Full wwPDB X-ray Structure Validation Report (i)

Nov 1, 2023 – 06:45 AM EDT

PDB ID	:	3K1X
Title	:	Acidic Fibroblast Growth Factor (FGF-1) complexed with dobesilate
Authors	:	Romero, A.; Fernandez, I.S.; Gimenez-Gallego, G.
Deposited on	:	2009-09-29
Resolution	:	1.98 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 (i) 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 (i)) were used in the production of this report:

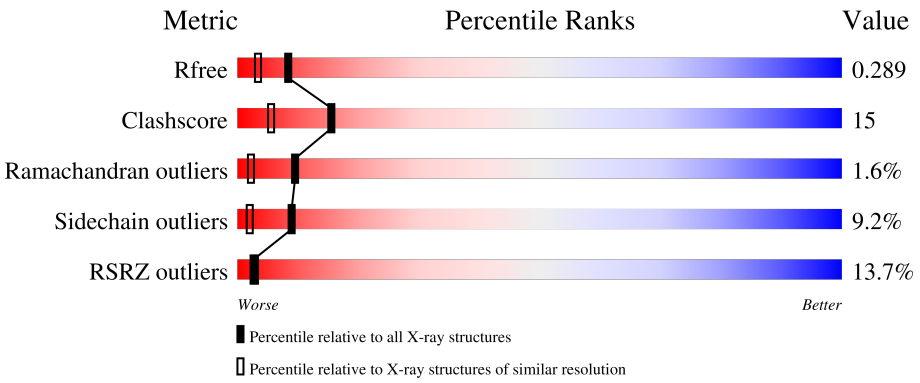
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.98 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}	130704	11647 (2.00-1.96)
Clashscore	141614	1014 (1.98-1.98)
Ramachandran outliers	138981	1006 (1.98-1.98)
Sidechain outliers	138945	1006 (1.98-1.98)
RSRZ outliers	127900	11410 (2.00-1.96)

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 <=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	130	15% 67% 28% 5% •
1	B	130	10% 80% 15% 5% •
1	C	130	10% 75% 21% •
1	D	130	9% 74% 18% 8%
1	E	130	25% 56% 36% 7% •

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Mol	Chain	Length	Quality of chain
1	F	130	13% 70% 21% 8%

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	DBX	A	131	-	-	X	-
2	DBX	B	131	-	-	X	-

2 Entry composition (i)

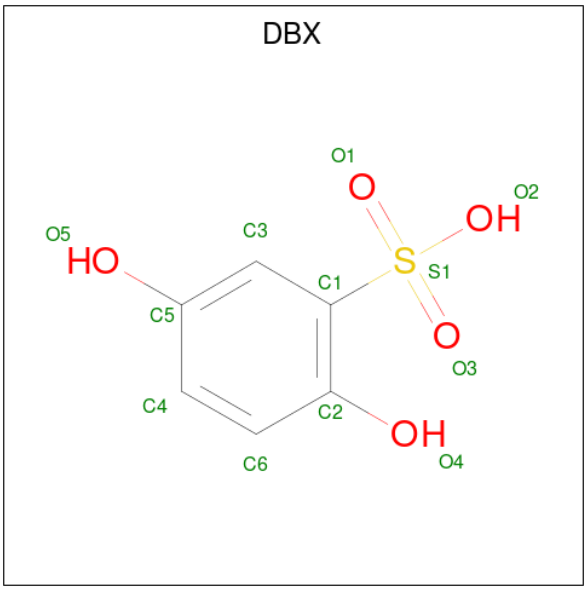
There are 3 unique types of molecules in this entry. The entry contains 6406 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Heparin-binding growth factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	130	1038	655	182	197	4	0	0	0
1	B	130	1038	655	182	197	4	0	0	0
1	C	130	1038	655	182	197	4	0	0	0
1	D	130	1038	655	182	197	4	0	0	0
1	E	130	1038	655	182	197	4	0	0	0
1	F	130	1038	655	182	197	4	0	0	0

- Molecule 2 is 2,5-dihydroxybenzenesulfonic acid (three-letter code: DBX) (formula: $C_6H_6O_5S$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	S		
2	A	1	12	6	5	1	0	0
			Total	C	O	S		
2	B	1	12	6	5	1	0	0

- Molecule 3 is water.

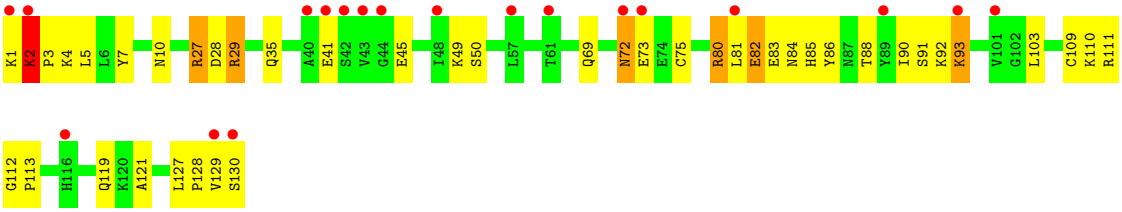
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	25	25	25	0	0
			Total	O		
3	B	37	37	37	0	0
			Total	O		
3	C	28	28	28	0	0
			Total	O		
3	D	35	35	35	0	0
			Total	O		
3	E	9	9	9	0	0
			Total	O		
3	F	20	20	20	0	0

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.

