



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:22 PM GMT

PDB ID : 1FBA
Title : THE CRYSTAL STRUCTURE OF FRUCTOSE-1,6-BISPHOSPHATE ALDOLASE FROM DROSOPHILA MELANOGASTER AT 2.5 ANGSTROMS RESOLUTION
Authors : Piontek, K.; Hester, G.; Brenner-Holzach, O.
Deposited on : 1992-06-08
Resolution : 1.90 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

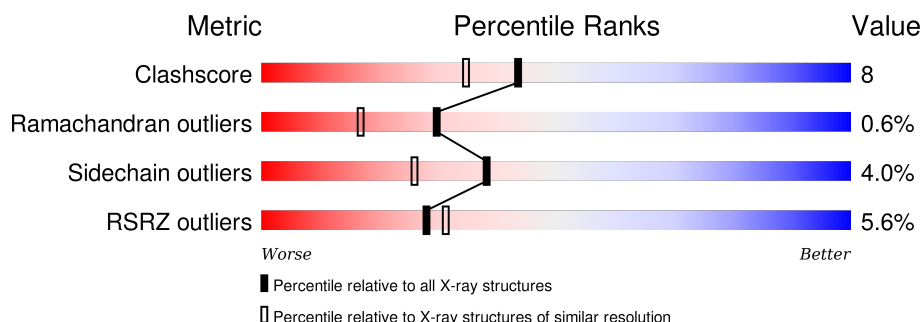
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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))
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	361	<div> <div>4%</div> <div>85%</div> <div>14%</div> <div>.</div> </div>
1	B	361	<div> <div>4%</div> <div>87%</div> <div>12%</div> <div>..</div> </div>
1	C	361	<div> <div>9%</div> <div>79%</div> <div>19%</div> <div>..</div> </div>
1	D	361	<div> <div>5%</div> <div>85%</div> <div>12%</div> <div>..</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12796 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 FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	361	Total	C	N	O	S	0	0	0
			2745	1728	480	531	6			
1	B	361	Total	C	N	O	S	0	0	0
			2745	1728	480	531	6			
1	C	361	Total	C	N	O	S	0	0	0
			2745	1728	480	531	6			
1	D	361	Total	C	N	O	S	0	0	0
			2745	1728	480	531	6			

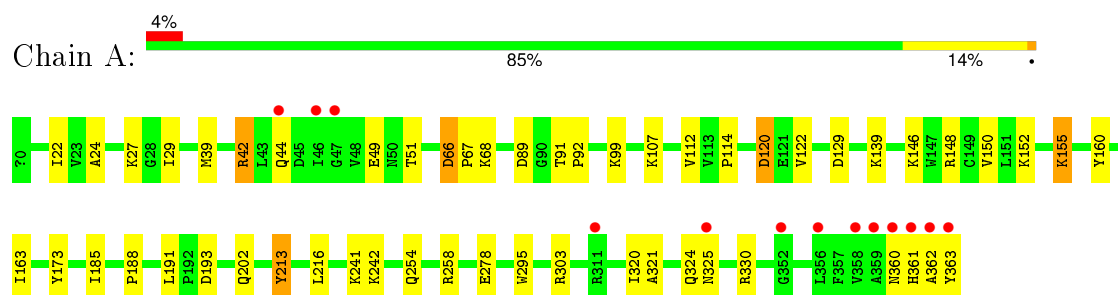
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	456	Total	O	0	0
			456	456		
2	B	477	Total	O	0	0
			477	477		
2	C	404	Total	O	0	0
			404	404		
2	D	479	Total	O	0	0
			479	479		

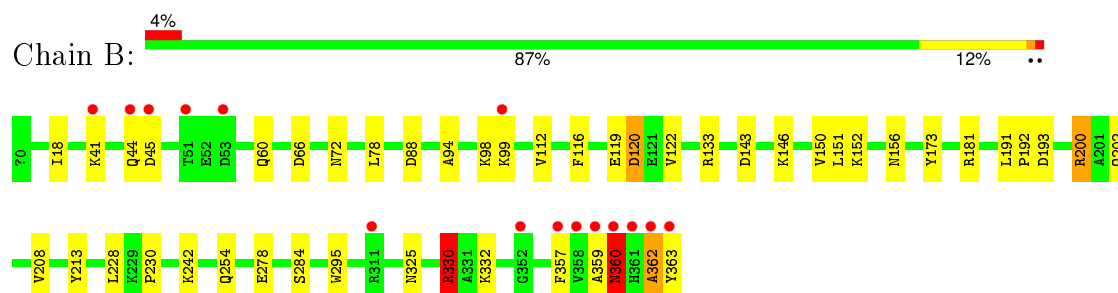
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

