRP:HE1	1:A:321:PRO:HD3	1.86	0.41
1:A:146:LEU:HD23	1:A:146:LEU:HA	1.89	0.40
1:A:422:MET:HG2	2:B:256:PHE:CE2	2.57	0.40
1:A:486:LEU:HG	1:A:550:HIS:CE1	2.56	0.40
2:B:420:LEU:HD23	2:B:424:ARG:HH22	1.85	0.40
1:A:75:LEU:HD13	1:A:91:TRP:O	2.21	0.40
2:B:358:GLU:HG3	2:B:365:LYS:HG2	2.03	0.40
2:B:402:ASN:ND2	2:B:439:ARG:HH21	2.19	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	503/763 (66%)	489 (97%)	13 (3%)	1 (0%)	43	56
2	B	499/518 (96%)	478 (96%)	20 (4%)	1 (0%)	43	56
All	All	1002/1281 (78%)	967 (96%)	33 (3%)	2 (0%)	43	56

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	437	ILE
2	B	236	VAL

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	453/679 (67%)	450 (99%)	3 (1%)	76	85
2	B	423/452 (94%)	419 (99%)	4 (1%)	70	82
All	All	876/1131 (78%)	869 (99%)	7 (1%)	73	84

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	82	ASP
1	A	234	VAL
1	A	246	LYS
2	B	42	MET
2	B	84	ASP
2	B	167	ASP
2	B	326	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	180	GLN
1	A	186	HIS

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Mol	Chain	Res	Type
1	A	451	GLN
1	A	455	HIS
1	A	528	GLN
2	B	74	GLN
2	B	502	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](#)

6 ligands are modelled in this entry.

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	$\# Z > 2$
3	SO4	A	803	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	A	804	-	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	B	601	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	A	802	-	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	A	801	-	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	B	602	-	4,4,4	0.23	0	6,6,6	0.08	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.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	601	SO4	2	0
3	B	602	SO4	1	0

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	517/763 (67%)	1.37	111 (21%) 2 2	48, 77, 140, 174	0
2	B	503/518 (97%)	1.11	93 (18%) 3 3	46, 72, 144, 190	0
All	All	1020/1281 (79%)	1.25	204 (20%) 3 2	46, 75, 143, 190	0

All (204) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	297	ASN	11.4
1	A	523	PRO	10.0
1	A	150	ASN	9.1
1	A	33	LEU	8.5
2	B	134	ASN	8.0
1	A	294	LEU	7.8
2	B	513	SER	7.3
2	B	121	ILE	7.2
1	A	279	TYR	7.1
1	A	440	SER	7.0
1	A	0	PHE	6.9
1	A	323	THR	6.8
1	A	437	ILE	6.8
1	A	148	MET	6.7
2	B	140	ASN	6.7
2	B	139	SER	6.6
2	B	135	GLN	6.6
2	B	341	ASP	6.5
1	A	3	ILE	6.4
2	B	137	SER	6.4
1	A	153	ARG	6.1
1	A	267	MET	6.1
1	A	293	PHE	6.1
1	A	42	ILE	6.0

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Mol	Chain	Res	Type	RSRZ
1	A	151	ALA	5.9
2	B	512	GLY	5.9
2	B	376	LYS	5.7
2	B	287	THR	5.7
1	A	438	ASP	5.7
1	A	1	MET	5.7
2	B	240	ILE	5.5
2	B	495	GLU	5.4
1	A	117	PRO	5.4
2	B	138	GLU	5.4
2	B	85	LYS	5.4
2	B	123	ARG	5.4
1	A	324	ASN	5.3
1	A	436	LYS	5.3
2	B	120	GLY	5.2
1	A	370	SER	5.2
1	A	152	GLU	5.1
1	A	136	ILE	5.0
2	B	343	LYS	4.9
1	A	514	SER	4.9
2	B	127	ARG	4.8
2	B	493	THR	4.8
2	B	239	GLU	4.8
2	B	281	GLU	4.8
1	A	2	LYS	4.7
1	A	434	ARG	4.6
2	B	511	SER	4.6
2	B	280	LYS	4.5
1	A	365	PRO	4.4
2	B	470	THR	4.4
2	B	342	SER	4.4
1	A	325	ASN	4.3
1	A	441	LEU	4.3
1	A	55	SER	4.2
1	A	322	ARG	4.2
1	A	433	PRO	4.1
2	B	286	GLY	4.1
2	B	82	ASP	4.0
2	B	344	LYS	4.0
1	A	292	ASP	4.0
1	A	563	LYS	4.0
1	A	321	PRO	3.9

