Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 10:36 PM GMT

PDB ID	:	1UB3
Title	:	Crystal Structure of Tetrameric Structure of Aldolase from thermus thermophilus HB8
Authors	:	Lokanath, N.K.; Miyano, M.; Yokoyama, S.; Kuramitsu, S.; Kunishima, N.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on	:	2003-03-28
Resolution	:	1.40 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

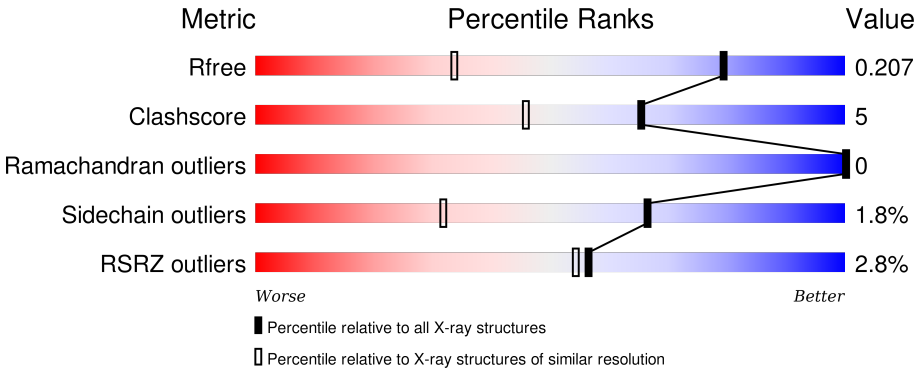
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.40 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}	91344	1199 (1.40-1.40)
Clashscore	102246	1295 (1.40-1.40)
Ramachandran outliers	100387	1259 (1.40-1.40)
Sidechain outliers	100360	1258 (1.40-1.40)
RSRZ outliers	91569	1198 (1.40-1.40)

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 <=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	220	83% 13%
1	B	220	3% 82% 10%
1	C	220	80% 14% 5%
1	D	220	6% 74% 20%

2 Entry composition

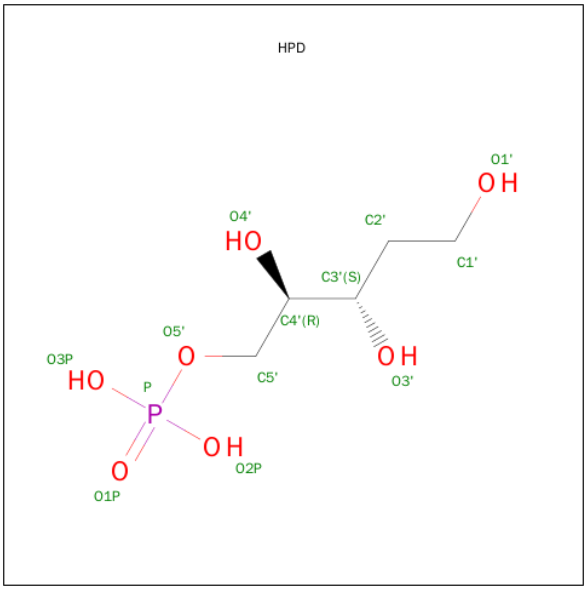
There are 3 unique types of molecules in this entry. The entry contains 6816 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Aldolase protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	211	Total	C	N	O	S	0	0	0
			1581	1004	281	292	4			
1	B	211	Total	C	N	O	S	0	0	0
			1584	1006	281	292	5			
1	C	210	Total	C	N	O	S	0	0	0
			1576	1001	280	291	4			
1	D	211	Total	C	N	O	S	0	0	0
			1581	1004	281	292	4			

- Molecule 2 is 1-HYDROXY-PENTANE-3,4-DIOL-5-PHOSPHATE (three-letter code: HPD) (formula: $C_5H_{13}O_7P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			13	5	7	1		
2	B	1	Total	C	O	P	0	0
			13	5	7	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	1	Total C O P 13 5 7 1	0	0
2	D	1	Total C O P 13 5 7 1	0	0

- Molecule 3 is water.