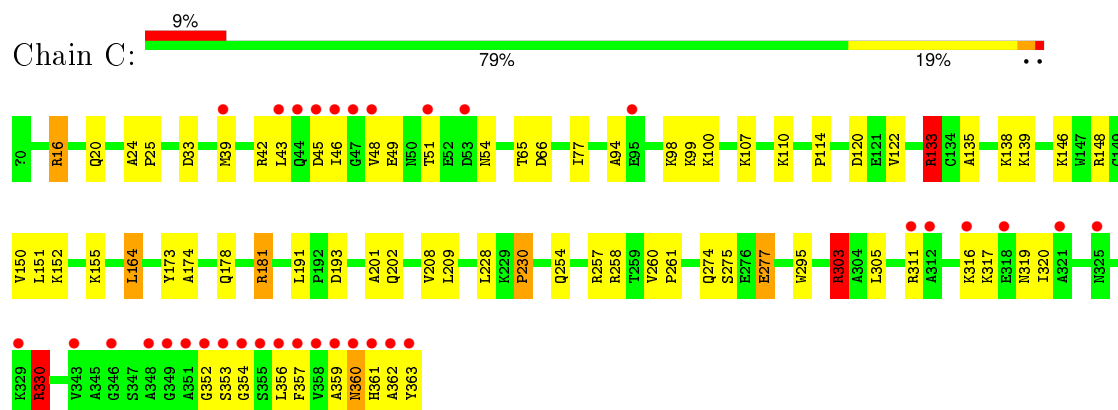
• Molecule 1: FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE



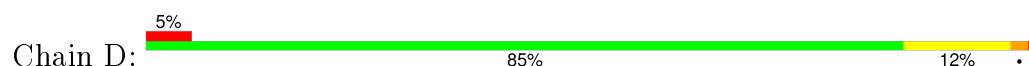
• Molecule 1: FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE

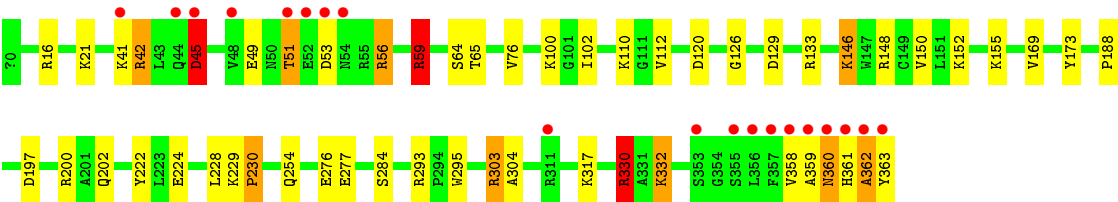


• Molecule 1: FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE



• Molecule 1: FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	86.60Å 116.80Å 151.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 1.90 7.99 – 1.96	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-1.90) 95.4 (7.99-1.96)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.72 (at 1.97Å)	Xtriage
Refinement program	PROLSQ, X-PLOR	Depositor
R, R_{free}	0.179 , (Not available) 0.162 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	15.2	Xtriage
Anisotropy	0.661	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 72.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 103410 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12796	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 3.96% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ACE

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	0.79	0/2789	1.11	11/3779 (0.3%)
1	B	0.80	0/2789	1.10	8/3779 (0.2%)
1	C	0.76	0/2789	1.18	18/3779 (0.5%)
1	D	0.79	0/2789	1.15	12/3779 (0.3%)
All	All	0.78	0/11156	1.14	49/15116 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
1	D	0	3
All	All	0	5

There are no bond length outliers.

