Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 01:51 PM GMT

PDB ID	:	3V9B
Title	:	Crystal structure of the catalytic domain of PDE4D2 with (S)-N-(3-{1-[1-(3-Cyclopropylmethoxy-4-difluoromethoxyphenyl)-2-(1-oxypyridin-4-yl)-ethyl]-1H-pyrazl-3-yl}phenyl)acetamide
Authors	:	Kim, H.T.; Chang, H.J.
Deposited on	:	2011-12-25
Resolution	:	2.10 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:

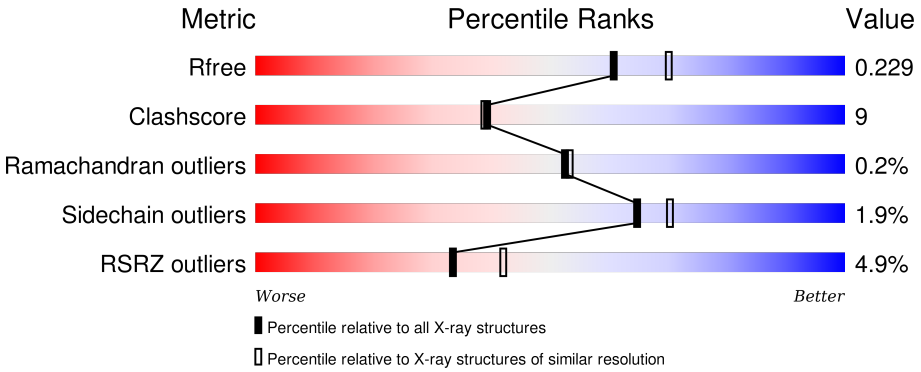
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.10 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	360	5% 75% 16% • 8%
1	B	360	3% 72% 18% • 9%
1	C	360	6% 68% 21% • 10%
1	D	360	3% 75% 15% • 9%

2 Entry composition

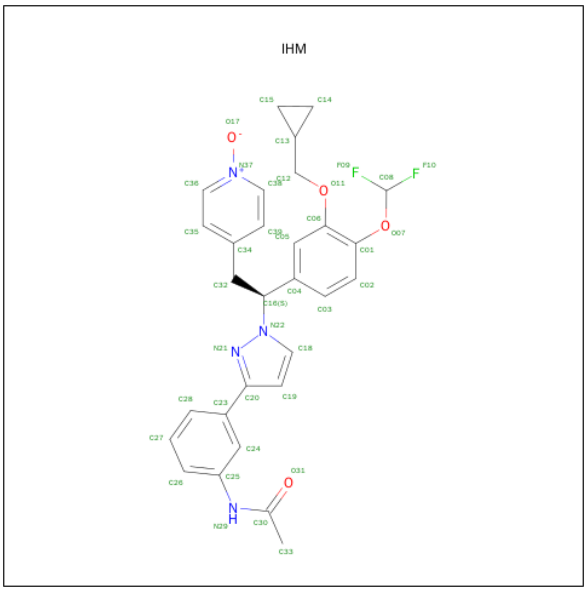
There are 4 unique types of molecules in this entry. The entry contains 11174 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 cAMP-specific 3',5'-cyclic phosphodiesterase 4D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	331	Total	C	N	O	S	0	0	0
			2678	1695	457	512	14			
1	B	327	Total	C	N	O	S	0	0	0
			2647	1673	452	508	14			
1	C	325	Total	C	N	O	S	0	0	0
			2631	1664	450	503	14			
1	D	326	Total	C	N	O	S	0	0	0
			2640	1669	451	506	14			

- Molecule 2 is N-(3-{1-[(1S)-1-[3-(CYCLOPROPYLMETHOXY)-4-(DIFLUOROMETHOXY)PHENYL]-2-(1-OXIDOPYRIDIN-4-YL)ETHYL]-1H-PYRAZOL-3-YL}PHENYL)ACETAMIDE (three-letter code: IHM) (formula: $C_{29}H_{28}F_2N_4O_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			39	29	2	4	4		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	F	N	O	0	0
			39	29	2	4	4		
2	C	1	Total	C	F	N	O	0	0
			39	29	2	4	4		
2	D	1	Total	C	F	N	O	0	0
			39	29	2	4	4		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Zn	0	0
			2	2		
3	A	2	Total	Zn	0	0
			2	2		
3	D	2	Total	Zn	0	0
			2	2		
3	C	2	Total	Zn	0	0
			2	2		