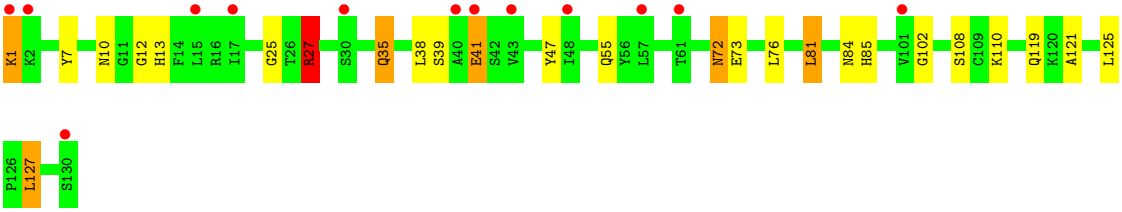
• Molecule 1: Heparin-binding growth factor 1

Chain A:



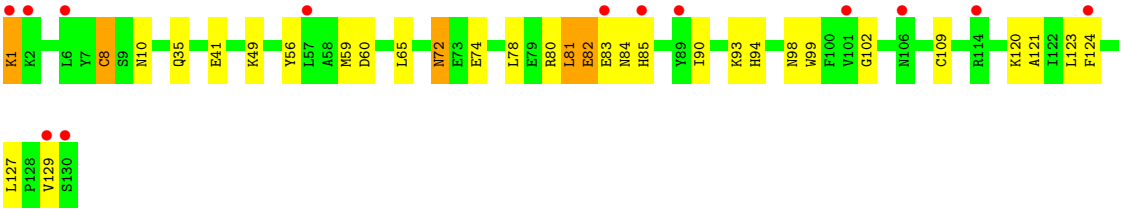
• Molecule 1: Heparin-binding growth factor 1

Chain B:



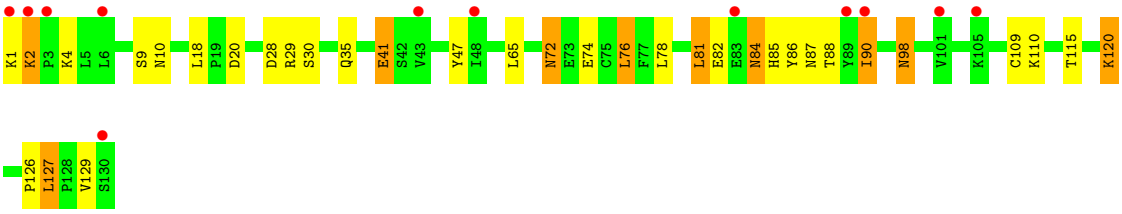
• Molecule 1: Heparin-binding growth factor 1

Chain C:



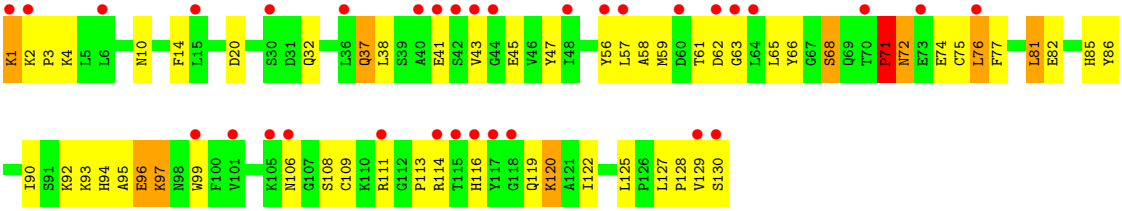
• Molecule 1: Heparin-binding growth factor 1

Chain D:



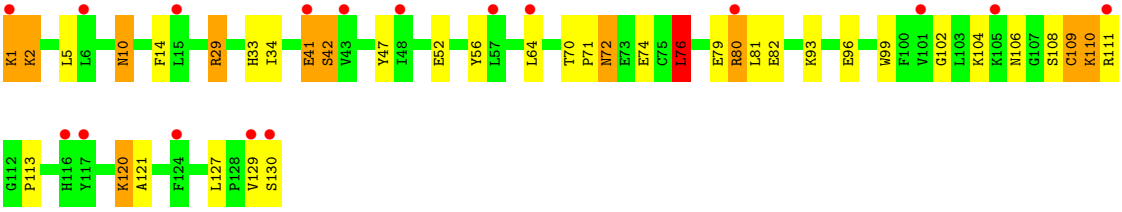
• Molecule 1: Heparin-binding growth factor 1

Chain E:



• Molecule 1: Heparin-binding growth factor 1

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	97.02Å 47.35Å 97.97Å 90.00° 106.64° 90.00°	Depositor
Resolution (Å)	24.48 – 1.98 24.48 – 1.98	Depositor EDS
% Data completeness (in resolution range)	98.5 (24.48-1.98) 98.5 (24.48-1.98)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.17 (at 1.98Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.227 , 0.290 0.228 , 0.289	Depositor DCC
R_{free} test set	2981 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	29.6	Xtriage
Anisotropy	0.349	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.41 , 54.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.016 for l,-k,h	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6406	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 68.59 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.2597e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: DBX

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	1.27	2/1061 (0.2%)	1.13	5/1429 (0.3%)
1	B	1.24	1/1061 (0.1%)	1.19	6/1429 (0.4%)
1	C	1.24	2/1061 (0.2%)	1.12	2/1429 (0.1%)
1	D	1.25	1/1061 (0.1%)	1.17	5/1429 (0.3%)
1	E	1.05	1/1061 (0.1%)	0.99	1/1429 (0.1%)
1	F	1.12	1/1061 (0.1%)	1.07	1/1429 (0.1%)
All	All	1.20	8/6366 (0.1%)	1.11	20/8574 (0.2%)

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	D	0	1
1	E	0	1
1	F	0	1
All	All	0	3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	8	CYS	CB-SG	-8.14	1.68	1.82
1	A	7	TYR	CG-CD2	6.20	1.47	1.39
1	F	80	ARG	CB-CG	5.96	1.68	1.52
1	E	14	PHE	CE2-CZ	5.70	1.48	1.37
1	B	108	SER	CB-OG	-5.42	1.35	1.42
1	A	86	TYR	CZ-OH	5.34	1.47	1.37
1	C	99	TRP	CB-CG	5.26	1.59	1.50
1	D	9	SER	CB-OG	5.06	1.48	1.42

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	29	ARG	NE-CZ-NH2	-7.80	116.40	120.30
1	E	129	VAL	N-CA-C	-7.00	92.10	111.00
1	A	27	ARG	NE-CZ-NH1	-6.69	116.96	120.30
1	B	27	ARG	NE-CZ-NH1	6.66	123.63	120.30
1	D	90	ILE	CG1-CB-CG2	-6.20	97.76	111.40
1	B	127	LEU	CA-CB-CG	6.12	129.39	115.30
1	C	59	MET	CG-SD-CE	-6.06	90.51	100.20
1	B	27	ARG	CG-CD-NE	5.95	124.30	111.80
1	D	18	LEU	CB-CG-CD1	-5.88	101.00	111.00
1	D	127	LEU	CA-CB-CG	5.80	128.64	115.30
1	B	125	LEU	CB-CG-CD1	-5.67	101.36	111.00
1	C	80	ARG	CD-NE-CZ	5.57	131.40	123.60
1	D	76	LEU	CA-CB-CG	5.48	127.91	115.30
1	A	5	LEU	CB-CG-CD2	-5.45	101.73	111.00
1	B	27	ARG	CD-NE-CZ	5.40	131.15	123.60
1	B	81	LEU	CA-CB-CG	5.27	127.43	115.30
1	A	28	ASP	CB-CA-C	-5.21	99.98	110.40
1	A	127	LEU	CA-CB-CG	5.13	127.11	115.30
1	D	20	ASP	CB-CG-OD1	5.10	122.89	118.30
1	F	76	LEU	CB-CG-CD1	5.02	119.54	111.00

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	84	ASN	Peptide
1	E	128	PRO	Peptide
1	F	41	GLU	Peptide

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	1038	0	1028	43	0
1	B	1038	0	1028	23	0
1	C	1038	0	1028	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1038	0	1028	21	0
1	E	1038	0	1028	41	0
1	F	1038	0	1028	34	0
2	A	12	0	5	8	0
2	B	12	0	4	6	0
3	A	25	0	0	1	0
3	B	37	0	0	0	0
3	C	28	0	0	0	0
3	D	35	0	0	2	0
3	E	9	0	0	1	0
3	F	20	0	0	3	0
All	All	6406	0	6177	184	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 15.