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Mol	Chain	Res	Type	RSRZ
2	B	496	TYR	3.9
1	A	526	ASP	3.9
1	A	45	ALA	3.9
1	A	27	HIS	3.9
2	B	87	CYS	3.9
1	A	564	PRO	3.9
1	A	435	TYR	3.8
2	B	243	ILE	3.8
2	B	494	SER	3.8
1	A	186	HIS	3.7
1	A	524	LYS	3.7
1	A	291	VAL	3.7
1	A	116	ASP	3.7
1	A	266	PRO	3.7
1	A	439	GLY	3.6
2	B	136	ARG	3.6
2	B	418	LYS	3.5
2	B	124	GLY	3.5
2	B	448	GLY	3.5
1	A	212	VAL	3.5
1	A	43	PRO	3.4
1	A	120	CYS	3.4
2	B	236	VAL	3.4
2	B	285	VAL	3.4
1	A	525	ARG	3.3
1	A	32	MET	3.3
2	B	510	PHE	3.3
2	B	86	THR	3.3
1	A	326	ILE	3.3
1	A	47	ILE	3.2
2	B	241	ASP	3.2
2	B	126	LEU	3.2
2	B	507	HIS	3.2
2	B	83	TYR	3.2
1	A	313	THR	3.2
1	A	114	ARG	3.1
2	B	128	HIS	3.1
1	A	312	GLU	3.1
2	B	142	PHE	3.1
2	B	119	LEU	3.1
2	B	232	GLU	3.0
2	B	283	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	25	ARG	3.0
2	B	435	LYS	3.0
1	A	41	ILE	3.0
2	B	340	ALA	3.0
1	A	219	SER	3.0
1	A	147	LEU	2.9
1	A	113	PRO	2.9
1	A	167	LYS	2.9
1	A	112	ASN	2.9
1	A	154	VAL	2.9
1	A	225	GLU	2.9
1	A	213	GLY	2.9
1	A	99	GLN	2.8
2	B	469	GLU	2.8
2	B	84	ASP	2.8
2	B	234	PHE	2.8
1	A	115	ALA	2.8
1	A	146	LEU	2.8
2	B	439	ARG	2.8
2	B	454	LYS	2.8
2	B	432	THR	2.7
1	A	371	LYS	2.7
1	A	183	ILE	2.7
1	A	132	THR	2.7
2	B	132	THR	2.7
1	A	81	SER	2.7
2	B	421	ARG	2.7
1	A	155	GLY	2.7
1	A	30	PHE	2.7
2	B	141	ARG	2.7
2	B	238	GLU	2.6
1	A	195	HIS	2.6
2	B	425	LYS	2.6
1	A	431	LEU	2.6
2	B	298	SER	2.6
2	B	302	ILE	2.6
1	A	442	GLU	2.6
1	A	19	TYR	2.6
1	A	185	GLU	2.6
1	A	345	ARG	2.5
1	A	46	PRO	2.5
2	B	427	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	248	ASN	2.5
1	A	119	CYS	2.4
2	B	117	GLY	2.4
1	A	264	ASN	2.4
1	A	15	ASP	2.4
1	A	217	LEU	2.4
1	A	16	HIS	2.4
1	A	356	ASN	2.4
2	B	282	GLY	2.4
1	A	349	CYS	2.4
1	A	14	VAL	2.4
1	A	118	GLU	2.4
1	A	192	ASN	2.3
1	A	29	GLU	2.3
1	A	111	PRO	2.3
2	B	466	LEU	2.3
1	A	17	CYS	2.3
2	B	429	LYS	2.3
2	B	284	GLU	2.3
2	B	79	ASN	2.3
2	B	402	ASN	2.3
2	B	497	ALA	2.3
1	A	228	PRO	2.3
2	B	473	PRO	2.3
2	B	492	GLY	2.3
1	A	432	ASP	2.3
2	B	417	GLN	2.2
1	A	485	SER	2.2
2	B	394	LYS	2.2
2	B	300	ASN	2.2
2	B	431	GLN	2.2
2	B	377	GLU	2.2
2	B	400	ALA	2.2
2	B	242	PRO	2.2
2	B	195	LYS	2.2
1	A	26	GLN	2.1
2	B	133	GLN	2.1
1	A	241	ARG	2.1
1	A	282	GLU	2.1
1	A	53	THR	2.1
1	A	320	THR	2.1
1	A	265	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	358	ARG	2.1
1	A	484	GLU	2.1
2	B	150	SER	2.1
2	B	147	PRO	2.1
2	B	465	THR	2.1
1	A	201	LYS	2.1
1	A	223	LYS	2.1
2	B	471	ALA	2.1
1	A	317	LYS	2.1
2	B	509	ASP	2.0
2	B	129	SER	2.0
1	A	513	ILE	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](#)

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
3	SO4	B	602	5/5	0.41	0.20	242,244,246,258	0
3	SO4	A	801	5/5	0.52	0.14	209,210,213,219	0
3	SO4	A	802	5/5	0.54	0.36	198,203,217,221	0
3	SO4	A	804	5/5	0.68	0.26	169,170,173,207	0
3	SO4	A	803	5/5	0.71	0.15	153,155,163,174	0
3	SO4	B	601	5/5	0.88	0.14	123,124,151,160	0

6.5 Other polymers [i](#)

There are no such residues in this entry.