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	16	ARG	NE-CZ-NH1	12.18	126.39	120.30
1	C	330	ARG	NE-CZ-NH1	11.86	126.23	120.30
1	D	16	ARG	CD-NE-CZ	11.45	139.63	123.60
1	C	133	ARG	NE-CZ-NH1	10.76	125.68	120.30
1	C	16	ARG	NE-CZ-NH1	10.09	125.34	120.30
1	B	200	ARG	NE-CZ-NH1	9.15	124.87	120.30
1	C	133	ARG	NE-CZ-NH2	-9.01	115.80	120.30
1	C	16	ARG	NE-CZ-NH2	-8.95	115.82	120.30
1	C	133	ARG	CD-NE-CZ	8.54	135.55	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	330	ARG	CD-NE-CZ	8.37	135.32	123.60
1	D	59	ARG	NE-CZ-NH1	8.27	124.44	120.30
1	A	66	ASP	CB-CG-OD1	7.87	125.39	118.30
1	C	181	ARG	NE-CZ-NH1	7.61	124.11	120.30
1	A	330	ARG	NE-CZ-NH1	7.37	123.99	120.30
1	B	66	ASP	CB-CG-OD1	7.37	124.93	118.30
1	C	303	ARG	NE-CZ-NH1	6.94	123.77	120.30
1	B	330	ARG	NE-CZ-NH1	6.71	123.66	120.30
1	A	258	ARG	NE-CZ-NH1	6.48	123.54	120.30
1	C	330	ARG	NE-CZ-NH2	-6.40	117.10	120.30
1	C	257	ARG	NE-CZ-NH1	6.34	123.47	120.30
1	D	303	ARG	NE-CZ-NH1	6.28	123.44	120.30
1	A	303	ARG	NE-CZ-NH1	-6.25	117.18	120.30
1	B	200	ARG	NE-CZ-NH2	-6.25	117.18	120.30
1	D	16	ARG	NE-CZ-NH2	-6.21	117.20	120.30
1	A	330	ARG	CD-NE-CZ	6.18	132.25	123.60
1	D	42	ARG	NE-CZ-NH1	6.16	123.38	120.30
1	D	59	ARG	CD-NE-CZ	6.14	132.20	123.60
1	A	129	ASP	CB-CG-OD1	6.13	123.82	118.30
1	B	330	ARG	CG-CD-NE	5.95	124.29	111.80
1	C	277	GLU	CA-CB-CG	5.89	126.37	113.40
1	D	129	ASP	CB-CG-OD1	5.76	123.49	118.30
1	A	330	ARG	CG-CD-NE	5.61	123.58	111.80
1	C	120	ASP	CB-CG-OD1	5.55	123.29	118.30
1	C	133	ARG	CG-CD-NE	5.54	123.44	111.80
1	C	303	ARG	CD-NE-CZ	5.52	131.32	123.60
1	A	42	ARG	NE-CZ-NH2	-5.48	117.56	120.30
1	B	45	ASP	CB-CG-OD1	5.48	123.23	118.30
1	D	330	ARG	CG-CD-NE	5.47	123.29	111.80
1	A	213	TYR	CA-CB-CG	-5.34	103.25	113.40
1	D	197	ASP	CB-CG-OD1	5.33	123.10	118.30
1	D	45	ASP	CB-CG-OD1	5.27	123.04	118.30
1	C	258	ARG	NE-CZ-NH1	5.19	122.90	120.30
1	B	181	ARG	NE-CZ-NH1	5.13	122.86	120.30
1	C	181	ARG	NE-CZ-NH2	-5.07	117.77	120.30
1	D	42	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	A	120	ASP	CB-CG-OD2	-5.04	113.76	118.30
1	C	66	ASP	CB-CG-OD1	5.04	122.83	118.30
1	B	213	TYR	CA-CB-CG	-5.01	103.88	113.40
1	A	89	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	42	ARG	Sidechain
1	C	133	ARG	Sidechain
1	D	293	ARG	Sidechain
1	D	330	ARG	Sidechain
1	D	56	ARG	Sidechain

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	2745	0	2769	39	0
1	B	2745	0	2769	36	0
1	C	2745	0	2769	59	0
1	D	2745	0	2769	46	0
2	A	456	0	0	10	0
2	B	477	0	0	7	0
2	C	404	0	0	9	0
2	D	479	0	0	13	0
All	All	12796	0	11076	179	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 8.