All (184) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:LYS:O	1:A:2:LYS:HB2	1.49	1.09
1:A:121:ALA:HB2	2:A:131:DBX:H6	1.33	1.07
1:A:2:LYS:HG2	1:A:3:PRO:HD2	1.12	1.07
1:A:45:GLU:OE1	1:A:92:LYS:NZ	1.97	0.98
1:C:90:ILE:HD11	1:C:98:ASN:HA	1.48	0.96
1:A:129:VAL:HG22	1:A:130:SER:H	1.31	0.92
1:E:72:ASN:HD22	1:E:74:GLU:H	1.18	0.91
1:A:2:LYS:CG	1:A:3:PRO:HD2	2.00	0.89
1:F:2:LYS:HB2	1:F:2:LYS:NZ	1.90	0.87
1:F:14:PHE:CE2	1:F:29:ARG:HG3	2.12	0.84
1:F:129:VAL:HG22	1:F:130:SER:H	1.42	0.83
1:E:72:ASN:ND2	1:E:74:GLU:H	1.75	0.83
1:A:129:VAL:CG2	1:A:130:SER:H	1.92	0.81
1:F:109:CYS:SG	1:F:110:LYS:O	2.39	0.81
1:F:2:LYS:HB2	1:F:2:LYS:HZ2	1.45	0.80
1:A:84:ASN:O	1:A:85:HIS:HB2	1.84	0.77
1:B:1:LYS:HD2	1:B:38:LEU:O	1.85	0.77
1:C:82:GLU:C	1:C:84:ASN:H	1.87	0.76
1:F:79:GLU:O	1:F:80:ARG:HD3	1.88	0.72
1:E:97:LYS:HD2	1:E:99:TRP:CE2	2.24	0.72
1:A:82:GLU:OE1	1:A:88:THR:HG23	1.90	0.71
1:A:129:VAL:HG22	1:A:130:SER:N	2.04	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:97:LYS:NZ	1:E:97:LYS:HB2	2.07	0.70
1:A:10:ASN:HD21	2:A:131:DBX:C6	2.06	0.69
1:F:79:GLU:C	1:F:80:ARG:HD3	2.13	0.68
1:D:74:GLU:OE2	3:D:137:HOH:O	2.11	0.67
1:B:1:LYS:HD2	1:B:39:SER:HA	1.75	0.67
1:E:37:GLN:HE21	1:E:37:GLN:HA	1.58	0.67
1:C:82:GLU:HB3	1:C:84:ASN:HB2	1.77	0.67
1:A:110:LYS:NZ	2:A:131:DBX:C4	2.58	0.66
1:E:66:TYR:HE1	1:E:68:SER:HG	1.43	0.66
1:A:2:LYS:HG2	1:A:3:PRO:CD	2.07	0.66
1:A:110:LYS:NZ	2:A:131:DBX:H4	2.11	0.66
1:D:72:ASN:HD22	1:D:74:GLU:H	1.44	0.66
1:D:84:ASN:HB3	1:D:86:TYR:H	1.61	0.65
1:A:4:LYS:NZ	1:A:128:PRO:HG3	2.11	0.65
1:C:82:GLU:HG2	1:C:123:LEU:HD21	1.79	0.65
1:A:110:LYS:HZ3	2:A:131:DBX:H4	1.62	0.65
1:E:97:LYS:HB2	1:E:97:LYS:HZ2	1.62	0.65
1:D:81:LEU:HD21	1:D:85:HIS:HA	1.77	0.65
1:F:33:HIS:CD2	1:F:52:GLU:HG2	2.33	0.64
2:B:131:DBX:O1	2:B:131:DBX:O4	2.10	0.64
1:A:110:LYS:HZ1	2:A:131:DBX:C4	2.11	0.64
1:E:97:LYS:HD2	1:E:99:TRP:CZ2	2.33	0.63
1:B:121:ALA:HB2	2:B:131:DBX:H6	1.80	0.62
1:A:92:LYS:HG2	1:E:43:VAL:HG21	1.81	0.62
1:C:82:GLU:HG3	1:C:84:ASN:ND2	2.14	0.62
1:D:90:ILE:HD11	1:D:98:ASN:HA	1.81	0.61
1:C:82:GLU:C	1:C:84:ASN:N	2.53	0.61
1:E:58:ALA:HB2	1:E:75:CYS:SG	2.40	0.61
1:E:56:TYR:CE1	1:E:71:PRO:HD3	2.36	0.60
1:E:96:GLU:H	1:E:96:GLU:CD	2.04	0.60
1:E:32:GLN:HB2	3:E:145:HOH:O	2.00	0.59
1:E:59:MET:O	1:E:74:GLU:HB3	2.02	0.59
1:F:41:GLU:CG	1:F:47:TYR:CE2	2.86	0.59
1:A:10:ASN:ND2	2:A:131:DBX:C6	2.65	0.59
1:A:4:LYS:HZ3	1:A:128:PRO:HG3	1.67	0.58
1:F:99:TRP:CZ2	1:F:113:PRO:HG3	2.39	0.58
1:D:28:ASP:OD1	1:D:30:SER:HB2	2.03	0.58
1:A:111:ARG:HB2	1:A:111:ARG:NH1	2.19	0.57
1:E:106:ASN:OD1	1:E:108:SER:OG	2.16	0.57
1:D:82:GLU:C	1:D:84:ASN:H	2.06	0.57
1:B:72:ASN:C	1:B:72:ASN:HD22	2.08	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:63:GLY:O	1:E:111:ARG:HA	2.05	0.56
