



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 02:26 PM UTC

PDB ID : 2HLZ / pdb_00002hlz
Title : Crystal Structure of human ketohexokinase
Authors : Rabeh, W.M.; Tempel, W.; Nedyalkova, L.; Landry, R.; Arrowsmith, C.H.;
Edwards, A.M.; Sundstrom, M.; Weigelt, J.; Bochkarev, A.; Park, H.; Struc-
tural Genomics Consortium (SGC)
Deposited on : 2006-07-10
Resolution : 1.85 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 : 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

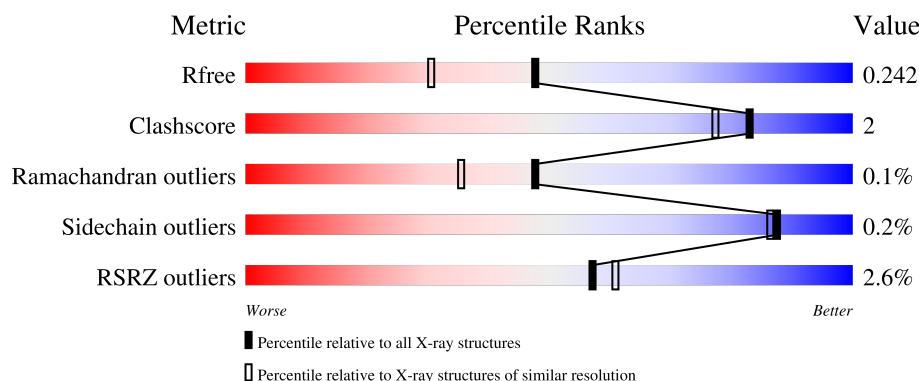
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

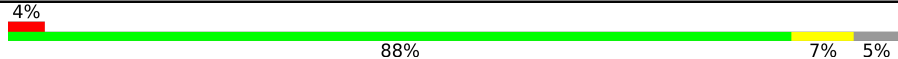
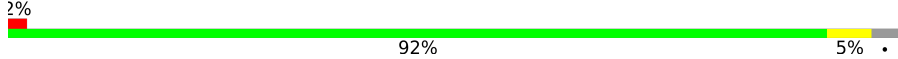
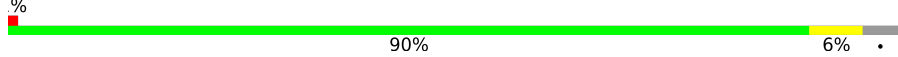
The reported resolution of this entry is 1.85 Å.

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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	312	
1	B	312	
1	C	312	
1	D	312	

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
2	UNX	A	701	-	-	-	X
2	UNX	A	707	-	-	-	X
2	UNX	A	708	-	-	-	X
2	UNX	A	712	-	-	-	X
2	UNX	A	713	-	-	-	X
2	UNX	A	715	-	-	-	X
2	UNX	A	726	-	-	-	X
2	UNX	A	732	-	-	-	X
2	UNX	B	702	-	-	-	X
2	UNX	B	705	-	-	-	X
2	UNX	B	706	-	-	-	X
2	UNX	B	710	-	-	-	X
2	UNX	B	711	-	-	-	X
2	UNX	B	718	-	-	-	X
2	UNX	B	721	-	-	-	X
2	UNX	B	731	-	-	-	X
2	UNX	C	703	-	-	-	X
2	UNX	C	716	-	-	-	X
2	UNX	C	722	-	-	-	X
2	UNX	C	723	-	-	-	X
2	UNX	C	724	-	-	-	X
2	UNX	C	725	-	-	-	X
2	UNX	C	729	-	-	-	X
2	UNX	C	730	-	-	-	X
2	UNX	D	704	-	-	-	X
2	UNX	D	709	-	-	-	X
2	UNX	D	714	-	-	-	X
2	UNX	D	717	-	-	-	X
2	UNX	D	719	-	-	-	X
2	UNX	D	720	-	-	-	X
2	UNX	D	727	-	-	-	X
2	UNX	D	728	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9449 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 Ketohexokinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	S	Se	0	1	0
			2229	1418	383	418	7	3			
1	B	296	Total	C	N	O	S	Se	0	2	0
			2238	1421	383	424	7	3			
1	C	302	Total	C	N	O	S	Se	0	1	0
			2284	1450	397	427	7	3			
1	D	301	Total	C	N	O	S	Se	0	3	0
			2294	1457	397	430	7	3			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	GLY	-	cloning artifact	UNP P50053
A	-12	SER	-	cloning artifact	UNP P50053
A	-11	SER	-	cloning artifact	UNP P50053
A	-10	HIS	-	expression tag	UNP P50053
A	-9	HIS	-	expression tag	UNP P50053
A	-8	HIS	-	expression tag	UNP P50053
A	-7	HIS	-	expression tag	UNP P50053
A	-6	HIS	-	expression tag	UNP P50053
A	-5	HIS	-	expression tag	UNP P50053
A	-4	SER	-	cloning artifact	UNP P50053
A	-3	SER	-	cloning artifact	UNP P50053
A	-2	GLY	-	cloning artifact	UNP P50053
A	-1	LEU	-	cloning artifact	UNP P50053
A	0	VAL	-	cloning artifact	UNP P50053
A	1	PRO	-	cloning artifact	UNP P50053
A	2	ARG	-	cloning artifact	UNP P50053
A	3	GLY	-	cloning artifact	UNP P50053
A	4	SER	-	cloning artifact	UNP P50053
A	49	ILE	VAL	conflict	UNP P50053
A	60	MSE	MET	modified residue	UNP P50053
A	63	MSE	MET	modified residue	UNP P50053