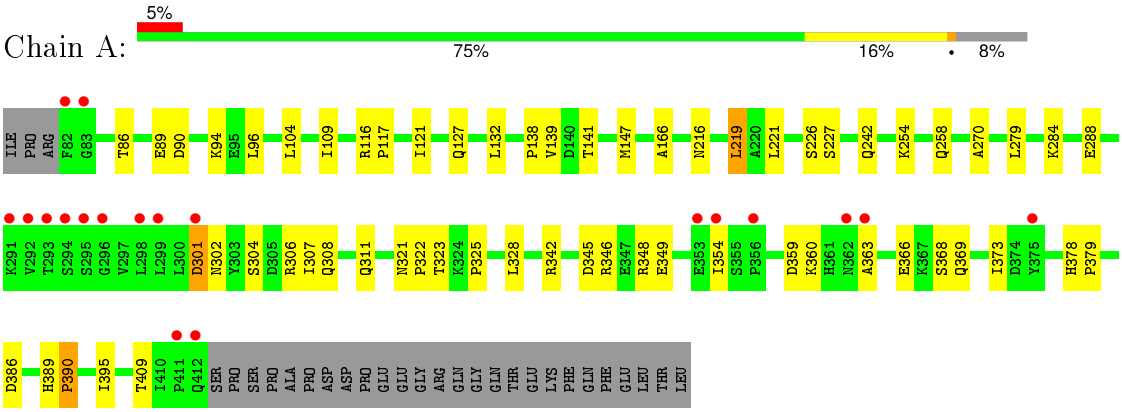
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	104	Total	O	0	0
			104	104		
4	B	99	Total	O	0	0
			99	99		
4	C	95	Total	O	0	0
			95	95		
4	D	116	Total	O	0	0
			116	116		

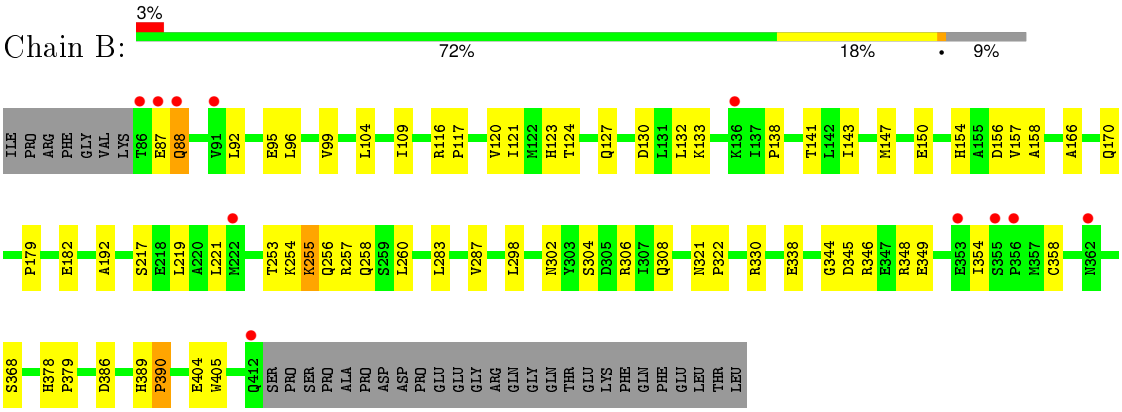
3 Residue-property plots (i)

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.

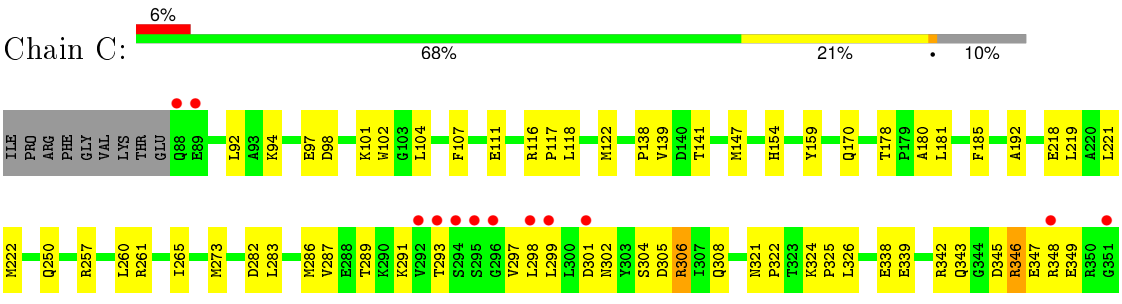
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D