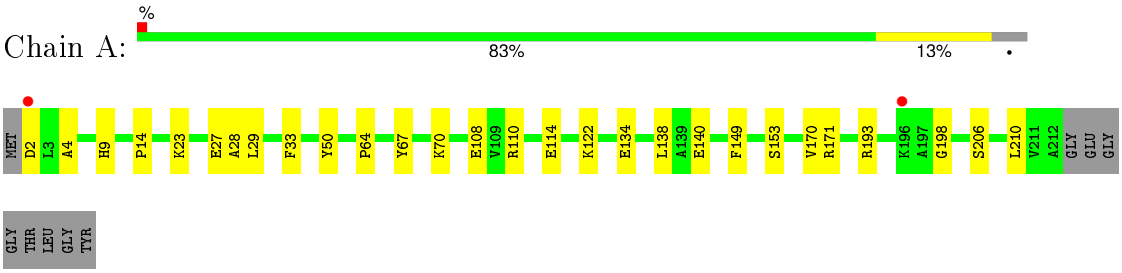
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	115	Total O 115 115	0	0
3	B	100	Total O 100 100	0	0
3	C	127	Total O 127 127	0	0
3	D	100	Total O 100 100	0	0

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.

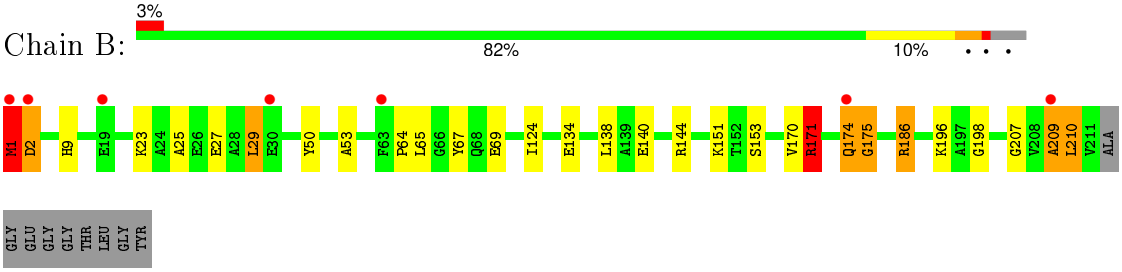
- Molecule 1: Aldolase protein

Chain A:



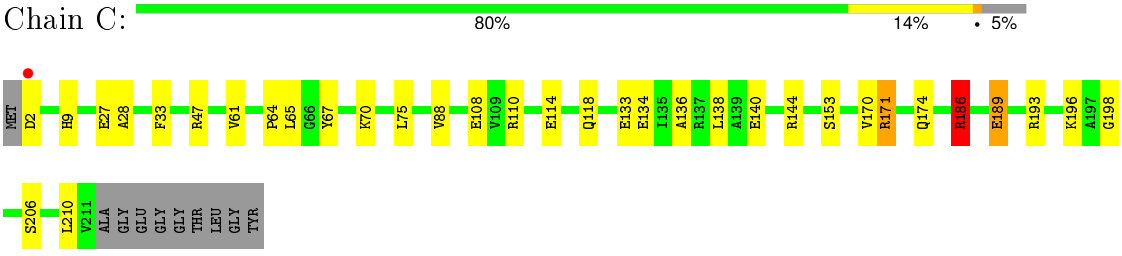
- Molecule 1: Aldolase protein

Chain B:



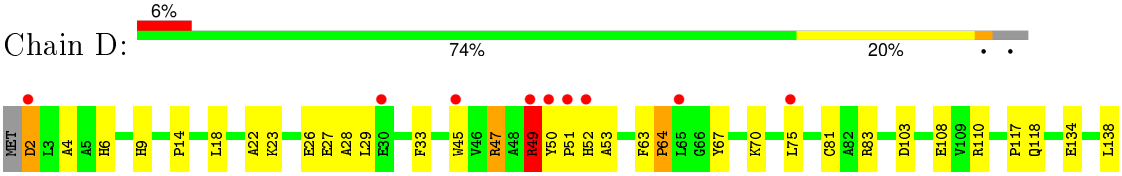
- Molecule 1: Aldolase protein

Chain C:



- Molecule 1: Aldolase protein

Chain D:




A139
E140
R144
S153
L168
L169
V170
Q174
E189
T190
R193
M194
G198
G207
V208
A209
L210
V211
A212
GLY
GLU
GLY
GLY
THR
LEU
GLY
TYR