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Chain	Residue	Modelled	Actual	Comment	Reference
A	149	MSE	MET	modified residue	UNP P50053
B	-13	GLY	-	cloning artifact	UNP P50053
B	-12	SER	-	cloning artifact	UNP P50053
B	-11	SER	-	cloning artifact	UNP P50053
B	-10	HIS	-	expression tag	UNP P50053
B	-9	HIS	-	expression tag	UNP P50053
B	-8	HIS	-	expression tag	UNP P50053
B	-7	HIS	-	expression tag	UNP P50053
B	-6	HIS	-	expression tag	UNP P50053
B	-5	HIS	-	expression tag	UNP P50053
B	-4	SER	-	cloning artifact	UNP P50053
B	-3	SER	-	cloning artifact	UNP P50053
B	-2	GLY	-	cloning artifact	UNP P50053
B	-1	LEU	-	cloning artifact	UNP P50053
B	0	VAL	-	cloning artifact	UNP P50053
B	1	PRO	-	cloning artifact	UNP P50053
B	2	ARG	-	cloning artifact	UNP P50053
B	3	GLY	-	cloning artifact	UNP P50053
B	4	SER	-	cloning artifact	UNP P50053
B	49	ILE	VAL	conflict	UNP P50053
B	60	MSE	MET	modified residue	UNP P50053
B	63	MSE	MET	modified residue	UNP P50053
B	149	MSE	MET	modified residue	UNP P50053
C	-13	GLY	-	cloning artifact	UNP P50053
C	-12	SER	-	cloning artifact	UNP P50053
C	-11	SER	-	cloning artifact	UNP P50053
C	-10	HIS	-	expression tag	UNP P50053
C	-9	HIS	-	expression tag	UNP P50053
C	-8	HIS	-	expression tag	UNP P50053
C	-7	HIS	-	expression tag	UNP P50053
C	-6	HIS	-	expression tag	UNP P50053
C	-5	HIS	-	expression tag	UNP P50053
C	-4	SER	-	cloning artifact	UNP P50053
C	-3	SER	-	cloning artifact	UNP P50053
C	-2	GLY	-	cloning artifact	UNP P50053
C	-1	LEU	-	cloning artifact	UNP P50053
C	0	VAL	-	cloning artifact	UNP P50053
C	1	PRO	-	cloning artifact	UNP P50053
C	2	ARG	-	cloning artifact	UNP P50053
C	3	GLY	-	cloning artifact	UNP P50053
C	4	SER	-	cloning artifact	UNP P50053
C	49	ILE	VAL	conflict	UNP P50053