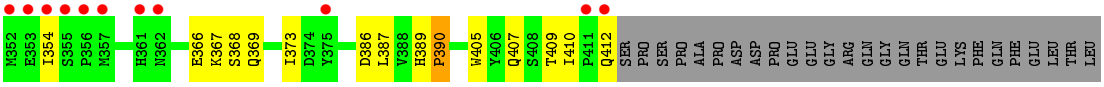


- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



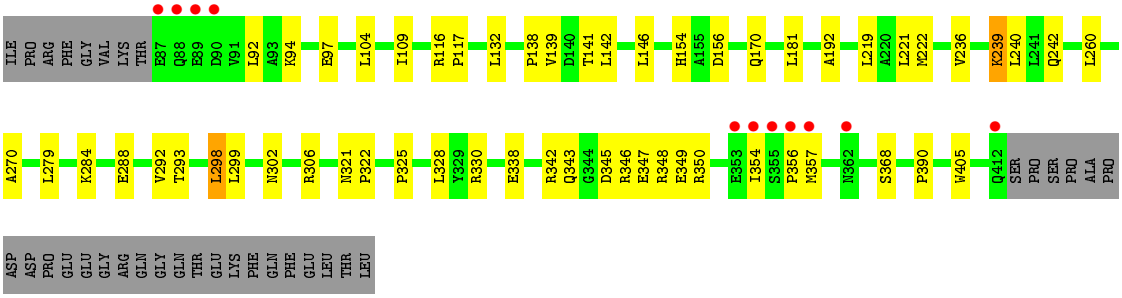
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D





- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	98.59Å 110.29Å 161.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.41 – 2.10 48.13 – 2.10	Depositor EDS
% Data completeness (in resolution range)	88.6 (35.41-2.10) 88.4 (48.13-2.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	2.41 (at 2.10Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.206 , 0.236 0.201 , 0.229	Depositor DCC
R_{free} test set	4903 reflections (5.64%)	DCC
Wilson B-factor (Å^2)	20.9	Xtriage
Anisotropy	0.496	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 55.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	1 of 97750 reflections (0.001%)	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	11174	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.92% 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: ZN, IHM

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	0.32	0/2733	0.52	0/3712
1	B	0.31	0/2701	0.52	0/3670
1	C	0.32	0/2685	0.52	0/3648
1	D	0.33	0/2694	0.54	0/3660
All	All	0.32	0/10813	0.53	0/14690

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2678	0	2633	42	0
1	B	2647	0	2599	55	0
1	C	2631	0	2586	58	0
1	D	2640	0	2592	37	0
2	A	39	0	27	1	0
2	B	39	0	27	1	0
2	C	39	0	27	2	0
2	D	39	0	27	1	0
3	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	A	104	0	0	2	0
4	B	99	0	0	1	0
4	C	95	0	0	3	0
4	D	116	0	0	4	0
All	All	11174	0	10518	190	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 9.