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	63.82Å 96.89Å 137.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.25 – 1.40 29.25 – 1.40	Depositor EDS
% Data completeness (in resolution range)	97.8 (29.25-1.40) 97.9 (29.25-1.40)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$< I/\sigma(I) >$ [1]	2.86 (at 1.40Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.202 , 0.211 0.199 , 0.207	Depositor DCC
R_{free} test set	16428 reflections (9.96%)	DCC
Wilson B-factor (Å^2)	14.7	Xtriage
Anisotropy	0.449	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 43.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Outliers	0 of 165045 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6816	wwPDB-VP
Average B, all atoms (Å^2)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: HPD

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	0.43	0/1608	0.83	5/2180 (0.2%)
1	B	1.02	9/1611 (0.6%)	0.87	10/2183 (0.5%)
1	C	0.80	10/1603 (0.6%)	0.86	6/2173 (0.3%)
1	D	1.04	20/1608 (1.2%)	1.09	20/2180 (0.9%)
All	All	0.86	39/6430 (0.6%)	0.92	41/8716 (0.5%)

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	B	0	3
1	C	0	3
1	D	0	3
All	All	0	9

All (39) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	209	ALA	C-N	-22.61	0.82	1.34
1	B	174	GLN	C-N	-22.49	0.92	1.33
1	D	208	VAL	C-N	-11.77	1.06	1.34
1	D	210	LEU	C-N	-11.05	1.08	1.34
1	C	189	GLU	CD-OE2	-11.04	1.13	1.25
1	D	29	LEU	C-N	-10.96	1.08	1.34
1	D	174	GLN	C-N	-10.54	1.14	1.33
1	C	196	LYS	C-N	-9.83	1.11	1.34
1	D	2	ASP	C-N	-9.77	1.11	1.34
1	D	117	PRO	C-N	-9.68	1.11	1.34
1	D	6	HIS	C-N	-9.56	1.12	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	133	GLU	CD-OE1	-9.46	1.15	1.25
1	C	2	ASP	C-N	-8.37	1.14	1.34
1	D	26	GLU	C-N	-8.26	1.15	1.34
1	B	207	GLY	C-N	-7.55	1.16	1.34
1	C	118	GLN	C-N	-7.52	1.16	1.34
1	D	193	ARG	C-N	-7.43	1.17	1.34
1	D	52	HIS	C-N	-6.98	1.18	1.34
1	B	29	LEU	C-N	-6.88	1.18	1.34
1	C	171	ARG	C-N	-6.82	1.18	1.34
1	D	49	ARG	C-N	-6.69	1.18	1.34
1	D	110	ARG	CZ-NH2	-6.68	1.24	1.33
1	B	210	LEU	C-N	-6.59	1.18	1.34
1	C	136	ALA	C-N	-6.28	1.19	1.34
1	D	110	ARG	CZ-NH1	6.08	1.41	1.33
1	C	133	GLU	C-N	-5.97	1.20	1.34
1	D	209	ALA	C-N	-5.93	1.20	1.34
1	B	175	GLY	C-N	-5.86	1.20	1.34
1	D	207	GLY	C-N	-5.79	1.20	1.34
1	B	25	ALA	C-N	-5.75	1.20	1.34
1	D	4	ALA	C-N	5.48	1.46	1.34
1	B	196	LYS	C-N	5.48	1.46	1.34
1	D	22	ALA	C-N	5.47	1.46	1.34
1	D	193	ARG	CZ-NH2	-5.37	1.26	1.33
1	C	189	GLU	CD-OE1	5.36	1.31	1.25
1	D	193	ARG	CZ-NH1	5.31	1.40	1.33
1	B	186	ARG	C-N	-5.16	1.22	1.34
1	D	2	ASP	CG-OD2	-5.07	1.13	1.25
1	C	186	ARG	CZ-NH2	5.00	1.39	1.33