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Chain	Residue	Modelled	Actual	Comment	Reference
C	60	MSE	MET	modified residue	UNP P50053
C	63	MSE	MET	modified residue	UNP P50053
C	149	MSE	MET	modified residue	UNP P50053
D	-13	GLY	-	cloning artifact	UNP P50053
D	-12	SER	-	cloning artifact	UNP P50053
D	-11	SER	-	cloning artifact	UNP P50053
D	-10	HIS	-	expression tag	UNP P50053
D	-9	HIS	-	expression tag	UNP P50053
D	-8	HIS	-	expression tag	UNP P50053
D	-7	HIS	-	expression tag	UNP P50053
D	-6	HIS	-	expression tag	UNP P50053
D	-5	HIS	-	expression tag	UNP P50053
D	-4	SER	-	cloning artifact	UNP P50053
D	-3	SER	-	cloning artifact	UNP P50053
D	-2	GLY	-	cloning artifact	UNP P50053
D	-1	LEU	-	cloning artifact	UNP P50053
D	0	VAL	-	cloning artifact	UNP P50053
D	1	PRO	-	cloning artifact	UNP P50053
D	2	ARG	-	cloning artifact	UNP P50053
D	3	GLY	-	cloning artifact	UNP P50053
D	4	SER	-	cloning artifact	UNP P50053
D	49	ILE	VAL	conflict	UNP P50053
D	60	MSE	MET	modified residue	UNP P50053
D	63	MSE	MET	modified residue	UNP P50053
D	149	MSE	MET	modified residue	UNP P50053

- Molecule 2 is UNKNOWN ATOM OR ION (CCD ID: UNX) (formula: X).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	8	Total X 8 8	0	0
2	B	8	Total X 8 8	0	0
2	C	8	Total X 8 8	0	0
2	D	8	Total X 8 8	0	0

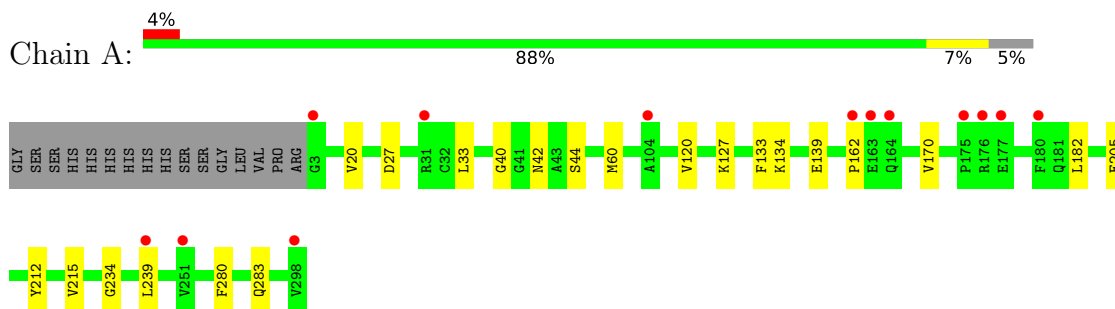
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	67	Total 67	O 67	0	0
3	B	86	Total 86	O 86	0	0
3	C	105	Total 105	O 105	0	0
3	D	114	Total 114	O 114	0	0

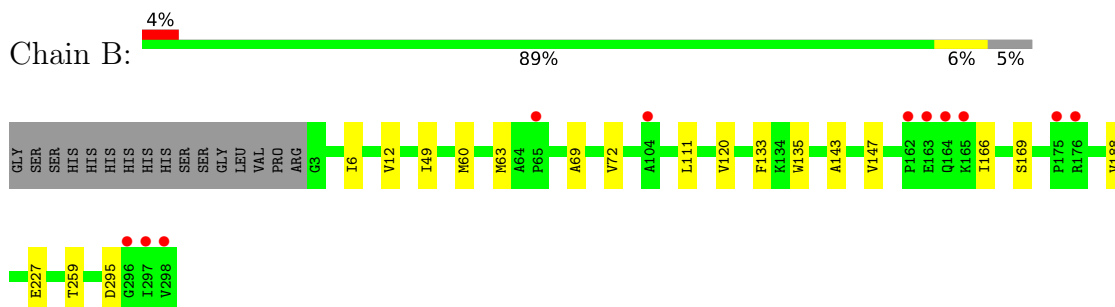
3 Residue-property plots [i](#)

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.

