



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:51 PM UTC

PDB ID : 4O46 / pdb_00004o46
Title : 14-3-3-gamma in complex with influenza NS1 C-terminal tail phosphorylated at S228
Authors : Qin, S.; Liu, Y.; Tempel, W.; Arrowsmith, C.H.; Bountra, C.; Edwards, A.M.; Min, J.; Structural Genomics Consortium (SGC)
Deposited on : 2013-12-18
Resolution : 2.90 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

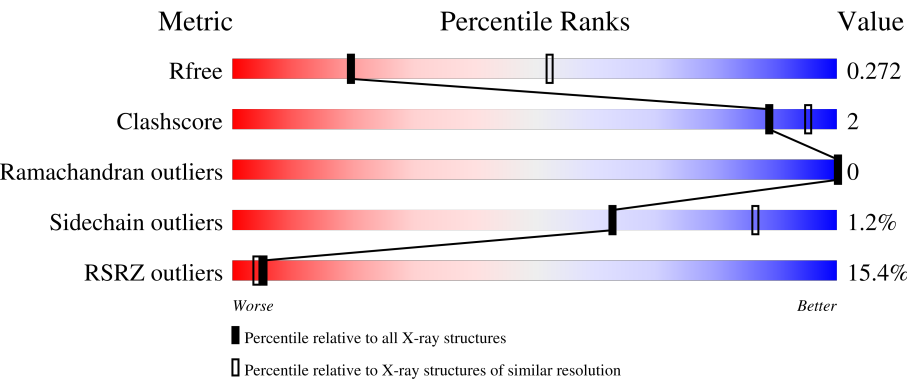
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	256	8% 86%6%8%
1	B	256	4% 86%5%9%
1	C	256	7% 87%.8%
1	D	256	9% 86%6%8%
1	E	256	7% 84%8%8%

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Mol	Chain	Length	Quality of chain
1	F	256	
2	G	15	
2	H	15	
2	I	15	
2	J	15	
2	K	15	
2	L	15	
3	M	24	
3	N	24	
3	O	24	
3	V	24	

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
4	UNX	A	301	-	-	-	X
4	UNX	A	302	-	-	-	X
4	UNX	A	303	-	-	-	X
4	UNX	A	304	-	-	-	X
4	UNX	A	305	-	-	-	X
4	UNX	A	306	-	-	-	X
4	UNX	A	307	-	-	-	X
4	UNX	A	308	-	-	-	X
4	UNX	B	301	-	-	-	X
4	UNX	B	302	-	-	-	X
4	UNX	B	303	-	-	-	X
4	UNX	B	304	-	-	-	X
4	UNX	B	305	-	-	-	X
4	UNX	B	306	-	-	-	X
4	UNX	B	307	-	-	-	X
4	UNX	B	308	-	-	-	X
4	UNX	B	309	-	-	-	X
4	UNX	B	310	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	UNX	B	311	-	-	-	X
4	UNX	B	312	-	-	-	X
4	UNX	B	313	-	-	-	X
4	UNX	B	314	-	-	-	X
4	UNX	B	315	-	-	-	X
4	UNX	B	316	-	-	-	X
4	UNX	B	317	-	-	-	X
4	UNX	B	318	-	-	-	X
4	UNX	C	301	-	-	-	X
4	UNX	C	302	-	-	-	X
4	UNX	C	303	-	-	-	X
4	UNX	C	304	-	-	-	X
4	UNX	C	305	-	-	-	X
4	UNX	C	306	-	-	-	X
4	UNX	C	307	-	-	-	X
4	UNX	C	308	-	-	-	X
4	UNX	C	309	-	-	-	X
4	UNX	C	310	-	-	-	X
4	UNX	C	311	-	-	-	X
4	UNX	C	312	-	-	-	X
4	UNX	C	313	-	-	-	X
4	UNX	D	301	-	-	-	X
4	UNX	D	302	-	-	-	X
4	UNX	D	303	-	-	-	X
4	UNX	D	304	-	-	-	X
4	UNX	D	305	-	-	-	X
4	UNX	D	306	-	-	-	X
4	UNX	D	307	-	-	-	X
4	UNX	D	308	-	-	-	X
4	UNX	D	309	-	-	-	X
4	UNX	E	301	-	-	-	X
4	UNX	E	302	-	-	-	X
4	UNX	E	303	-	-	-	X
4	UNX	E	304	-	-	-	X
4	UNX	F	301	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10919 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 14-3-3 protein gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	235	Total	C	N	O	S	0	1	0
			1811	1135	314	353	9			
1	B	234	Total	C	N	O	S	0	0	0
			1818	1142	306	361	9			
1	C	235	Total	C	N	O	S	0	1	0
			1804	1134	303	358	9			
1	D	235	Total	C	N	O	S	0	0	0
			1777	1116	304	347	10			
1	E	236	Total	C	N	O	S	0	0	0
			1814	1138	312	355	9			
1	F	206	Total	C	N	O	S	0	0	0
			1354	841	243	265	5			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	248	SER	-	expression tag	UNP P61981
A	249	LEU	-	expression tag	UNP P61981
A	250	GLU	-	expression tag	UNP P61981
A	251	HIS	-	expression tag	UNP P61981
A	252	HIS	-	expression tag	UNP P61981
A	253	HIS	-	expression tag	UNP P61981
A	254	HIS	-	expression tag	UNP P61981
A	255	HIS	-	expression tag	UNP P61981
A	256	HIS	-	expression tag	UNP P61981
B	248	SER	-	expression tag	UNP P61981
B	249	LEU	-	expression tag	UNP P61981
B	250	GLU	-	expression tag	UNP P61981
B	251	HIS	-	expression tag	UNP P61981
B	252	HIS	-	expression tag	UNP P61981
B	253	HIS	-	expression tag	UNP P61981
B	254	HIS	-	expression tag	UNP P61981
B	255	HIS	-	expression tag	UNP P61981