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	193	ARG	NE-CZ-NH2	-15.25	112.67	120.30
1	B	171	ARG	NE-CZ-NH2	-14.75	112.93	120.30
1	A	193	ARG	NE-CZ-NH1	13.33	126.97	120.30
1	D	103	ASP	CB-CG-OD2	-12.87	106.72	118.30
1	D	103	ASP	CB-CG-OD1	12.78	129.80	118.30
1	B	171	ARG	NE-CZ-NH1	11.53	126.07	120.30
1	C	2	ASP	CB-CG-OD1	-11.14	108.27	118.30
1	C	2	ASP	CB-CG-OD2	9.84	127.16	118.30
1	D	49	ARG	NE-CZ-NH2	-9.41	115.60	120.30
1	D	193	ARG	NE-CZ-NH2	-9.37	115.61	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	2	ASP	N-CA-CB	-9.05	94.31	110.60
1	D	110	ARG	NE-CZ-NH2	-8.92	115.84	120.30
1	D	211	VAL	C-N-CA	8.50	142.95	121.70
1	B	174	GLN	C-N-CA	8.45	140.04	122.30
1	D	211	VAL	O-C-N	-8.36	109.32	122.70
1	D	110	ARG	CD-NE-CZ	-8.26	112.04	123.60
1	D	210	LEU	O-C-N	-8.20	109.58	122.70
1	D	193	ARG	CD-NE-CZ	-8.10	112.26	123.60
1	A	140	GLU	O-C-N	-7.88	110.09	122.70
1	D	81	CYS	CA-CB-SG	-7.03	101.35	114.00
1	B	1	MET	O-C-N	6.93	133.79	122.70
1	B	2	ASP	O-C-N	6.68	133.40	122.70
1	C	174	GLN	CG-CD-OE1	-6.54	108.52	121.60
1	D	110	ARG	CG-CD-NE	6.46	125.37	111.80
1	D	51	PRO	C-N-CA	-6.45	105.58	121.70
1	D	49	ARG	NE-CZ-NH1	6.35	123.47	120.30
1	D	2	ASP	CB-CG-OD2	-6.12	112.79	118.30
1	C	171	ARG	NE-CZ-NH2	-6.08	117.26	120.30
1	D	47	ARG	CD-NE-CZ	-5.85	115.41	123.60
1	B	171	ARG	CD-NE-CZ	5.83	131.77	123.60
1	B	1	MET	CA-C-N	-5.55	104.99	117.20
1	C	189	GLU	O-C-N	-5.55	113.82	122.70
1	B	2	ASP	CA-C-N	-5.50	105.09	117.20
1	B	210	LEU	O-C-N	-5.47	113.95	122.70
1	C	186	ARG	CG-CD-NE	-5.42	100.42	111.80
1	D	2	ASP	CA-CB-CG	5.39	125.25	113.40
1	D	110	ARG	NE-CZ-NH1	5.37	122.98	120.30
1	B	209	ALA	O-C-N	-5.28	114.25	122.70
1	D	211	VAL	CA-C-N	5.21	128.67	117.20
1	A	171	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	A	140	GLU	CA-C-N	5.08	128.37	117.20

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	171	ARG	Sidechain
1	B	175	GLY	Mainchain
1	B	186	ARG	Sidechain
1	C	171	ARG	Sidechain
1	C	186	ARG	Sidechain
1	C	189	GLU	Mainchain

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Mol	Chain	Res	Type	Group
1	D	193	ARG	Sidechain
1	D	210	LEU	Mainchain
1	D	49	ARG	Sidechain

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	1581	0	1609	14	0
1	B	1584	0	1611	21	0
1	C	1576	0	1599	16	0
1	D	1581	0	1598	20	0
2	A	13	0	10	0	0
2	B	13	0	10	0	0
2	C	13	0	10	0	0
2	D	13	0	10	0	0
3	A	115	0	0	1	0
3	B	100	0	0	0	0
3	C	127	0	0	0	0
3	D	100	0	0	0	0
All	All	6816	0	6457	64	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 5.