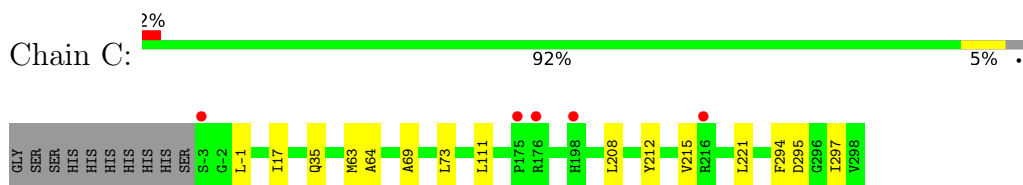
- Molecule 1: Ketohexokinase



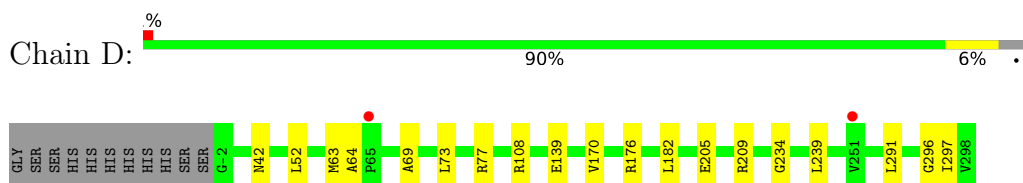
- Molecule 1: Ketohexokinase



- Molecule 1: Ketohexokinase



- Molecule 1: Ketohexokinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	66.93Å 71.67Å 82.69Å 105.06° 107.33° 93.09°	Depositor
Resolution (Å)	29.66 – 1.85 29.66 – 1.85	Depositor EDS
% Data completeness (in resolution range)	94.6 (29.66-1.85) 94.5 (29.66-1.85)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.29 (at 1.85Å)	Xtriage
Refinement program	REFMAC refmac_5.2.0019	Depositor
R, R_{free}	0.214 , 0.249 (Not available) , 0.242	Depositor DCC
R_{free} test set	4258 reflections (3.56%)	wwPDB-VP
Wilson B-factor (Å ²)	18.8	Xtriage
Anisotropy	0.003	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 40.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9449	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.55% 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: 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	0.93	0/2270	0.89	3/3071 (0.1%)
1	B	0.96	0/2283	0.92	1/3091 (0.0%)
1	C	0.99	0/2329	0.87	1/3153 (0.0%)
1	D	0.99	0/2345	0.92	2/3175 (0.1%)
All	All	0.97	0/9227	0.90	7/12490 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	234	GLY	CA-C-N	6.77	126.73	119.28
1	D	234	GLY	C-N-CA	6.77	126.73	119.28
1	B	295	ASP	N-CA-C	5.97	117.79	111.28
1	C	295	ASP	N-CA-C	5.87	117.35	111.07
1	A	234	GLY	CA-C-N	5.17	124.97	119.28
1	A	234	GLY	C-N-CA	5.17	124.97	119.28
1	A	133	PHE	N-CA-C	5.04	117.66	109.24