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Chain	Residue	Modelled	Actual	Comment	Reference
B	256	HIS	-	expression tag	UNP P61981
C	248	SER	-	expression tag	UNP P61981
C	249	LEU	-	expression tag	UNP P61981
C	250	GLU	-	expression tag	UNP P61981
C	251	HIS	-	expression tag	UNP P61981
C	252	HIS	-	expression tag	UNP P61981
C	253	HIS	-	expression tag	UNP P61981
C	254	HIS	-	expression tag	UNP P61981
C	255	HIS	-	expression tag	UNP P61981
C	256	HIS	-	expression tag	UNP P61981
D	248	SER	-	expression tag	UNP P61981
D	249	LEU	-	expression tag	UNP P61981
D	250	GLU	-	expression tag	UNP P61981
D	251	HIS	-	expression tag	UNP P61981
D	252	HIS	-	expression tag	UNP P61981
D	253	HIS	-	expression tag	UNP P61981
D	254	HIS	-	expression tag	UNP P61981
D	255	HIS	-	expression tag	UNP P61981
D	256	HIS	-	expression tag	UNP P61981
E	248	SER	-	expression tag	UNP P61981
E	249	LEU	-	expression tag	UNP P61981
E	250	GLU	-	expression tag	UNP P61981
E	251	HIS	-	expression tag	UNP P61981
E	252	HIS	-	expression tag	UNP P61981
E	253	HIS	-	expression tag	UNP P61981
E	254	HIS	-	expression tag	UNP P61981
E	255	HIS	-	expression tag	UNP P61981
E	256	HIS	-	expression tag	UNP P61981
F	248	SER	-	expression tag	UNP P61981
F	249	LEU	-	expression tag	UNP P61981
F	250	GLU	-	expression tag	UNP P61981
F	251	HIS	-	expression tag	UNP P61981
F	252	HIS	-	expression tag	UNP P61981
F	253	HIS	-	expression tag	UNP P61981
F	254	HIS	-	expression tag	UNP P61981
F	255	HIS	-	expression tag	UNP P61981
F	256	HIS	-	expression tag	UNP P61981

- Molecule 2 is a protein called Nonstructural protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	6	Total	C	N	O	P	0	0	0
			42	24	7	10	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	6	Total	C	N	O	P	0	0	0
			42	24	6	11	1			
2	I	6	Total	C	N	O	P	0	0	0
			44	25	7	11	1			
2	J	6	Total	C	N	O	P	0	0	0
			40	23	6	10	1			
2	K	6	Total	C	N	O	P	0	0	0
			41	24	6	10	1			
2	L	2	Total	C	N	O	P	0	0	0
			15	6	2	6	1			

- Molecule 3 is a protein called Unidentified polymer.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	M	20	Total	C	N	O	0	0	0
			100	60	20	20			
3	N	9	Total	C	N	O	0	0	0
			45	27	9	9			
3	O	10	Total	C	N	O	0	0	0
			50	30	10	10			
3	V	13	Total	C	N	O	0	0	0
			65	39	13	13			