All (179) 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:122:VAL:HG21	1:B:362:ALA:HB1	1.37	1.02
1:B:330:ARG:HD2	2:B:615:HOH:O	1.64	0.98
1:D:359:ALA:O	1:D:360:ASN:HB2	1.69	0.92
1:A:325:ASN:HB3	2:A:550:HOH:O	1.68	0.92
1:C:152:LYS:HE2	1:C:362:ALA:HB3	1.55	0.88
1:C:359:ALA:O	1:C:360:ASN:HB2	1.75	0.87
1:D:152:LYS:HE2	1:D:362:ALA:HB3	1.61	0.82
1:B:112:VAL:HG21	1:B:362:ALA:HA	1.62	0.82
1:A:152:LYS:NZ	1:A:362:ALA:HB3	1.95	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:191:LEU:HD22	1:C:361:HIS:CD2	2.16	0.81
1:D:148:ARG:HH22	1:D:361:HIS:CG	1.97	0.81
1:A:160:TYR:HA	2:A:708:HOH:O	1.79	0.81
1:B:94:ALA:O	1:B:98:LYS:HG2	1.80	0.80
1:A:114:PRO:HB3	1:A:363:TYR:CE1	2.19	0.78
1:C:164:LEU:C	1:C:164:LEU:HD23	2.04	0.78
1:D:362:ALA:O	1:D:363:TYR:HB2	1.84	0.77
1:B:122:VAL:CG2	1:B:362:ALA:HB1	2.13	0.76
1:D:112:VAL:HG21	1:D:362:ALA:HA	1.67	0.75
1:A:241:LYS:HE3	2:A:690:HOH:O	1.85	0.75
1:A:152:LYS:HZ3	1:A:362:ALA:HB3	1.51	0.74
1:C:46:ILE:HG13	1:C:48:VAL:HG23	1.69	0.73
1:B:152:LYS:NZ	1:B:362:ALA:O	2.22	0.73
1:C:191:LEU:HD13	1:C:361:HIS:HD2	1.55	0.72
1:B:120:ASP:OD2	1:B:363:TYR:CD2	2.43	0.71
1:B:120:ASP:OD2	1:B:363:TYR:HD2	1.74	0.70
1:D:330:ARG:HD2	2:D:604:HOH:O	1.89	0.70
1:C:146:LYS:HE2	2:C:1050:HOH:O	1.93	0.69
1:C:362:ALA:O	1:C:363:TYR:HB2	1.92	0.69
1:D:148:ARG:NH2	1:D:361:HIS:ND1	2.40	0.69
1:C:191:LEU:HD13	1:C:361:HIS:CD2	2.29	0.68
1:C:152:LYS:CE	1:C:362:ALA:HB3	2.24	0.67
1:C:51:THR:HG23	1:C:54:ASN:H	1.60	0.66
1:A:185:ILE:HD13	2:A:793:HOH:O	1.94	0.66
1:C:303:ARG:HH11	1:C:303:ARG:HB3	1.60	0.66
1:B:44:GLN:HB2	2:B:722:HOH:O	1.96	0.65
1:A:362:ALA:O	1:A:363:TYR:CD2	2.51	0.64
1:B:150:VAL:HG11	1:B:362:ALA:CB	2.28	0.63
1:D:152:LYS:HZ1	1:D:363:TYR:HD1	1.46	0.63
1:C:191:LEU:HD22	1:C:361:HIS:CG	2.34	0.62
1:A:362:ALA:O	1:A:363:TYR:HD2	1.82	0.62
1:D:21:LYS:HG3	2:D:459:HOH:O	1.99	0.62
1:B:228:LEU:HG	1:B:230:PRO:HD3	1.81	0.62
1:A:148:ARG:NH2	1:A:361:HIS:ND1	2.47	0.62
1:A:163:ILE:HB	2:A:708:HOH:O	1.99	0.62
1:C:317:LYS:HD2	1:C:320:ILE:HD11	1.82	0.61