All (190) 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:C:368:SER:HB3	2:C:1:IHM:H10	1.47	0.95
1:B:368:SER:HB3	2:B:1:IHM:H10	1.49	0.94
1:D:356:PRO:O	1:D:357:MET:HG2	1.70	0.91
1:B:348:ARG:HB2	1:B:354:ILE:HD11	1.50	0.91
1:A:368:SER:HB3	2:A:1:IHM:H10	1.52	0.90
1:B:254:LYS:HG2	1:B:258:GLN:HE21	1.48	0.79
1:B:304:SER:O	1:B:308:GLN:HG3	1.83	0.78
1:C:306:ARG:HH11	1:C:306:ARG:HB3	1.50	0.77
1:A:302:ASN:ND2	1:A:304:SER:HB2	2.01	0.76
1:B:254:LYS:HG2	1:B:258:GLN:NE2	2.01	0.75
1:D:368:SER:HB3	2:D:1:IHM:H10	1.71	0.73
1:A:302:ASN:HD22	1:A:304:SER:HB2	1.52	0.72
1:C:348:ARG:HB2	1:C:354:ILE:HD11	1.70	0.70
1:D:356:PRO:HA	4:D:500:HOH:O	1.91	0.70
1:C:250:GLN:HA	1:C:257:ARG:HH21	1.57	0.69
1:D:321:ASN:HB2	1:D:322:PRO:HD3	1.76	0.67
1:C:139:VAL:HG23	4:C:498:HOH:O	1.94	0.67
1:B:96:LEU:O	1:B:99:VAL:HG23	1.94	0.66
1:B:321:ASN:HB2	1:B:322:PRO:HD3	1.77	0.66
1:A:321:ASN:HB2	1:A:322:PRO:HD3	1.79	0.64
1:B:253:THR:OG1	1:B:256:GLN:HG3	1.97	0.64
1:A:216:ASN:ND2	1:A:221:LEU:HD21	2.13	0.63
1:A:304:SER:O	1:A:308:GLN:HG3	1.98	0.63
1:C:321:ASN:HB2	1:C:322:PRO:HD3	1.81	0.63
1:A:302:ASN:O	1:A:306:ARG:HG2	1.99	0.62
1:C:221:LEU:HD23	1:C:221:LEU:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:ARG:HG3	1:A:346:ARG:HH21	1.65	0.62
1:C:345:ASP:O	1:C:349:GLU:HG3	1.99	0.62
1:A:342:ARG:HE	1:A:346:ARG:HH12	1.47	0.62
1:C:218:GLU:HG2	1:C:222:MET:CE	2.30	0.61
1:D:343:GLN:O	1:D:347:GLU:HG3	2.01	0.60
1:B:330:ARG:HD2	4:B:513:HOH:O	2.03	0.59
1:D:284:LYS:O	1:D:288:GLU:HG3	2.01	0.58
1:B:143:ILE:O	1:B:147:MET:HG3	2.03	0.58
1:B:87:GLU:HG3	1:B:88:GLN:H	1.69	0.57
1:D:306:ARG:NH2	4:D:492:HOH:O	2.36	0.57
1:C:342:ARG:O	1:C:346:ARG:HG2	2.05	0.57
1:C:221:LEU:C	1:C:221:LEU:HD23	2.25	0.57
1:A:348:ARG:HB2	1:A:354:ILE:HD11	1.87	0.57
1:B:96:LEU:HD11	1:B:120:VAL:CG2	2.34	0.56
1:C:250:GLN:HA	1:C:257:ARG:NH2	2.20	0.56
1:B:346:ARG:HD2	4:D:451:HOH:O	2.05	0.56
1:B:345:ASP:O	1:B:349:GLU:HG3	2.06	0.55
1:C:138:PRO:HG2	1:C:141:THR:OG1	2.07	0.55
1:C:192:ALA:HB2	1:C:260:LEU:HD12	1.89	0.55
1:D:345:ASP:O	1:D:349:GLU:HG3	2.07	0.55
1:A:147:MET:SD	1:C:349:GLU:HB3	2.47	0.55
1:A:359:ASP:O	1:A:363:ALA:HB2	2.06	0.54
1:C:366:GLU:CD	1:C:366:GLU:H	2.11	0.54
1:A:342:ARG:NE	1:A:346:ARG:HH12	2.06	0.54
1:A:127:GLN:HG3	1:A:132:LEU:HD13	1.90	0.53
4:A:489:HOH:O	1:C:346:ARG:HD2	2.08	0.53