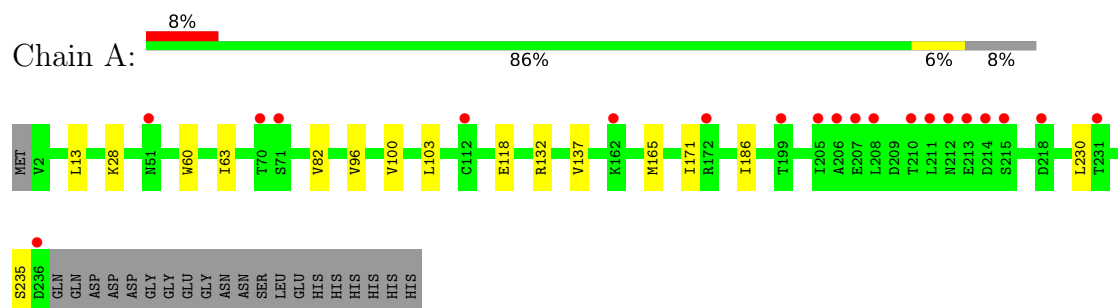
- Molecule 4 is UNKNOWN ATOM OR ION (CCD ID: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	10	Total	X	0	0
			10	10		
4	B	18	Total	X	0	0
			18	18		
4	C	14	Total	X	0	0
			14	14		
4	D	9	Total	X	0	0
			9	9		
4	E	5	Total	X	0	0
			5	5		
4	F	1	Total	X	0	0
			1	1		

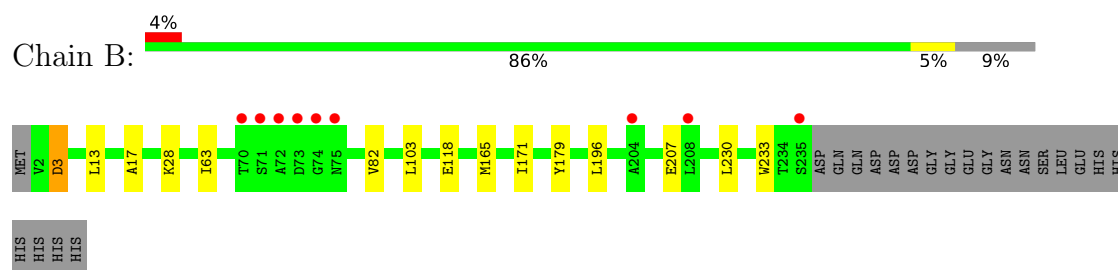
3 Residue-property plots [i](#)

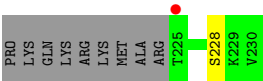
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: 14-3-3 protein gamma

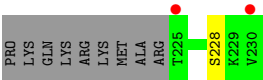


• Molecule 1: 14-3-3 protein gamma

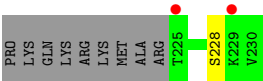




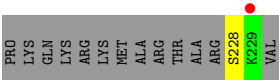
• Molecule 2: Nonstructural protein 1



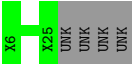
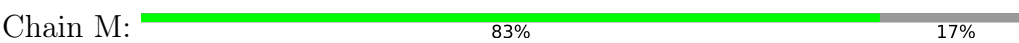
• Molecule 2: Nonstructural protein 1



• Molecule 2: Nonstructural protein 1



• Molecule 3: Unidentified polymer



• Molecule 3: Unidentified polymer



• Molecule 3: Unidentified polymer



• Molecule 3: Unidentified polymer



X7	X19	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK
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4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	121.83Å 121.83Å 314.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.53 – 2.90 38.53 – 2.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (38.53-2.90) 99.9 (38.53-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.31 (at 2.90Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.10.0, BUSTER 2.10.0	Depositor
R, R_{free}	0.226 , 0.249 0.249 , 0.272	Depositor DCC
R_{free} test set	1510 reflections (2.83%)	wwPDB-VP
Wilson B-factor (Å ²)	56.7	Xtriage
Anisotropy	0.313	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 72.4	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	0.90	EDS
Total number of atoms	10919	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.25% 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

5.1 Standard geometry

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

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	0.74	0/1844	1.42	1/2501 (0.0%)
1	B	0.73	0/1846	1.42	1/2503 (0.0%)
1	C	0.74	0/1837	1.42	1/2496 (0.0%)
1	D	0.74	0/1803	1.41	0/2446
1	E	0.74	0/1841	1.45	2/2497 (0.1%)
1	F	0.78	0/1363	1.54	2/1855 (0.1%)
2	G	0.55	0/30	0.94	0/37
2	H	0.60	0/30	0.96	0/38
2	I	0.59	0/32	0.98	0/40
2	J	0.57	0/28	1.03	0/35
2	K	0.59	0/29	0.98	0/36
2	L	0.23	0/4	0.11	0/4
All	All	0.74	0/10687	1.44	7/14488 (0.0%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	212	ASN	CA-CB-CG	9.64	122.24	112.60
1	E	235	SER	N-CA-C	-6.81	104.61	113.12
1	B	3	ASP	CA-CB-CG	6.01	118.61	112.60
1	E	74	GLY	N-CA-C	5.44	119.40	113.58
1	A	235	SER	N-CA-C	-5.28	105.12	112.45
1	F	80	GLU	CA-C-N	5.26	127.76	120.29
1	F	80	GLU	C-N-CA	5.26	127.76	120.29