1:D:228:LEU:HG	1:D:230:PRO:HD3	1.83	0.61
1:A:362:ALA:O	1:A:363:TYR:HB2	2.01	0.60
1:C:114:PRO:HB3	1:C:363:TYR:CE2	2.37	0.60
1:A:152:LYS:CE	1:A:362:ALA:HB3	2.32	0.59
1:B:242:LYS:HE2	1:B:278:GLU:OE2	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:ARG:HH22	1:A:361:HIS:CG	2.21	0.58
1:C:316:LYS:HE2	2:C:1273:HOH:O	2.03	0.58
1:D:152:LYS:HE2	1:D:362:ALA:CB	2.32	0.58
1:D:155:LYS:HE2	2:D:401:HOH:O	2.04	0.57
1:C:98:LYS:HE2	2:C:1205:HOH:O	2.04	0.57
1:B:146:LYS:HG2	2:B:538:HOH:O	2.05	0.57
1:C:164:LEU:C	1:C:164:LEU:CD2	2.74	0.56
1:C:150:VAL:CG1	1:C:362:ALA:HB2	2.35	0.56
1:B:357:PHE:CE2	1:B:359:ALA:HB2	2.39	0.56
1:A:99:LYS:HB3	2:A:592:HOH:O	2.05	0.56
1:D:110:LYS:HD2	1:D:126:GLY:HA2	1.88	0.56
1:D:41:LYS:O	1:D:45:ASP:OD1	2.25	0.55
1:B:150:VAL:HG11	1:B:362:ALA:HB3	1.86	0.55
1:D:229:LYS:HD2	2:D:425:HOH:O	2.07	0.55
1:D:146:LYS:HE3	2:D:697:HOH:O	2.07	0.54
1:D:361:HIS:HD2	2:D:584:HOH:O	1.89	0.54
1:C:361:HIS:CE1	2:C:1134:HOH:O	2.61	0.54
1:D:65:THR:O	1:D:100:LYS:NZ	2.39	0.53
1:A:362:ALA:O	1:A:363:TYR:CB	2.56	0.53
1:D:42:ARG:HA	1:D:45:ASP:OD1	2.09	0.53
1:C:274:GLN:O	1:C:356:LEU:HD12	2.09	0.53
1:C:33:ASP:HB3	1:C:77:ILE:HG22	1.90	0.53
1:B:357:PHE:CZ	1:B:359:ALA:HB2	2.43	0.52
1:C:94:ALA:O	1:C:98:LYS:HG3	2.09	0.52
1:B:41:LYS:HD2	2:B:712:HOH:O	2.09	0.52
1:A:150:VAL:CG1	1:A:191:LEU:HD11	2.40	0.52
1:C:148:ARG:HH22	1:C:361:HIS:HB3	1.74	0.52
1:C:122:VAL:HG13	1:C:363:TYR:CE1	2.45	0.51
1:C:303:ARG:HH11	1:C:303:ARG:CB	2.22	0.51
1:D:152:LYS:HB3	2:D:428:HOH:O	2.09	0.51
1:A:152:LYS:HE2	1:A:362:ALA:HB3	1.92	0.51
1:B:18:ILE:HD13	1:B:143:ASP:HB3	1.92	0.51
1:C:228:LEU:HG	1:C:230:PRO:HD3	1.92	0.51
1:D:112:VAL:CG2	1:D:363:TYR:H	2.24	0.51
1:B:150:VAL:CG1	1:B:362:ALA:CB	2.89	0.51
1:B:202:GLN:HE22	1:B:254:GLN:HE21	1.59	0.50
1:C:202:GLN:HE22	1:C:254:GLN:HE21	1.58	0.50
1:A:242:LYS:HE3	1:A:278:GLU:OE2	2.11	0.50
1:D:49:GLU:HG2	1:D:51:THR:HG22	1.91	0.50
1:C:201:ALA:HB1	2:C:1303:HOH:O	2.11	0.50
1:D:150:VAL:CG1	1:D:362:ALA:HB2	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:PHE:HB2	2:B:373:HOH:O	2.12	0.50