1:E:97:LYS:HZ2	1:E:97:LYS:CB	2.18	0.56
1:B:110:LYS:NZ	1:B:119:GLN:NE2	2.54	0.56
1:B:12:GLY:O	1:B:27:ARG:HD3	2.06	0.56
1:C:49:LYS:HD2	1:C:56:TYR:CZ	2.42	0.55
1:E:57:LEU:HD11	1:E:65:LEU:HD22	1.89	0.55
1:C:1:LYS:HD2	1:C:1:LYS:N	2.22	0.55
1:B:35:GLN:H	1:B:35:GLN:NE2	2.05	0.55
1:A:1:LYS:O	1:A:2:LYS:CB	2.36	0.55
1:F:106:ASN:OD1	1:F:108:SER:OG	2.26	0.54
1:D:78:LEU:HB2	1:D:90:ILE:HG22	1.88	0.54
1:E:58:ALA:HA	1:E:74:GLU:O	2.07	0.54
1:D:82:GLU:C	1:D:84:ASN:N	2.61	0.54
1:C:82:GLU:O	1:C:84:ASN:N	2.27	0.54
1:E:66:TYR:HE1	1:E:68:SER:OG	1.90	0.54
1:B:84:ASN:O	1:B:85:HIS:HB2	2.08	0.54
1:F:79:GLU:O	1:F:80:ARG:CD	2.55	0.54
1:F:129:VAL:HG22	1:F:130:SER:N	2.18	0.53
1:D:110:LYS:HD3	1:D:115:THR:HG22	1.90	0.53
1:C:82:GLU:HG2	1:C:123:LEU:CD2	2.39	0.53
1:A:80:ARG:NH1	1:A:90:ILE:HD11	2.24	0.53
1:A:10:ASN:HB2	1:A:121:ALA:HA	1.91	0.52
1:D:81:LEU:CD2	1:D:85:HIS:HA	2.39	0.52
1:D:47:TYR:CZ	1:D:76:LEU:HD13	2.45	0.52
1:E:72:ASN:HD21	1:E:74:GLU:HB2	1.74	0.52
1:F:41:GLU:HG2	1:F:47:TYR:CE2	2.45	0.52
1:F:41:GLU:HG3	1:F:76:LEU:HD11	1.91	0.52
1:E:20:ASP:N	1:E:20:ASP:OD1	2.39	0.52
1:C:65:LEU:HD12	1:C:109:CYS:HB2	1.90	0.52
1:A:73:GLU:HG3	1:A:93:LYS:HD3	1.91	0.52
1:C:78:LEU:HB2	1:C:90:ILE:HG22	1.92	0.52
1:E:47:TYR:CE1	1:E:76:LEU:HD13	2.44	0.51
1:D:72:ASN:HD22	1:D:72:ASN:C	2.14	0.51
1:F:72:ASN:HD22	1:F:74:GLU:H	1.59	0.51
1:F:56:TYR:CE1	1:F:71:PRO:HD3	2.45	0.51
1:A:84:ASN:O	1:A:85:HIS:CB	2.53	0.51
1:C:82:GLU:HG3	1:C:84:ASN:HD22	1.75	0.51
1:A:129:VAL:CG2	1:A:130:SER:N	2.66	0.50
1:A:112:GLY:N	1:A:113:PRO:HD2	2.26	0.50
1:D:72:ASN:ND2	1:D:74:GLU:H	2.08	0.50
1:D:65:LEU:HD12	1:D:109:CYS:HB2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:82:GLU:HG3	1:D:88:THR:HG23	1.93	0.50
1:C:72:ASN:HD22	1:C:74:GLU:H	1.58	0.50
1:F:64:LEU:CD2	1:F:111:ARG:HG2	2.42	0.50
1:E:4:LYS:HD2	1:E:38:LEU:HD12	1.93	0.49
1:D:72:ASN:HD21	1:D:74:GLU:HB2	1.77	0.49
1:C:102:GLY:HA2	1:C:121:ALA:O	2.12	0.49
1:B:35:GLN:H	1:B:35:GLN:HE21	1.61	0.49
1:B:110:LYS:HE3	2:B:131:DBX:C4	2.43	0.49
1:B:110:LYS:HZ3	1:B:119:GLN:HE22	1.59	0.49
1:A:49:LYS:HE3	1:A:50:SER:O	2.12	0.49
1:C:8:CYS:HB2	1:C:124:PHE:CE2	2.49	0.48
1:E:47:TYR:CZ	1:E:76:LEU:HD13	2.49	0.48
1:F:93:LYS:HD3	3:F:138:HOH:O	2.12	0.48
1:A:80:ARG:HH11	1:A:90:ILE:HD11	1.79	0.47
1:B:121:ALA:HB2	2:B:131:DBX:C6	2.45	0.47
1:A:90:ILE:HG22	1:A:91:SER:O	2.15	0.47
1:C:90:ILE:CD1	1:C:98:ASN:HD22	2.28	0.47
1:A:80:ARG:HH11	1:A:90:ILE:CD1	2.28	0.47
1:B:10:ASN:HD21	2:B:131:DBX:C6	2.27	0.47
1:A:29:ARG:NH2	1:B:55:GLN:OE1	2.49	0.46
1:E:97:LYS:NZ	1:E:97:LYS:CB	2.76	0.46
1:A:72:ASN:ND2	1:A:75:CYS:SG	2.89	0.46
1:C:1:LYS:HD2	1:C:1:LYS:H3	1.80	0.46
1:C:93:LYS:HG2	1:C:94:HIS:CE1	2.51	0.46