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	1811	0	1694	9	0
1	B	1818	0	1710	9	0
1	C	1804	0	1675	6	0
1	D	1777	0	1642	9	0
1	E	1814	0	1710	11	0
1	F	1354	0	1052	4	0
2	G	42	0	36	0	0
2	H	42	0	33	1	0
2	I	44	0	41	0	0
2	J	40	0	29	0	0
2	K	41	0	31	0	0
2	L	15	0	7	0	0
3	M	100	0	22	0	0
3	N	45	0	11	0	0
3	O	50	0	12	0	0
3	V	65	0	15	0	0
4	A	10	0	0	0	0
4	B	18	0	0	0	0
4	C	14	0	0	0	0
4	D	9	0	0	0	0
4	E	5	0	0	0	0
4	F	1	0	0	0	0
All	All	10919	0	9720	38	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 2.

All (38) 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:B:13:LEU:HD11	1:D:82:VAL:HG22	1.84	0.58
1:D:28:LYS:HG3	1:D:103:LEU:HD21	1.87	0.56
1:A:13:LEU:HD11	1:C:82:VAL:HG22	1.89	0.54
1:E:118:GLU:HG3	1:E:165:MET:HE3	1.90	0.53
1:A:28:LYS:HG3	1:A:103:LEU:HD21	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:96:VAL:O	1:D:100:VAL:HG23	2.10	0.52
1:B:63:ILE:HD11	1:D:17:ALA:HB2	1.92	0.52
1:B:28:LYS:HG3	1:B:103:LEU:HD21	1.92	0.52
1:E:28:LYS:HG3	1:E:103:LEU:HD21	1.93	0.51
1:C:28:LYS:HG3	1:C:103:LEU:HD21	1.91	0.51
1:E:63:ILE:HD11	1:F:17:ALA:HB2	1.93	0.51
1:B:82:VAL:HG22	1:D:13:LEU:HD11	1.92	0.50
1:E:96:VAL:O	1:E:100:VAL:HG23	2.12	0.49
1:B:17:ALA:HB2	1:D:63:ILE:HD11	1.95	0.48
1:B:118:GLU:HG2	1:B:165:MET:HE3	1.96	0.48
1:E:17:ALA:HB2	1:F:63:ILE:HD11	1.96	0.48
1:A:63:ILE:HD11	1:C:17:ALA:HB2	1.96	0.47
1:A:96:VAL:O	1:A:100:VAL:HG23	2.14	0.47
1:A:118:GLU:HG2	1:A:165:MET:HE3	1.96	0.47
1:D:165:MET:HE1	1:D:171:ILE:HB	1.97	0.47
1:E:165:MET:HE1	1:E:171:ILE:HB	1.97	0.46
1:B:165:MET:HE1	1:B:171:ILE:HB	1.98	0.46
1:A:82:VAL:HG22	1:C:13:LEU:HD11	1.98	0.46
1:D:118:GLU:HG2	1:D:165:MET:HE3	1.98	0.45
1:A:165:MET:HE1	1:A:171:ILE:HB	1.99	0.45
1:E:132:ARG:HG3	1:E:186:ILE:HG13	2.01	0.43
1:E:60:TRP:CE2	1:E:137:VAL:HG12	2.55	0.42
1:A:132:ARG:HG3	1:A:186:ILE:HG13	2.02	0.41
1:B:179:TYR:HB3	1:B:196:LEU:HD21	2.02	0.41
1:C:132:ARG:HG3	1:C:186:ILE:HG13	2.02	0.41
1:D:60:TRP:CE2	1:D:137:VAL:HG12	2.55	0.41
1:E:13:LEU:HD11	1:F:82:VAL:HG22	2.02	0.41
1:E:179:TYR:HB3	1:E:196:LEU:HD21	2.03	0.41
1:E:78:LYS:O	1:E:82:VAL:HG23	2.21	0.41
1:A:60:TRP:CE2	1:A:137:VAL:HG12	2.57	0.40
1:B:233:TRP:HE1	2:H:226:ALA:HB2	1.86	0.40
1:F:96:VAL:O	1:F:100:VAL:HG23	2.22	0.40
1:C:60:TRP:CE2	1:C:137:VAL:HG12	2.56	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	234/256 (91%)	232 (99%)	2 (1%)	0	100	100
1	B	232/256 (91%)	230 (99%)	2 (1%)	0	100	100
1	C	234/256 (91%)	231 (99%)	3 (1%)	0	100	100
1	D	233/256 (91%)	230 (99%)	3 (1%)	0	100	100
1	E	234/256 (91%)	231 (99%)	3 (1%)	0	100	100
1	F	194/256 (76%)	191 (98%)	3 (2%)	0	100	100
2	G	3/15 (20%)	3 (100%)	0	0	100	100
2	H	3/15 (20%)	3 (100%)	0	0	100	100
2	I	3/15 (20%)	3 (100%)	0	0	100	100
2	J	3/15 (20%)	3 (100%)	0	0	100	100
2	K	3/15 (20%)	3 (100%)	0	0	100	100
All	All	1376/1611 (85%)	1360 (99%)	16 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	177/225 (79%)	176 (99%)	1 (1%)	78	93
1	B	181/225 (80%)	178 (98%)	3 (2%)	53	82
1	C	176/225 (78%)	173 (98%)	3 (2%)	53	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	167/225 (74%)	164 (98%)	3 (2%)	51	80
1	E	179/225 (80%)	179 (100%)	0	100	100
1	F	86/225 (38%)	84 (98%)	2 (2%)	44	76
2	G	2/12 (17%)	2 (100%)	0	100	100
2	H	2/12 (17%)	2 (100%)	0	100	100
2	I	3/12 (25%)	3 (100%)	0	100	100
2	J	1/12 (8%)	1 (100%)	0	100	100
2	K	1/12 (8%)	1 (100%)	0	100	100
All	All	975/1410 (69%)	963 (99%)	12 (1%)	63	86