1:D:41:LYS:NZ	1:D:358:VAL:HG21	2.27	0.49
1:A:321:ALA:O	1:A:325:ASN:ND2	2.31	0.49
1:D:49:GLU:HG3	2:D:648:HOH:O	2.12	0.49
1:A:49:GLU:HG2	1:A:51:THR:HG23	1.95	0.49
1:B:122:VAL:HG21	1:B:362:ALA:CB	2.26	0.49
1:A:320:ILE:O	1:A:324:GLN:HG3	2.13	0.48
1:A:107:LYS:HE3	2:A:565:HOH:O	2.13	0.48
1:D:41:LYS:HZ3	1:D:358:VAL:HG21	1.79	0.48
1:C:303:ARG:HH11	1:C:303:ARG:CG	2.26	0.48
1:B:150:VAL:HG11	1:B:362:ALA:HB2	1.93	0.48
1:A:146:LYS:HE3	2:A:566:HOH:O	2.13	0.47
1:A:146:LYS:HG3	2:A:566:HOH:O	2.13	0.47
1:A:114:PRO:HB3	1:A:363:TYR:CZ	2.49	0.47
1:C:110:LYS:HE3	2:C:1259:HOH:O	2.15	0.47
1:B:133:ARG:HD3	2:B:592:HOH:O	2.14	0.47
1:C:133:ARG:HG2	2:C:1120:HOH:O	2.14	0.47
1:D:362:ALA:O	1:D:363:TYR:CB	2.56	0.46
1:B:152:LYS:CE	1:B:362:ALA:O	2.63	0.46
1:A:155:LYS:HE2	1:C:155:LYS:HE2	1.98	0.46
1:C:275:SER:HB3	1:C:354:GLY:O	2.15	0.46
1:C:122:VAL:CG2	1:C:362:ALA:HB1	2.43	0.46
1:B:150:VAL:CG1	1:B:362:ALA:HB3	2.45	0.46
1:D:120:ASP:HA	1:D:363:TYR:OH	2.16	0.46
1:B:151:LEU:HD13	1:B:208:VAL:CG2	2.45	0.46
1:C:65:THR:O	1:C:100:LYS:NZ	2.48	0.46
1:D:317:LYS:HD2	2:D:702:HOH:O	2.15	0.46
1:D:112:VAL:HG21	1:D:363:TYR:H	1.80	0.45
1:D:222:TYR:CZ	1:D:224:GLU:HB2	2.52	0.45
1:C:151:LEU:HD13	1:C:208:VAL:CG2	2.46	0.45
1:C:316:LYS:HE3	1:C:319:ASN:OD1	2.17	0.45
1:B:359:ALA:O	1:B:360:ASN:HB2	2.15	0.45
1:B:72:ASN:HD21	1:B:332:LYS:HD2	1.81	0.45
1:C:317:LYS:CD	1:C:320:ILE:HD11	2.47	0.45
1:A:22:ILE:HG21	1:A:29:ILE:HD11	1.98	0.45
1:C:150:VAL:HG12	1:C:362:ALA:HB2	1.98	0.44
1:A:91:THR:HA	1:A:92:PRO:HD3	1.88	0.44
1:C:191:LEU:CD2	1:C:361:HIS:CG	3.00	0.44
1:C:16:ARG:O	1:C:20:GLN:HG3	2.17	0.44
1:C:305:LEU:HD23	1:C:330:ARG:HB3	1.99	0.44
1:B:60:GLN:OE1	1:B:88:ASP:N	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:133:ARG:HD3	2:D:691:HOH:O	2.17	0.44
1:A:139:LYS:HE3	1:A:139:LYS:HB2	1.81	0.44
1:C:49:GLU:O	1:C:54:ASN:ND2	2.51	0.44
1:D:64:SER:HB3	2:D:663:HOH:O	2.18	0.44
1:D:202:GLN:HE22	1:D:254:GLN:HE21	1.65	0.44
1:D:76:VAL:HG23	1:D:102:ILE:HG21	2.00	0.44
1:A:66:ASP:HA	1:A:67:PRO:HD2	1.80	0.43