All (64) 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:209:ALA:C	1:B:210:LEU:CA	2.01	1.28
1:B:209:ALA:O	1:B:210:LEU:N	1.72	1.21
1:B:209:ALA:CA	1:B:210:LEU:N	2.10	1.13
1:B:209:ALA:O	1:B:210:LEU:CA	2.09	0.98
1:B:209:ALA:C	1:B:210:LEU:N	0.82	0.86
1:A:14:PRO:HG3	1:C:65:LEU:HD22	1.63	0.80
1:D:140:GLU:HG3	1:D:144:ARG:NH1	1.97	0.80
1:C:140:GLU:HG3	1:C:144:ARG:NH1	2.02	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:75:LEU:HD13	1:D:75:LEU:HD13	1.72	0.72
1:B:65:LEU:HD22	1:D:14:PRO:HG3	1.70	0.71
1:D:190:THR:O	1:D:194:MET:HG3	1.90	0.71
1:B:171:ARG:O	1:B:174:GLN:NE2	2.28	0.65
1:B:140:GLU:HG3	1:B:144:ARG:NH1	2.12	0.64
1:D:140:GLU:HG3	1:D:144:ARG:HH11	1.66	0.61
1:B:209:ALA:O	1:B:210:LEU:HA	2.00	0.60
1:B:9:HIS:HE1	1:B:27:GLU:OE1	1.84	0.59
1:C:70:LYS:HG3	1:C:108:GLU:HA	1.86	0.58
1:A:9:HIS:HE1	1:A:27:GLU:OE1	1.89	0.56
1:B:170:VAL:HG21	1:B:198:GLY:HA3	1.89	0.54
1:C:9:HIS:HE1	1:C:27:GLU:OE1	1.91	0.53
1:C:134:GLU:O	1:C:138:LEU:HG	2.09	0.53
1:B:50:TYR:HB3	1:B:53:ALA:HB2	1.91	0.52
1:C:206:SER:O	1:C:210:LEU:HG	2.09	0.52
1:D:18:LEU:HD11	1:D:45:TRP:CD2	2.44	0.52
1:A:170:VAL:HG21	1:A:198:GLY:HA3	1.92	0.51
1:D:9:HIS:HE1	1:D:27:GLU:OE1	1.94	0.50
1:D:23:LYS:O	1:D:27:GLU:HG3	2.12	0.50
1:B:209:ALA:O	1:B:210:LEU:C	2.51	0.49
1:A:64:PRO:HD2	1:C:64:PRO:HD2	1.95	0.49
1:C:170:VAL:HG11	1:C:198:GLY:HA3	1.94	0.49
1:D:168:LEU:C	1:D:168:LEU:HD23	2.33	0.49
1:D:49:ARG:HG3	1:D:50:TYR:CE1	2.48	0.49
1:B:23:LYS:O	1:B:27:GLU:HG3	2.12	0.48
1:B:29:LEU:HD11	1:B:50:TYR:CE2	2.49	0.47
1:C:47:ARG:HD2	1:D:118:GLN:HG2	1.96	0.47
1:A:134:GLU:O	1:A:138:LEU:HG	2.15	0.47
1:A:114:GLU:HB2	3:A:887:HOH:O	2.14	0.47
1:D:70:LYS:HG3	1:D:108:GLU:HA	1.97	0.47
1:A:122:LYS:HG2	1:A:149:PHE:HB2	1.97	0.46
1:C:186:ARG:HD3	1:C:206:SER:OG	2.15	0.46
1:C:110:ARG:O	1:C:114:GLU:HG3	2.16	0.45
1:A:70:LYS:HG3	1:A:108:GLU:HA	1.99	0.45
1:A:29:LEU:HD11	1:A:50:TYR:CE2	2.52	0.45
1:D:170:VAL:HG21	1:D:198:GLY:HA3	1.99	0.45
1:D:50:TYR:HB3	1:D:53:ALA:HB2	2.00	0.44
1:B:209:ALA:C	1:B:210:LEU:C	2.75	0.44
1:C:28:ALA:HA	1:C:33:PHE:HD2	1.83	0.43
1:A:206:SER:O	1:A:210:LEU:HD13	2.19	0.43
1:C:193:ARG:HH11	1:C:193:ARG:HG2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:69:GLU:CD	1:D:83:ARG:HH11	2.20	0.43
1:A:110:ARG:O	1:A:114:GLU:HG3	2.20	0.42
1:B:64:PRO:HD2	1:D:64:PRO:HD2	2.02	0.41
1:D:134:GLU:O	1:D:138:LEU:HG	2.20	0.41
1:B:134:GLU:O	1:B:138:LEU:HG	2.20	0.41
1:B:124:ILE:HG12	1:B:151:LYS:HD3	2.02	0.41
1:A:23:LYS:O	1:A:27:GLU:HG3	2.21	0.41
1:C:110:ARG:NH2	1:C:144:ARG:O	2.49	0.41
1:C:61:VAL:HG23	1:C:88:VAL:HG13	2.02	0.41
1:A:2:ASP:OD2	1:A:4:ALA:HB3	2.22	0.40
1:A:28:ALA:HA	1:A:33:PHE:CD2	2.56	0.40
1:B:1:MET:HB2	1:B:2:ASP:H	1.67	0.40
1:D:63:PHE:HA	1:D:64:PRO:HA	1.87	0.40
1:D:28:ALA:HA	1:D:33:PHE:HD2	1.86	0.40
1:D:47:ARG:HA	1:D:47:ARG:HD3	1.84	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	209/220 (95%)	208 (100%)	1 (0%)	0	100	100
1	B	209/220 (95%)	209 (100%)	0	0	100	100
1	C	208/220 (94%)	207 (100%)	1 (0%)	0	100	100
1	D	209/220 (95%)	209 (100%)	0	0	100	100
All	All	835/880 (95%)	833 (100%)	2 (0%)	0	100	100