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	230	LEU
1	B	3	ASP
1	B	207	GLU
1	B	230	LEU
1	C	205	ILE
1	C	212	ASN
1	C	230	LEU
1	D	86	ARG
1	D	87	GLU
1	D	230	LEU
1	F	35	GLU
1	F	80	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	ASN
1	A	164	HIS
1	A	212	ASN
1	B	6	GLN
1	B	164	HIS
1	B	224	GLN
1	C	106	ASN
1	C	164	HIS
1	C	212	ASN

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Mol	Chain	Res	Type
1	D	29	ASN
1	D	106	ASN
1	D	164	HIS
1	D	212	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

6 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
2	SEP	K	228	2	8,9,10	0.83	0	7,12,14	1.34	1 (14%)
2	SEP	H	228	2	8,9,10	0.98	0	7,12,14	1.27	1 (14%)
2	SEP	J	228	2	8,9,10	1.02	1 (12%)	7,12,14	1.58	1 (14%)
2	SEP	L	228	2	8,9,10	1.01	0	7,12,14	2.96	1 (14%)
2	SEP	I	228	2	8,9,10	0.81	0	7,12,14	1.34	1 (14%)
2	SEP	G	228	2	8,9,10	0.96	0	7,12,14	1.18	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SEP	K	228	2	-	0/6/8/10	-
2	SEP	H	228	2	-	0/6/8/10	-
2	SEP	J	228	2	-	0/6/8/10	-
2	SEP	L	228	2	-	2/6/8/10	-
2	SEP	I	228	2	-	0/6/8/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SEP	G	228	2	-	0/6/8/10	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	228	SEP	P-OG	-2.02	1.53	1.60

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	228	SEP	OG-CB-CA	7.19	115.14	108.14
2	J	228	SEP	OG-CB-CA	2.69	110.76	108.14
2	K	228	SEP	OG-CB-CA	2.62	110.69	108.14
2	H	228	SEP	OG-CB-CA	2.50	110.58	108.14
2	I	228	SEP	OG-CB-CA	2.27	110.35	108.14

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	L	228	SEP	N-CA-CB-OG
2	L	228	SEP	C-CA-CB-OG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 57 ligands modelled in this entry, 57 are unknown - 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