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	2229	0	2204	11	0
1	B	2238	0	2197	14	0
1	C	2284	0	2250	9	0
1	D	2294	0	2265	11	0
2	A	8	0	0	0	0
2	B	8	0	0	0	0
2	C	8	0	0	0	0
2	D	8	0	0	0	0
3	A	67	0	0	0	0
3	B	86	0	0	0	0
3	C	105	0	0	0	0
3	D	114	0	0	0	0
All	All	9449	0	8916	43	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 (43) 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:60:MSE:HE2	1:B:120:VAL:HG11	1.60	0.83
1:A:205:GLU:HG3	1:A:239:LEU:HD21	1.69	0.73
1:D:205:GLU:HG3	1:D:239:LEU:HD13	1.74	0.69
1:B:60:MSE:HE2	1:B:120:VAL:CG1	2.22	0.68
1:B:12:VAL:HG21	1:B:72[B]:VAL:HG11	1.83	0.60
1:B:227[A]:GLU:H	1:B:227[A]:GLU:CD	2.09	0.60
1:C:64:ALA:O	1:C:69:ALA:HB2	2.02	0.60
1:B:12:VAL:HG21	1:B:72[B]:VAL:CG1	2.35	0.56
1:D:170[A]:VAL:HG11	1:D:182:LEU:HB3	1.87	0.56
1:C:294:PHE:O	1:C:297:ILE:HG23	2.06	0.56
1:A:127:LYS:HB2	1:C:-1:LEU:HD23	1.88	0.56
1:A:42:ASN:HB2	1:A:139:GLU:CD	2.32	0.54
1:A:20:VAL:HA	1:A:33[B]:LEU:HD13	1.91	0.53
1:A:212:TYR:O	1:A:215:VAL:HG22	2.09	0.53
1:C:212:TYR:O	1:C:215:VAL:HG22	2.09	0.51
1:A:60:MSE:HE2	1:A:120:VAL:CG1	2.43	0.49
1:B:69:ALA:HA	1:B:72[A]:VAL:HG22	1.95	0.48
1:B:111:LEU:HD12	1:B:111:LEU:N	2.29	0.47
1:A:280:PHE:HA	1:A:283:GLN:HE21	1.81	0.46
1:D:42:ASN:HB2	1:D:139:GLU:CD	2.41	0.46
1:A:60:MSE:HE2	1:A:120:VAL:HG11	1.98	0.45
1:C:111:LEU:HD12	1:C:111:LEU:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:ASP:HA	1:D:108:ARG:O	2.16	0.45
1:B:63:MSE:HE1	1:B:72[B]:VAL:HG12	1.99	0.45
1:D:73:LEU:O	1:D:77:ARG:HG3	2.17	0.44
1:D:64:ALA:O	1:D:69:ALA:HB2	2.17	0.44
1:A:170:VAL:HG11	1:A:182:LEU:HB3	2.00	0.44
1:C:63:MSE:HE3	1:C:73:LEU:CD2	2.48	0.44
1:D:63:MSE:HE3	1:D:73:LEU:HD21	1.99	0.43
1:D:205:GLU:HG3	1:D:239:LEU:CD1	2.44	0.43
1:C:63:MSE:HE3	1:C:73:LEU:HD21	2.00	0.43
1:D:209:ARG:NH2	1:D:239:LEU:HD12	2.34	0.43
1:B:133:PHE:O	1:B:166:ILE:HG12	2.19	0.42
1:D:291:LEU:HD13	1:D:296:GLY:HA3	2.02	0.42
1:C:17:ILE:O	1:C:35:GLN:HA	2.20	0.42
1:C:208:LEU:HD23	1:C:221:LEU:HG	2.02	0.41
1:B:143:ALA:O	1:B:147:VAL:HG23	2.21	0.41
1:D:52:LEU:HD13	1:D:297:ILE:HG12	2.02	0.41
1:B:6:ILE:HG12	1:B:135:TRP:HB3	2.03	0.41
1:A:40:GLY:O	1:A:44:SER:HB3	2.21	0.40
1:B:49:ILE:HG13	1:B:259:THR:HA	2.04	0.40
1:B:169:SER:HA	1:B:188:VAL:O	2.20	0.40

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	295/312 (95%)	291 (99%)	3 (1%)	1 (0%)	36	25
1	B	296/312 (95%)	289 (98%)	7 (2%)	0	100	100
1	C	301/312 (96%)	299 (99%)	2 (1%)	0	100	100
1	D	302/312 (97%)	298 (99%)	4 (1%)	0	100	100
All	All	1194/1248 (96%)	1177 (99%)	16 (1%)	1 (0%)	48	35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	PRO

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	232/257 (90%)	231 (100%)	1 (0%)	84	82
1	B	234/257 (91%)	234 (100%)	0	100	100
1	C	239/257 (93%)	239 (100%)	0	100	100
1	D	242/257 (94%)	241 (100%)	1 (0%)	84	82
All	All	947/1028 (92%)	945 (100%)	2 (0%)	87	86