1:A:138:PRO:HG2	1:A:141:THR:OG1	2.09	0.53
1:A:90:ASP:OD1	1:A:94:LYS:HE2	2.09	0.53
1:B:330:ARG:HD3	1:B:405:TRP:CH2	2.44	0.52
1:A:116:ARG:N	1:A:117:PRO:CD	2.72	0.52
1:A:342:ARG:HE	1:A:346:ARG:NH1	2.07	0.52
1:C:302:ASN:OD1	1:C:304:SER:HB3	2.09	0.52
1:C:98:ASP:OD1	1:C:101:LYS:HD2	2.09	0.52
1:B:116:ARG:N	1:B:117:PRO:CD	2.73	0.52
1:D:348:ARG:HB3	1:D:354:ILE:HD11	1.91	0.52
1:C:261:ARG:NH1	1:C:265:ILE:HD11	2.24	0.52
1:C:283:LEU:O	1:C:287:VAL:HG23	2.11	0.51
1:C:306:ARG:HH11	1:C:306:ARG:CB	2.20	0.51
1:A:138:PRO:HG2	1:A:141:THR:CB	2.41	0.51
1:B:378:HIS:HB3	1:B:379:PRO:HD3	1.91	0.51
1:B:217:SER:O	1:B:221:LEU:HD13	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:179:PRO:O	1:B:182:GLU:HG3	2.11	0.51
1:D:302:ASN:O	1:D:306:ARG:HG3	2.11	0.51
1:B:138:PRO:HG2	1:B:141:THR:HB	1.92	0.51
1:A:270:ALA:HB1	1:A:279:LEU:HD11	1.93	0.51
1:C:282:ASP:HB3	1:C:308:GLN:NE2	2.25	0.50
1:C:289:THR:O	1:C:291:LYS:HG3	2.11	0.50
1:C:116:ARG:N	1:C:117:PRO:CD	2.74	0.50
1:C:104:LEU:HD22	1:C:170:GLN:HG3	1.94	0.50
1:D:138:PRO:HG2	1:D:141:THR:CB	2.42	0.50
1:B:104:LEU:HD22	1:B:170:GLN:HG3	1.94	0.50
1:B:117:PRO:HA	1:B:120:VAL:HG12	1.93	0.50
1:C:326:LEU:HD21	1:C:405:TRP:CE2	2.46	0.50
1:B:154:HIS:HB3	1:B:156:ASP:OD1	2.12	0.49
1:D:222:MET:HE3	4:D:52:HOH:O	2.12	0.49
1:D:142:LEU:O	1:D:146:LEU:HG	2.12	0.49
1:B:257:ARG:HB2	1:B:257:ARG:NH1	2.27	0.49
1:C:343:GLN:O	1:C:347:GLU:HG3	2.12	0.49
1:D:116:ARG:N	1:D:117:PRO:CD	2.75	0.49
1:A:86:THR:OG1	1:A:89:GLU:HG3	2.13	0.49
1:B:138:PRO:HG2	1:B:141:THR:CB	2.43	0.49
1:C:180:ALA:O	1:C:297:VAL:HG13	2.13	0.49
1:D:132:LEU:HD22	1:D:139:VAL:HG22	1.95	0.48
1:B:116:ARG:O	1:B:120:VAL:HG12	2.13	0.48
1:B:121:ILE:HD12	1:B:166:ALA:HB1	1.96	0.48
1:A:121:ILE:HD12	1:A:166:ALA:HB1	1.94	0.48
1:B:192:ALA:HB2	1:B:260:LEU:HD12	1.96	0.48
1:D:138:PRO:HG2	1:D:141:THR:HB	1.96	0.48
1:B:130:ASP:OD1	1:B:133:LYS:HD2	2.13	0.48
1:D:138:PRO:HG2	1:D:141:THR:OG1	2.13	0.48
1:A:348:ARG:NH2	1:A:360:LYS:HE2	2.29	0.48
1:B:257:ARG:CB	1:B:257:ARG:HH11	2.26	0.48
1:D:346:ARG:O	1:D:350:ARG:HG3	2.13	0.48
1:C:94:LYS:O	1:C:97:GLU:HB2	2.14	0.48
1:A:345:ASP:OD1	1:A:348:ARG:NH2	2.47	0.47
1:C:185:PHE:HD1	1:C:306:ARG:HH12	1.63	0.47
1:D:219:LEU:HD23	1:D:222:MET:CE	2.44	0.47
1:B:143:ILE:HG22	1:B:147:MET:CE	2.45	0.47
1:B:87:GLU:HG3	1:B:88:GLN:HG3	1.96	0.47