1:A:122:VAL:CG2	1:A:362:ALA:HB1	2.49	0.43
1:D:359:ALA:O	1:D:360:ASN:CB	2.52	0.43
1:C:164:LEU:O	1:C:164:LEU:HD23	2.18	0.43
1:C:107:LYS:HG3	1:C:146:LYS:HD2	1.99	0.43
1:D:332:LYS:HD2	1:D:332:LYS:HA	1.76	0.43
1:B:152:LYS:HD2	2:B:589:HOH:O	2.18	0.43
1:B:94:ALA:O	1:B:98:LYS:CG	2.57	0.43
1:D:361:HIS:CD2	2:D:584:HOH:O	2.67	0.43
1:D:59:ARG:CG	1:D:59:ARG:HH11	2.32	0.42
1:B:152:LYS:HE2	1:B:362:ALA:O	2.18	0.42
1:B:150:VAL:CG1	1:B:362:ALA:HB2	2.49	0.42
1:D:330:ARG:HH11	1:D:330:ARG:HD2	1.67	0.42
1:C:122:VAL:HG21	1:C:362:ALA:HB1	2.02	0.42
1:C:352:GLY:HA3	2:C:1080:HOH:O	2.20	0.42
1:C:39:MET:O	1:C:43:LEU:HG	2.20	0.42
1:A:112:VAL:HG21	1:A:362:ALA:HA	2.00	0.42
1:D:146:LYS:CE	2:D:697:HOH:O	2.66	0.41
1:A:68:LYS:HE2	2:A:600:HOH:O	2.20	0.41
1:C:150:VAL:HG11	1:C:362:ALA:HB2	2.01	0.41
1:B:119:GLU:OE1	1:B:156:ASN:HB2	2.20	0.41
1:C:174:ALA:O	1:C:178:GLN:HG3	2.19	0.41
1:A:39:MET:HA	1:A:39:MET:CE	2.51	0.41
1:D:150:VAL:HG11	1:D:362:ALA:HB2	2.02	0.41
1:D:42:ARG:CZ	1:D:303:ARG:HD2	2.51	0.41
1:A:24:ALA:HB3	1:A:27:LYS:HD2	2.02	0.41
1:D:360:ASN:HB3	1:D:361:HIS:H	1.48	0.41
1:A:213:TYR:CE1	1:A:216:LEU:HD12	2.56	0.41
1:C:24:ALA:HA	1:C:25:PRO:HD3	1.89	0.40
1:C:362:ALA:O	1:C:363:TYR:CB	2.65	0.40
1:A:148:ARG:HH22	1:A:361:HIS:CB	2.35	0.40
1:C:135:ALA:O	1:C:139:LYS:HG3	2.21	0.40
1:D:276:GLU:HG2	1:D:304:ALA:O	2.22	0.40
1:C:357:PHE:CE2	1:C:359:ALA:HB2	2.57	0.40
1:C:146:LYS:HG3	2:C:1181:HOH:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:49:GLU:HG2	1:D:51:THR:CG2	2.51	0.40
1:C:260:VAL:HA	1:C:261:PRO:HD3	1.98	0.40
1:A:202:GLN:HE22	1:A:254:GLN:HE21	1.69	0.40
1:B:191:LEU:HA	1:B:192:PRO:HD3	1.97	0.40
1:C:122:VAL:HG13	1:C:363:TYR:CD1	2.57	0.40
1:C:138:LYS:HE2	1:C:181:ARG:HB2	2.02	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	359/361 (99%)	348 (97%)	9 (2%)	2 (1%)	30	17
1	B	359/361 (99%)	352 (98%)	5 (1%)	2 (1%)	30	17
1	C	359/361 (99%)	344 (96%)	13 (4%)	2 (1%)	30	17
1	D	359/361 (99%)	347 (97%)	9 (2%)	3 (1%)	24	11
All	All	1436/1444 (99%)	1391 (97%)	36 (2%)	9 (1%)	30	17