1:E:111:ARG:HB3	1:E:113:PRO:HD2	1.98	0.46
1:A:111:ARG:HB2	1:A:111:ARG:HH11	1.81	0.45
1:E:116:HIS:O	1:E:119:GLN:HB2	2.17	0.45
1:E:114:ARG:O	1:E:119:GLN:NE2	2.45	0.45
1:A:112:GLY:N	1:A:113:PRO:CD	2.80	0.45
1:F:41:GLU:O	1:F:42:SER:CB	2.65	0.45
1:F:129:VAL:CG2	1:F:130:SER:H	2.22	0.45
1:A:27:ARG:HH11	1:A:27:ARG:HD2	1.55	0.45
1:E:72:ASN:ND2	1:E:74:GLU:N	2.55	0.45
1:E:3:PRO:HD2	1:E:130:SER:HB2	1.97	0.45
1:F:1:LYS:N	3:F:149:HOH:O	2.49	0.45
1:F:10:ASN:HA	1:F:120:LYS:HE2	1.99	0.45
1:B:102:GLY:HA2	1:B:121:ALA:O	2.17	0.45
1:E:92:LYS:O	1:E:93:LYS:C	2.54	0.45
1:D:4:LYS:HE3	3:D:150:HOH:O	2.16	0.44
1:D:82:GLU:O	1:D:84:ASN:N	2.50	0.44
1:E:94:HIS:O	1:E:95:ALA:C	2.55	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:72:ASN:ND2	1:F:74:GLU:HB2	2.32	0.44
1:B:110:LYS:HZ3	1:B:119:GLN:NE2	2.14	0.44
1:A:72:ASN:HD22	1:A:72:ASN:C	2.21	0.44
1:B:10:ASN:HB2	1:B:121:ALA:HA	2.00	0.44
1:C:10:ASN:HA	1:C:120:LYS:HG2	1.99	0.44
1:F:72:ASN:HD21	1:F:74:GLU:HB2	1.82	0.44
1:D:10:ASN:HA	1:D:120:LYS:HG2	2.00	0.44
1:B:41:GLU:HG3	1:B:47:TYR:CE2	2.53	0.43
1:B:7:TYR:CZ	1:B:12:GLY:HA2	2.53	0.43
1:E:1:LYS:HB3	1:E:37:GLN:OE1	2.19	0.43
1:B:41:GLU:HG3	1:B:47:TYR:HE2	1.84	0.43
1:C:72:ASN:HD22	1:C:72:ASN:C	2.21	0.43
1:F:41:GLU:HG3	1:F:47:TYR:CE2	2.52	0.43
1:F:2:LYS:HB2	1:F:2:LYS:HZ3	1.80	0.43
1:F:64:LEU:HD23	1:F:111:ARG:HG2	1.99	0.43
1:F:1:LYS:HD2	3:F:149:HOH:O	2.19	0.43
1:B:110:LYS:HE3	2:B:131:DBX:H4	1.99	0.43
1:E:45:GLU:HA	1:E:77:PHE:O	2.19	0.43
3:A:149:HOH:O	1:C:60:ASP:HB2	2.18	0.43
1:B:27:ARG:HH11	1:B:27:ARG:HG3	1.84	0.43
1:E:10:ASN:HB2	1:E:120:LYS:C	2.40	0.42
1:A:119:GLN:HA	2:A:131:DBX:O2	2.19	0.42
1:E:66:TYR:CD1	1:E:66:TYR:C	2.93	0.42
1:C:81:LEU:CD2	1:C:85:HIS:HA	2.49	0.42
1:F:47:TYR:CE1	1:F:76:LEU:HD13	2.55	0.42
1:F:102:GLY:HA2	1:F:121:ALA:O	2.19	0.42
1:E:1:LYS:HE3	1:E:37:GLN:OE1	2.19	0.42
1:F:41:GLU:O	1:F:42:SER:OG	2.30	0.42
1:F:5:LEU:HD22	1:F:34:ILE:HG13	2.01	0.41
1:A:103:LEU:HD23	1:A:109:CYS:HA	2.02	0.41
1:A:69:GLN:HA	1:A:69:GLN:OE1	2.19	0.41
1:E:81:LEU:HD22	1:E:85:HIS:HA	2.03	0.41
1:A:111:ARG:C	1:A:113:PRO:HD2	2.40	0.41
1:F:70:THR:HG23	1:F:71:PRO:HD2	2.03	0.41
1:D:87:ASN:HD22	1:D:126:PRO:HG3	1.86	0.41
1:E:86:TYR:CE1	1:E:125:LEU:HD22	2.56	0.41
1:A:111:ARG:HH11	1:A:111:ARG:CB	2.34	0.40
1:E:119:GLN:O	1:E:122:ILE:HG12	2.21	0.40
1:B:13:HIS:HB3	1:B:25:GLY:HA3	2.04	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	128/130 (98%)	115 (90%)	11 (9%)	2 (2%)	9 2
1	B	128/130 (98%)	125 (98%)	3 (2%)	0	100 100
1	C	128/130 (98%)	118 (92%)	8 (6%)	2 (2%)	9 2
1	D	128/130 (98%)	119 (93%)	7 (6%)	2 (2%)	9 2
1	E	128/130 (98%)	114 (89%)	11 (9%)	3 (2%)	6 1
1	F	128/130 (98%)	122 (95%)	3 (2%)	3 (2%)	6 1
All	All	768/780 (98%)	713 (93%)	43 (6%)	12 (2%)	9 2