1:B:123:HIS:O	1:B:127:GLN:HG3	2.14	0.47
1:B:302:ASN:O	1:B:306:ARG:HG3	2.15	0.47
1:B:158:ALA:HB2	1:B:338:GLU:OE2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:255:LYS:N	1:B:255:LYS:HD2	2.29	0.47
1:A:345:ASP:O	1:A:349:GLU:HG3	2.15	0.46
1:C:289:THR:O	1:C:289:THR:HG22	2.15	0.46
1:B:254:LYS:O	1:B:258:GLN:HG3	2.15	0.46
1:D:330:ARG:HH11	1:D:405:TRP:HH2	1.63	0.46
1:C:286:MET:HE1	1:C:305:ASP:HA	1.98	0.46
1:C:293:THR:N	1:C:299:LEU:HD11	2.31	0.46
1:C:159:TYR:HB3	1:C:339:GLU:OE1	2.15	0.46
1:C:367:LYS:HG3	4:C:439:HOH:O	2.15	0.46
1:A:104:LEU:HD11	1:A:109:ILE:HD11	1.98	0.46
1:D:239:LYS:HE3	1:D:239:LYS:HA	1.97	0.45
1:C:389:HIS:HA	1:C:390:PRO:HA	1.80	0.45
1:B:154:HIS:HB2	1:B:157:VAL:HG23	1.98	0.45
1:D:260:LEU:HD13	1:D:260:LEU:C	2.37	0.45
1:B:254:LYS:C	1:B:258:GLN:HE21	2.20	0.45
1:A:138:PRO:HG2	1:A:141:THR:HB	1.97	0.45
1:B:116:ARG:HD3	1:B:150:GLU:OE1	2.16	0.45
1:D:350:ARG:HH21	1:D:350:ARG:HG2	1.81	0.45
1:D:192:ALA:HB2	1:D:260:LEU:HD22	1.99	0.45
1:B:132:LEU:HD12	1:B:132:LEU:H	1.80	0.45
1:D:181:LEU:HD21	1:D:298:LEU:HD12	1.98	0.45
1:B:92:LEU:HD11	1:B:109:ILE:HG23	1.99	0.45
1:D:104:LEU:HD22	1:D:170:GLN:HG3	1.99	0.45
1:A:96:LEU:HD23	1:A:109:ILE:HD13	1.99	0.45
1:B:99:VAL:HG21	1:B:124:THR:HG21	1.98	0.44
1:C:218:GLU:HG2	1:C:222:MET:HE2	2.00	0.44
1:C:154:HIS:N	1:C:154:HIS:CD2	2.86	0.44
1:B:345:ASP:OD1	1:B:348:ARG:NH2	2.51	0.44
1:B:120:VAL:HG13	1:B:121:ILE:N	2.33	0.44
1:B:143:ILE:O	1:B:147:MET:HE2	2.17	0.44
1:C:299:LEU:HD12	1:C:299:LEU:N	2.33	0.44
1:A:307:ILE:O	1:A:311:GLN:HG3	2.17	0.44
1:C:298:LEU:HD11	1:C:387:LEU:HG	1.99	0.44
1:A:139:VAL:HG23	4:A:498:HOH:O	2.17	0.44
1:B:87:GLU:HG3	1:B:88:GLN:N	2.30	0.44
1:A:323:THR:HB	1:A:395:ILE:HG23	1.99	0.44
1:C:291:LYS:O	1:C:299:LEU:HD13	2.17	0.43
1:C:219:LEU:HD13	4:C:468:HOH:O	2.18	0.43
1:C:338:GLU:OE2	1:C:342:ARG:NH2	2.51	0.43
1:A:219:LEU:HA	1:A:219:LEU:HD12	1.87	0.43
1:A:284:LYS:O	1:A:288:GLU:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:325:PRO:HD2	1:D:328:LEU:HD12	2.00	0.43
1:D:330:ARG:NH1	1:D:405:TRP:HH2	2.16	0.43
1:C:107:PHE:O	1:C:111:GLU:HG3	2.18	0.43
1:D:94:LYS:O	1:D:97:GLU:HB2	2.19	0.43
1:C:102:TRP:NE1	1:C:324:LYS:HD3	2.34	0.43
1:C:304:SER:O	1:C:308:GLN:HB2	2.19	0.42
1:B:389:HIS:CE1	1:B:390:PRO:HB3	2.54	0.42
1:D:236:VAL:O	1:D:240:LEU:HG	2.19	0.42