There are no Ramachandran outliers to report.

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	154/159 (97%)	152 (99%)	2 (1%)	76 48
1	B	155/159 (98%)	152 (98%)	3 (2%)	65 29
1	C	154/159 (97%)	152 (99%)	2 (1%)	76 48
1	D	154/159 (97%)	150 (97%)	4 (3%)	54 16
All	All	617/636 (97%)	606 (98%)	11 (2%)	66 32

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	67	TYR
1	A	153	SER
1	B	1	MET
1	B	67	TYR
1	B	153	SER
1	C	67	TYR
1	C	153	SER
1	D	2	ASP
1	D	64	PRO
1	D	67	TYR
1	D	153	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	HIS
1	A	178	GLN
1	B	9	HIS
1	B	178	GLN
1	C	9	HIS
1	C	178	GLN
1	D	6	HIS
1	D	9	HIS

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Mol	Chain	Res	Type
1	D	178	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

4 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	$\#\|Z\| > 2$
2	HPD	A	801	1	12,12,12	0.96	0	13,16,16	0.93	0
2	HPD	B	802	1	12,12,12	0.93	0	13,16,16	0.90	0
2	HPD	C	803	1	12,12,12	0.88	0	13,16,16	1.01	0
2	HPD	D	804	1	12,12,12	0.86	0	13,16,16	0.93	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	HPD	A	801	1	-	0/13/13/13	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HPD	B	802	1	-	0/13/13/13	0/0/0/0
2	HPD	C	803	1	-	0/13/13/13	0/0/0/0
2	HPD	D	804	1	-	0/13/13/13	0/0/0/0

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.

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, 95^{th} 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	211/220 (95%)	-0.00	2 (0%)	85	84	11, 16, 24, 31	0
1	B	211/220 (95%)	0.09	7 (3%)	50	47	11, 17, 28, 45	0
1	C	210/220 (95%)	-0.13	1 (0%)	91	90	10, 15, 25, 32	0
1	D	211/220 (95%)	0.17	14 (6%)	22	19	10, 17, 31, 41	0
All	All	843/880 (95%)	0.03	24 (2%)	56	54	10, 16, 28, 45	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	MET	7.8
1	D	212	ALA	4.5
1	A	2	ASP	3.6
1	D	49	ARG	3.6
1	D	52	HIS	3.5
1	B	2	ASP	3.2
1	C	2	ASP	3.0
1	B	19	GLU	3.0
1	D	2	ASP	2.8
1	B	30	GLU	2.8
1	A	196	LYS	2.7
1	D	45	TRP	2.6
1	D	210	LEU	2.5
1	D	30	GLU	2.5
1	B	209	ALA	2.4
1	D	189	GLU	2.4
1	B	63	PHE	2.3
1	D	50	TYR	2.3
1	B	174	GLN	2.2
1	D	65	LEU	2.2
1	D	211	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	75	LEU	2.1
1	D	174	GLN	2.1
1	D	51	PRO	2.1

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)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
2	HPD	B	802	13/13	0.95	0.10	-0.04	15,16,17,24	0
2	HPD	A	801	13/13	0.96	0.09	-0.35	15,15,17,22	0
2	HPD	D	804	13/13	0.97	0.08	-0.72	14,16,16,22	0
2	HPD	C	803	13/13	0.96	0.07	-1.10	14,16,18,22	0

6.5 Other polymers (i)

There are no such residues in this entry.