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 ⓘ

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	235/256 (91%)	0.47	20 (8%) 16 14	30, 55, 100, 121	2 (0%)
1	B	234/256 (91%)	0.12	9 (3%) 44 36	30, 48, 77, 113	1 (0%)
1	C	235/256 (91%)	0.42	19 (8%) 18 15	31, 54, 93, 123	2 (0%)
1	D	235/256 (91%)	0.60	24 (10%) 12 10	36, 66, 108, 131	0
1	E	236/256 (92%)	0.69	18 (7%) 20 16	45, 68, 112, 149	0
1	F	206/256 (80%)	2.34	120 (58%) 0 0	65, 114, 156, 187	0
2	G	5/15 (33%)	1.54	1 (20%) 3 2	67, 68, 73, 75	0
2	H	5/15 (33%)	0.95	0 100 100	56, 58, 66, 71	0
2	I	5/15 (33%)	1.19	1 (20%) 3 2	57, 61, 73, 84	0
2	J	5/15 (33%)	1.57	2 (40%) 1 0	65, 69, 77, 89	0
2	K	5/15 (33%)	1.54	2 (40%) 1 0	63, 63, 73, 76	0
2	L	1/15 (6%)	3.23	1 (100%) 0 0	125, 125, 125, 125	0
3	M	0/24	-	-	-	-
3	N	0/24	-	-	-	-
3	O	0/24	-	-	-	-
3	V	0/24	-	-	-	-
All	All	1407/1722 (81%)	0.75	217 (15%) 5 4	30, 63, 128, 187	5 (0%)

All (217) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	176	ALA	7.9
1	F	135	ALA	6.5
1	D	116	GLN	6.0
1	F	115	THR	5.7
1	D	235	SER	5.7
1	F	124	LEU	5.3
1	C	235	SER	5.2