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	C	83	GLU
1	D	41	GLU
1	E	41	GLU
1	F	42	SER
1	C	41	GLU
1	A	93	LYS
1	D	2	LYS
1	F	10	ASN
1	F	104	LYS
1	E	71	PRO
1	E	61	THR

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	114/114 (100%)	106 (93%)	8 (7%)	15 6
1	B	114/114 (100%)	105 (92%)	9 (8%)	12 3
1	C	114/114 (100%)	107 (94%)	7 (6%)	18 8
1	D	114/114 (100%)	103 (90%)	11 (10%)	8 1
1	E	114/114 (100%)	98 (86%)	16 (14%)	3 1
1	F	114/114 (100%)	102 (90%)	12 (10%)	7 1
All	All	684/684 (100%)	621 (91%)	63 (9%)	9 2

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	35	GLN
1	A	41	GLU
1	A	72	ASN
1	A	80	ARG
1	A	81	LEU
1	A	82	GLU
1	A	83	GLU
1	B	1	LYS
1	B	27	ARG
1	B	35	GLN
1	B	41	GLU
1	B	72	ASN
1	B	73	GLU
1	B	76	LEU
1	B	81	LEU
1	B	127	LEU
1	C	1	LYS
1	C	35	GLN
1	C	72	ASN
1	C	81	LEU
1	C	82	GLU
1	C	127	LEU
1	C	129	VAL
1	D	1	LYS
1	D	2	LYS
1	D	29	ARG
1	D	35	GLN

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Mol	Chain	Res	Type
1	D	41	GLU
1	D	72	ASN
1	D	81	LEU
1	D	98	ASN
1	D	120	LYS
1	D	127	LEU
1	D	129	VAL
1	E	1	LYS
1	E	2	LYS
1	E	37	GLN
1	E	62	ASP
1	E	68	SER
1	E	71	PRO
1	E	72	ASN
1	E	76	LEU
1	E	81	LEU
1	E	82	GLU
1	E	90	ILE
1	E	96	GLU
1	E	97	LYS
1	E	109	CYS
1	E	120	LYS
1	E	127	LEU
1	F	1	LYS
1	F	2	LYS
1	F	29	ARG
1	F	72	ASN
1	F	76	LEU
1	F	81	LEU
1	F	82	GLU
1	F	96	GLU
1	F	109	CYS
1	F	110	LYS
1	F	120	LYS
1	F	127	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	GLN
1	A	72	ASN
1	B	35	GLN

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Mol	Chain	Res	Type
1	B	72	ASN
1	B	98	ASN
1	C	13	HIS
1	C	35	GLN
1	C	72	ASN
1	C	84	ASN
1	C	98	ASN
1	D	72	ASN
1	E	13	HIS
1	E	69	GLN
1	E	72	ASN
1	E	98	ASN
1	F	37	GLN
1	F	72	ASN
1	F	85	HIS
1	F	98	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	DBX	B	131	-	11,12,12	1.75	1 (9%)	15,18,18	1.54	3 (20%)
2	DBX	A	131	-	11,12,12	2.26	1 (9%)	15,18,18	1.06	1 (6%)

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	DBX	B	131	-	-	6/6/6/6	0/1/1/1
2	DBX	A	131	-	-	6/6/6/6	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	131	DBX	C2-C1	-7.01	1.34	1.40
2	B	131	DBX	C2-C1	-5.45	1.36	1.40

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	131	DBX	O1-S1-C1	3.80	112.94	106.51
2	A	131	DBX	O1-S1-C1	-2.34	102.55	106.51
2	B	131	DBX	C6-C2-C1	2.32	120.61	118.75
2	B	131	DBX	O3-S1-C1	2.27	110.34	106.51

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	131	DBX	C2-C1-S1-O2
2	A	131	DBX	C3-C1-S1-O1
2	A	131	DBX	C3-C1-S1-O2
2	A	131	DBX	C3-C1-S1-O3
2	B	131	DBX	C2-C1-S1-O1
2	B	131	DBX	C2-C1-S1-O3
2	B	131	DBX	C3-C1-S1-O1
2	B	131	DBX	C3-C1-S1-O2
2	B	131	DBX	C3-C1-S1-O3
2	A	131	DBX	C2-C1-S1-O1

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Mol	Chain	Res	Type	Atoms
2	A	131	DBX	C2-C1-S1-O3
2	B	131	DBX	C2-C1-S1-O2

There are no ring outliers.