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	134	LYS
1	D	176	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	160	GLN
1	A	283	GLN
1	B	261	ASN
1	C	164	GLN
1	D	38	GLN
1	D	275	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 32 ligands modelled in this entry, 32 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 [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	293/312 (93%)	0.33	13 (4%)	39 42	11, 20, 34, 47	1 (0%)
1	B	293/312 (93%)	0.10	11 (3%)	44 48	9, 17, 30, 44	2 (0%)
1	C	299/312 (95%)	0.07	5 (1%)	69 73	10, 17, 31, 38	1 (0%)
1	D	298/312 (95%)	0.00	2 (0%)	84 87	8, 17, 28, 36	3 (1%)
All	All	1183/1248 (94%)	0.12	31 (2%)	57 61	8, 18, 31, 47	7 (0%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	163	GLU	4.4
1	C	175	PRO	4.1
1	A	162	PRO	4.1
1	C	-3	SER	3.6
1	A	177	GLU	3.4
1	B	65	PRO	3.1
1	A	163	GLU	3.1
1	C	176	ARG	3.0
1	B	164	GLN	3.0
1	A	298	VAL	2.9
1	B	298	VAL	2.8
1	A	175	PRO	2.8
1	A	180	PHE	2.7
1	A	239	LEU	2.7
1	B	176	ARG	2.5
1	B	162	PRO	2.5
1	B	296	GLY	2.4
1	B	165	LYS	2.4
1	C	216	ARG	2.3
1	A	164	GLN	2.2
1	D	65	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	31	ARG	2.2
1	B	104	ALA	2.2
1	A	104	ALA	2.1
1	A	176	ARG	2.1
1	C	198	HIS	2.1
1	B	297	ILE	2.1
1	A	3	GLY	2.1
1	B	175	PRO	2.1
1	D	251	VAL	2.0
1	A	251	VAL	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
2	UNX	D	727	1/1	-0.55	1.15	2,2,2,2	1
2	UNX	C	722	1/1	-0.45	1.19	2,2,2,2	1
2	UNX	D	720	1/1	-0.26	1.25	2,2,2,2	1
2	UNX	A	707	1/1	-0.18	1.50	2,2,2,2	1
2	UNX	A	715	1/1	-0.15	1.22	2,2,2,2	1
2	UNX	B	718	1/1	-0.07	1.18	2,2,2,2	1
2	UNX	D	704	1/1	-0.02	1.12	2,2,2,2	1
2	UNX	B	731	1/1	0.01	1.33	2,2,2,2	1
2	UNX	A	732	1/1	0.04	1.30	2,2,2,2	1
2	UNX	D	714	1/1	0.07	1.27	2,2,2,2	1
2	UNX	C	703	1/1	0.09	1.23	2,2,2,2	1
2	UNX	A	712	1/1	0.09	1.50	2,2,2,2	1
2	UNX	B	721	1/1	0.16	1.31	2,2,2,2	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	UNX	C	730	1/1	0.19	2.13	2,2,2,2	1
2	UNX	A	726	1/1	0.22	1.47	2,2,2,2	1
2	UNX	C	724	1/1	0.23	1.62	2,2,2,2	1
2	UNX	B	706	1/1	0.23	1.32	2,2,2,2	1
2	UNX	C	725	1/1	0.24	1.32	2,2,2,2	1
2	UNX	C	723	1/1	0.25	1.41	2,2,2,2	1
2	UNX	C	716	1/1	0.26	1.20	2,2,2,2	1
2	UNX	A	713	1/1	0.28	1.44	2,2,2,2	1
2	UNX	A	701	1/1	0.31	1.44	2,2,2,2	1
2	UNX	A	708	1/1	0.35	1.39	2,2,2,2	1
2	UNX	B	710	1/1	0.35	1.29	2,2,2,2	1
2	UNX	D	717	1/1	0.39	1.54	2,2,2,2	1
2	UNX	C	729	1/1	0.41	1.23	2,2,2,2	1
2	UNX	D	709	1/1	0.45	1.29	2,2,2,2	1
2	UNX	D	728	1/1	0.46	1.59	2,2,2,2	1
2	UNX	B	705	1/1	0.52	1.42	4,4,4,4	1
2	UNX	B	711	1/1	0.52	1.42	2,2,2,2	1
2	UNX	B	702	1/1	0.53	1.64	2,2,2,2	1
2	UNX	D	719	1/1	0.74	1.52	2,2,2,2	1

6.5 Other polymers [i](#)

There are no such residues in this entry.