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Mol	Chain	Res	Type	RSRZ
1	F	183	TYR	5.2
1	F	215	SER	4.9
1	F	73	ASP	4.8
1	F	121	VAL	4.7
1	F	122	PHE	4.5
1	E	213	GLU	4.5
1	D	72	ALA	4.4
1	F	137	VAL	4.4
1	A	236	ASP	4.4
1	A	213	GLU	4.4
1	E	209	ASP	4.4
1	F	77	LYS	4.4
1	F	112	CYS	4.4
1	F	157	ALA	4.3
1	F	192	GLN	4.3
1	E	237	GLN	4.2
1	F	235	SER	4.2
1	F	204	ALA	4.2
1	F	119	SER	4.1
1	F	216	TYR	4.0
1	F	155	SER	4.0
1	F	180	SER	4.0
1	A	210	THR	4.0
1	F	136	GLU	4.0
1	D	71	SER	4.0
1	F	26	ALA	3.9
1	D	215	SER	3.9
1	F	131	TYR	3.9
1	F	187	GLN	3.9
1	A	205	ILE	3.9
1	F	230	LEU	3.8
1	F	161	SER	3.8
1	F	87	GLU	3.7
1	F	228	ASP	3.7
1	F	105	ASP	3.7
1	F	231	THR	3.7
1	F	171	ILE	3.7
1	F	108	LEU	3.6
1	F	203	ASP	3.6
1	F	79	ILE	3.6
1	F	125	LYS	3.6
1	B	73	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
1	F	188	ASN	3.5
1	D	213	GLU	3.5
1	F	186	ILE	3.5
1	C	213	GLU	3.5
1	F	226	LEU	3.5
1	C	210	THR	3.5
1	F	70	THR	3.5
1	F	199	THR	3.5
1	F	109	ILE	3.4
1	F	159	GLU	3.4
1	D	115	THR	3.4
1	F	101	LEU	3.4
1	F	78	LYS	3.4
1	F	100	VAL	3.4
1	F	196	LEU	3.4
1	F	177	LEU	3.3
1	E	2	VAL	3.3
1	F	174	GLY	3.3
1	F	88	LYS	3.3
1	C	1	MET	3.3
1	F	223	MET	3.3
1	C	206	ALA	3.3
1	A	212	ASN	3.3
1	F	224	GLN	3.3
1	F	3	ASP	3.2
2	G	225	THR	3.2
2	L	229	LYS	3.2
1	F	201	PHE	3.2
1	A	215	SER	3.2
1	F	2	VAL	3.2
1	D	111	ASN	3.1
1	A	211	LEU	3.1
1	C	212	ASN	3.1
1	F	172	ARG	3.1
1	D	117	TYR	3.1
1	F	202	ASP	3.1
1	F	120	LYS	3.0
1	F	71	SER	3.0
1	D	70	THR	3.0
2	K	225	THR	3.0
1	F	104	LEU	3.0
1	E	105	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	F	133	TYR	2.9
1	A	218	ASP	2.9
1	D	163	GLU	2.9
1	C	72	ALA	2.9
1	F	200	ALA	2.9
1	D	210	THR	2.9
1	F	134	LEU	2.9
1	F	221	LEU	2.9
1	F	94	GLU	2.9
1	E	9	GLN	2.9
1	F	181	VAL	2.9
1	D	216	TYR	2.9
1	F	184	TYR	2.9
1	E	214	ASP	2.9
1	E	211	LEU	2.9
1	A	70	THR	2.8
1	F	69	LYS	2.8
1	F	114	GLU	2.8
1	A	206	ALA	2.8
1	B	235	SER	2.8
1	C	71	SER	2.8
1	F	85	TYR	2.8
1	E	95	ALA	2.8
1	C	70	THR	2.8
1	D	73	ASP	2.8
1	A	71	SER	2.8
1	C	6	GLN	2.7
1	F	110	LYS	2.7
1	B	74	GLY	2.7
1	F	118	GLU	2.7
1	C	205	ILE	2.7
1	B	71	SER	2.7
1	F	222	ILE	2.7
1	A	112	CYS	2.7
1	D	191	GLU	2.7
1	F	189	ALA	2.7
1	F	132	ARG	2.7
1	A	208	LEU	2.7
1	F	234	THR	2.6
1	F	197	ALA	2.6
1	F	62	VAL	2.6
1	F	96	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	214	ASP	2.6
1	E	195	HIS	2.6
1	F	154	TYR	2.6
1	F	66	ILE	2.6
1	D	211	LEU	2.6
1	F	220	THR	2.6
2	I	225	THR	2.6
1	F	151	GLU	2.5
1	F	217	LYS	2.5
1	F	7	LEU	2.4
1	F	160	ILE	2.4
1	C	76	GLU	2.4
1	D	166	GLN	2.4
1	F	195	HIS	2.4
1	F	89	ILE	2.4
1	B	72	ALA	2.4
1	B	70	THR	2.4
1	F	31	THR	2.4
1	E	33	LEU	2.4
1	F	191	GLU	2.4
1	A	231	THR	2.4
1	F	30	VAL	2.3
2	K	229	LYS	2.3
1	C	74	GLY	2.3
1	F	218	ASP	2.3
1	C	211	LEU	2.3
1	E	210	THR	2.3
1	F	127	LYS	2.3
1	B	75	ASN	2.3
1	F	233	TRP	2.3
1	A	162	LYS	2.3
1	F	182	PHE	2.3
1	F	156	GLU	2.3
1	D	1	MET	2.3
1	D	209	ASP	2.3
1	C	117	TYR	2.3
1	F	179	TYR	2.3
1	A	51	ASN	2.3
1	A	199	THR	2.3
1	D	113	SER	2.3
1	F	49	TYR	2.3
1	F	142	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	F	59	SER	2.2
1	F	150	SER	2.2
1	F	47	VAL	2.2
1	F	219	SER	2.2
1	F	5	GLU	2.2
1	F	144	ALA	2.2
1	F	153	ALA	2.2
1	D	231	THR	2.2
1	C	193	ALA	2.2
2	J	225	THR	2.2
1	F	46	SER	2.2
1	B	204	ALA	2.2
1	E	5	GLU	2.2
1	A	172	ARG	2.1
1	C	214	ASP	2.1
1	B	208	LEU	2.1
1	F	173	LEU	2.1
1	F	149	SER	2.1
1	A	207	GLU	2.1
1	C	207	GLU	2.1
1	D	67	GLU	2.1
1	E	207	GLU	2.1
1	E	221	LEU	2.1
1	D	2	VAL	2.1
1	F	51	ASN	2.1
2	J	230	VAL	2.1
1	F	33	LEU	2.1
1	F	84	ALA	2.1
1	F	194	CYS	2.1
1	F	123	TYR	2.1
1	E	16	GLN	2.0
1	E	194	CYS	2.0
1	F	146	VAL	2.0
1	E	212	ASN	2.0
1	D	205	ILE	2.0
1	F	80	GLU	2.0
1	F	148	GLU	2.0
1	C	16	GLN	2.0
1	F	190	PRO	2.0
1	F	175	LEU	2.0
1	F	229	ASN	2.0
1	F	82	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
2	SEP	L	228	10/11	0.70	0.17	119,121,122,122	0
2	SEP	J	228	10/11	0.95	0.10	59,61,66,66	0
2	SEP	G	228	10/11	0.95	0.08	55,58,61,62	0
2	SEP	I	228	10/11	0.96	0.07	49,52,53,54	0
2	SEP	K	228	10/11	0.97	0.07	49,52,58,58	0
2	SEP	H	228	10/11	0.97	0.07	45,48,55,55	0