2 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	131	DBX	6	0
2	A	131	DBX	8	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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	130/130 (100%)	0.97	19 (14%)	2	2	16, 33, 58, 67	0
1	B	130/130 (100%)	0.55	13 (10%)	7	8	15, 28, 45, 56	0
1	C	130/130 (100%)	0.69	13 (10%)	7	8	18, 31, 51, 61	0
1	D	130/130 (100%)	0.62	12 (9%)	9	10	19, 30, 50, 66	0
1	E	130/130 (100%)	1.46	33 (25%)	0	0	27, 47, 66, 72	0
1	F	130/130 (100%)	0.81	17 (13%)	3	3	22, 37, 52, 64	0
All	All	780/780 (100%)	0.85	107 (13%)	3	3	15, 34, 60, 72	0

All (107) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	130	SER	9.8
1	E	130	SER	8.9
1	A	43	VAL	8.3
1	A	1	LYS	7.9
1	C	2	LYS	7.6
1	A	130	SER	6.8
1	E	1	LYS	6.5
1	D	130	SER	6.4
1	E	64	LEU	6.3
1	C	129	VAL	5.9
1	E	118	GLY	5.8
1	C	130	SER	5.6
1	F	129	VAL	5.6
1	B	130	SER	5.4
1	F	41	GLU	5.0
1	E	116	HIS	4.8
1	A	73	GLU	4.6
1	F	43	VAL	4.5
1	E	41	GLU	4.5

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Mol	Chain	Res	Type	RSRZ
1	D	2	LYS	4.5
1	A	57	LEU	4.3
1	F	1	LYS	4.3
1	E	42	SER	4.2
1	F	116	HIS	4.1
1	A	41	GLU	4.0
1	E	62	ASP	3.9
1	E	43	VAL	3.8
1	B	43	VAL	3.7
1	F	117	TYR	3.7
1	E	73	GLU	3.7
1	A	101	VAL	3.6
1	D	101	VAL	3.6
1	A	42	SER	3.6
1	E	129	VAL	3.5
1	A	89	TYR	3.5
1	E	114	ARG	3.5
1	D	1	LYS	3.5
1	A	61	THR	3.4
1	A	40	ALA	3.4
1	A	93	LYS	3.4
1	E	106	ASN	3.3
1	D	105	LYS	3.3
1	F	101	VAL	3.3
1	C	1	LYS	3.3
1	C	101	VAL	3.1
1	B	48	ILE	3.0
1	B	41	GLU	3.0
1	A	48	ILE	3.0
1	A	2	LYS	3.0
1	D	89	TYR	3.0
1	E	56	TYR	3.0
1	E	105	LYS	3.0
1	F	64	LEU	2.9
1	E	6	LEU	2.9
1	C	124	PHE	2.9
1	E	40	ALA	2.8
1	B	57	LEU	2.8
1	E	48	ILE	2.8
1	B	101	VAL	2.8
1	C	85	HIS	2.8
1	E	30	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	E	101	VAL	2.8
1	C	89	TYR	2.7
1	A	129	VAL	2.7
1	E	115	THR	2.7
1	D	83	GLU	2.7
1	B	17	ILE	2.6
1	F	57	LEU	2.6
1	E	2	LYS	2.6
1	B	2	LYS	2.6
1	E	15	LEU	2.6
1	E	57	LEU	2.6
1	E	111	ARG	2.5
1	E	60	ASP	2.5
1	D	6	LEU	2.5
1	B	15	LEU	2.5
1	C	106	ASN	2.5
1	E	99	TRP	2.4
1	F	15	LEU	2.4
1	E	76	LEU	2.4
1	C	57	LEU	2.4
1	E	117	TYR	2.4
1	F	6	LEU	2.3
1	C	83	GLU	2.3
1	C	114	ARG	2.3
1	E	70	THR	2.3
1	B	1	LYS	2.3
1	E	63	GLY	2.3
1	B	30	SER	2.3
1	B	40	ALA	2.2
1	F	48	ILE	2.2
1	A	116	HIS	2.2
1	A	44	GLY	2.2
1	E	44	GLY	2.2
1	D	3	PRO	2.2
1	D	43	VAL	2.2
1	D	48	ILE	2.2
1	D	90	ILE	2.2
1	B	61	THR	2.1
1	A	81	LEU	2.1
1	E	36	LEU	2.1
1	F	105	LYS	2.1
1	F	124	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	F	111	ARG	2.1
1	F	80	ARG	2.1
1	A	72	ASN	2.0
1	C	6	LEU	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 monosaccharides 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	DBX	A	131	12/12	0.84	0.26	67,70,71,72	0
2	DBX	B	131	12/12	0.87	0.22	89,91,93,93	0

6.5 Other polymers (i)

There are no such residues in this entry.