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	362	ALA
1	C	360	ASN
1	D	360	ASN
1	B	360	ASN
1	C	353	SER
1	A	360	ASN
1	D	362	ALA
1	A	188	PRO
1	D	188	PRO

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	287/287 (100%)	281 (98%)	6 (2%)	61	55
1	B	287/287 (100%)	276 (96%)	11 (4%)	40	28
1	C	287/287 (100%)	273 (95%)	14 (5%)	31	18
1	D	287/287 (100%)	272 (95%)	15 (5%)	29	17
All	All	1148/1148 (100%)	1102 (96%)	46 (4%)	38	26

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	GLN
1	A	120	ASP
1	A	155	LYS
1	A	173	TYR
1	A	193	ASP
1	A	295	TRP
1	B	78	LEU
1	B	99	LYS
1	B	120	ASP
1	B	173	TYR
1	B	193	ASP
1	B	200	ARG
1	B	284	SER
1	B	295	TRP
1	B	325	ASN
1	B	330	ARG
1	B	360	ASN
1	C	42	ARG
1	C	45	ASP
1	C	99	LYS
1	C	133	ARG
1	C	164	LEU
1	C	173	TYR
1	C	193	ASP

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Mol	Chain	Res	Type
1	C	209	LEU
1	C	230	PRO
1	C	277	GLU
1	C	295	TRP
1	C	303	ARG
1	C	311	ARG
1	C	330	ARG
1	D	45	ASP
1	D	51	THR
1	D	53	ASP
1	D	56	ARG
1	D	59	ARG
1	D	146	LYS
1	D	169	VAL
1	D	173	TYR
1	D	200	ARG
1	D	230	PRO
1	D	277	GLU
1	D	284	SER
1	D	295	TRP
1	D	330	ARG
1	D	332	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	237	GLN
1	A	254	GLN
1	A	319	ASN
1	A	360	ASN
1	B	72	ASN
1	B	85	GLN
1	B	161	GLN
1	B	237	GLN
1	B	254	GLN
1	B	319	ASN
1	C	85	GLN
1	C	161	GLN
1	C	254	GLN
1	C	361	HIS
1	D	72	ASN
1	D	85	GLN

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Mol	Chain	Res	Type
1	D	161	GLN
1	D	254	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 carbohydrates 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 [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	360/361 (99%)	0.10	13 (3%) 46 50	2, 11, 42, 79	0
1	B	360/361 (99%)	0.05	15 (4%) 40 44	3, 12, 36, 89	0
1	C	360/361 (99%)	0.41	34 (9%) 11 12	3, 16, 55, 86	0
1	D	360/361 (99%)	0.09	19 (5%) 30 33	2, 11, 45, 86	0
All	All	1440/1444 (99%)	0.16	81 (5%) 28 31	2, 13, 45, 89	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	363	TYR	11.0
1	D	363	TYR	9.9
1	D	361	HIS	8.9
1	A	363	TYR	7.3
1	A	362	ALA	7.1
1	B	361	HIS	6.9
1	C	361	HIS	6.9
1	C	363	TYR	6.7
1	B	360	ASN	6.7
1	D	359	ALA	6.4
1	A	360	ASN	6.1
1	D	360	ASN	6.0
1	C	360	ASN	5.5
1	A	361	HIS	5.5
1	B	358	VAL	5.3
1	D	362	ALA	5.2
1	B	359	ALA	5.0
1	C	45	ASP	5.0
1	C	46	ILE	4.8
1	B	362	ALA	4.6
1	D	41	LYS	4.5

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Mol	Chain	Res	Type	RSRZ
1	C	356	LEU	4.4
1	C	358	VAL	4.3
1	C	47	GLY	4.3
1	C	44	GLN	4.3
1	C	311	ARG	4.1
1	A	359	ALA	4.1
1	A	46	ILE	4.0
1	C	362	ALA	3.9
1	C	357	PHE	3.9
1	C	343	VAL	3.8
1	D	53	ASP	3.8
1	C	51	THR	3.6
1	A	356	LEU	3.6
1	C	352	GLY	3.5
1	D	357	PHE	3.4
1	B	41	LYS	3.3
1	D	45	ASP	3.2
1	D	356	LEU	3.2
1	D	51	THR	3.2
1	C	346	GLY	3.1
1	C	349	GLY	3.1
1	C	353	SER	3.1
1	D	353	SER	3.0
1	C	348	ALA	3.0
1	C	354	GLY	3.0
1	A	358	VAL	2.9
1	D	44	GLN	2.9
1	D	48	VAL	2.9
1	A	311	ARG	2.8
1	C	318	GLU	2.8
1	D	355	SER	2.7
1	C	53	ASP	2.7
1	D	358	VAL	2.7
1	B	311	ARG	2.6
1	B	44	GLN	2.6
1	C	312	ALA	2.6
1	A	44	GLN	2.6
1	B	45	ASP	2.5
1	A	352	GLY	2.5
1	B	357	PHE	2.4
1	C	351	ALA	2.4
1	C	355	SER	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	352	GLY	2.4
1	C	48	VAL	2.4
1	C	325	ASN	2.3
1	A	47	GLY	2.3
1	B	51	THR	2.3
1	C	39	MET	2.3
1	C	95	GLU	2.3
1	B	99	LYS	2.3
1	D	52	GLU	2.2
1	C	43	LEU	2.2
1	C	316	LYS	2.2
1	C	359	ALA	2.1
1	D	54	ASN	2.1
1	C	321	ALA	2.1
1	C	329	LYS	2.1
1	A	325	ASN	2.0
1	B	53	ASP	2.0
1	D	311	ARG	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 carbohydrates 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.