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
4	UNX	A	307	1/1	-0.73	1.46	30,30,30,30	1
4	UNX	D	309	1/1	-0.67	1.54	30,30,30,30	1
4	UNX	B	317	1/1	-0.62	1.15	30,30,30,30	1
4	UNX	C	301	1/1	-0.44	1.66	30,30,30,30	1
4	UNX	A	303	1/1	-0.44	1.52	30,30,30,30	1
4	UNX	D	307	1/1	-0.39	1.61	30,30,30,30	1
4	UNX	C	304	1/1	-0.29	1.76	30,30,30,30	1
4	UNX	C	313	1/1	-0.26	1.60	30,30,30,30	1
4	UNX	D	301	1/1	-0.21	1.98	30,30,30,30	1
4	UNX	E	301	1/1	-0.20	2.41	30,30,30,30	1
4	UNX	E	302	1/1	-0.19	2.55	30,30,30,30	1
4	UNX	D	303	1/1	-0.18	1.54	30,30,30,30	1
4	UNX	B	315	1/1	-0.10	2.26	30,30,30,30	1
4	UNX	E	303	1/1	-0.10	1.53	30,30,30,30	1
4	UNX	A	308	1/1	-0.08	2.35	30,30,30,30	1
4	UNX	C	305	1/1	-0.07	2.37	30,30,30,30	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	UNX	B	309	1/1	-0.05	2.48	30,30,30,30	1
4	UNX	B	314	1/1	-0.00	2.19	30,30,30,30	1
4	UNX	F	301	1/1	0.01	2.14	30,30,30,30	1
4	UNX	A	302	1/1	0.07	1.93	30,30,30,30	1
4	UNX	C	308	1/1	0.09	2.10	30,30,30,30	1
4	UNX	A	304	1/1	0.09	1.70	30,30,30,30	1
4	UNX	B	303	1/1	0.10	1.53	30,30,30,30	1
4	UNX	D	305	1/1	0.12	1.66	30,30,30,30	1
4	UNX	B	307	1/1	0.14	2.52	30,30,30,30	1
4	UNX	C	309	1/1	0.14	1.83	30,30,30,30	1
4	UNX	B	305	1/1	0.14	1.87	30,30,30,30	1
4	UNX	A	306	1/1	0.18	1.87	30,30,30,30	1
4	UNX	B	306	1/1	0.18	1.62	30,30,30,30	1
4	UNX	C	307	1/1	0.19	1.59	30,30,30,30	1
4	UNX	C	312	1/1	0.27	2.01	30,30,30,30	1
4	UNX	C	311	1/1	0.28	1.88	30,30,30,30	1
4	UNX	D	304	1/1	0.29	1.80	30,30,30,30	1
4	UNX	C	306	1/1	0.29	1.72	30,30,30,30	1
4	UNX	A	305	1/1	0.29	1.94	30,30,30,30	1
4	UNX	B	316	1/1	0.29	2.45	30,30,30,30	1
4	UNX	B	301	1/1	0.36	2.05	30,30,30,30	1
4	UNX	E	304	1/1	0.38	3.32	30,30,30,30	1
4	UNX	D	308	1/1	0.38	2.06	30,30,30,30	1
4	UNX	B	304	1/1	0.39	1.62	30,30,30,30	1
4	UNX	C	303	1/1	0.40	1.76	30,30,30,30	1
4	UNX	C	302	1/1	0.40	1.34	30,30,30,30	1
4	UNX	D	306	1/1	0.41	2.57	30,30,30,30	1
4	UNX	B	311	1/1	0.42	1.54	30,30,30,30	1
4	UNX	B	308	1/1	0.43	2.57	30,30,30,30	1
4	UNX	C	310	1/1	0.45	2.02	30,30,30,30	1
4	UNX	D	302	1/1	0.45	1.56	30,30,30,30	1
4	UNX	B	312	1/1	0.49	2.18	30,30,30,30	1
4	UNX	B	318	1/1	0.50	1.66	30,30,30,30	1
4	UNX	A	301	1/1	0.53	1.74	30,30,30,30	1
4	UNX	B	310	1/1	0.61	1.67	30,30,30,30	1
4	UNX	B	313	1/1	0.67	1.36	30,30,30,30	1
4	UNX	B	302	1/1	0.70	2.01	30,30,30,30	1
4	UNX	A	309	1/1	0.85	0.16	30,30,30,30	0
4	UNX	E	305	1/1	0.89	0.11	30,30,30,30	0
4	UNX	C	314	1/1	0.93	0.08	30,30,30,30	0
4	UNX	A	310	1/1	0.96	0.06	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.