1:D:270:ALA:HB1	1:D:279:LEU:HD11	2.02	0.42
1:C:118:LEU:O	1:C:122:MET:HB2	2.20	0.42
1:A:366:GLU:HG2	1:A:409:THR:HG22	2.00	0.42
1:A:242:GLN:OE1	1:D:242:GLN:HG2	2.20	0.42
1:A:369:GLN:O	1:A:373:ILE:HG13	2.19	0.42
1:C:178:THR:HG22	1:C:181:LEU:HD12	2.01	0.42
1:C:389:HIS:CE1	1:C:390:PRO:HB3	2.54	0.42
1:B:283:LEU:O	1:B:287:VAL:HG23	2.20	0.42
1:D:338:GLU:OE2	1:D:342:ARG:NH2	2.52	0.42
1:A:325:PRO:HD2	1:A:328:LEU:HD12	2.02	0.42
1:C:306:ARG:HH11	1:C:306:ARG:CG	2.33	0.41
1:C:324:LYS:O	1:C:325:PRO:C	2.58	0.41
1:A:389:HIS:CE1	1:A:390:PRO:HB3	2.55	0.41
1:C:273:MET:HG2	2:C:1:IHM:C36	2.50	0.41
1:B:389:HIS:HA	1:B:390:PRO:HA	1.84	0.41
1:D:299:LEU:C	1:D:299:LEU:HD23	2.40	0.41
1:C:407:GLN:NE2	1:C:410:ILE:HD12	2.35	0.41
1:C:138:PRO:HG2	1:C:141:THR:CB	2.50	0.41
1:B:179:PRO:HA	1:B:182:GLU:HG3	2.01	0.41
1:B:95:GLU:OE1	1:B:95:GLU:HA	2.19	0.41
1:A:254:LYS:HD3	1:A:258:GLN:HG3	2.02	0.41
1:D:104:LEU:HD11	1:D:109:ILE:HD11	2.03	0.41
1:A:226:SER:O	1:A:227:SER:C	2.59	0.41
1:C:293:THR:CG2	1:C:299:LEU:HD11	2.51	0.41
1:D:292:VAL:HG12	1:D:293:THR:O	2.21	0.41
1:C:369:GLN:O	1:C:373:ILE:HG13	2.20	0.41
1:C:409:THR:HG22	1:C:409:THR:O	2.19	0.41
1:D:154:HIS:HB3	1:D:156:ASP:OD1	2.21	0.41
1:A:378:HIS:HB3	1:A:379:PRO:HD3	2.02	0.40
1:A:346:ARG:CG	1:A:346:ARG:HH21	2.31	0.40
1:B:117:PRO:HA	1:B:120:VAL:CG1	2.50	0.40
1:B:344:GLY:HA3	1:B:358:CYS:O	2.21	0.40
1:B:138:PRO:HG2	1:B:141:THR:OG1	2.22	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	329/360 (91%)	318 (97%)	10 (3%)	1 (0%)	46 45
1	B	325/360 (90%)	309 (95%)	16 (5%)	0	100 100
1	C	323/360 (90%)	305 (94%)	17 (5%)	1 (0%)	46 45
1	D	324/360 (90%)	310 (96%)	14 (4%)	0	100 100
All	All	1301/1440 (90%)	1242 (96%)	57 (4%)	2 (0%)	52 53

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	301	ASP
1	A	301	ASP

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	302/328 (92%)	298 (99%)	4 (1%)	76 82
1	B	299/328 (91%)	292 (98%)	7 (2%)	58 62
1	C	297/328 (90%)	290 (98%)	7 (2%)	57 61
1	D	298/328 (91%)	293 (98%)	5 (2%)	68 74
All	All	1196/1312 (91%)	1173 (98%)	23 (2%)	65 70

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	219	LEU
1	A	301	ASP
1	A	386	ASP
1	A	390	PRO
1	B	88	GLN
1	B	219	LEU
1	B	255	LYS
1	B	298	LEU
1	B	386	ASP
1	B	390	PRO
1	B	404	GLU
1	C	92	LEU
1	C	147	MET
1	C	306	ARG
1	C	346	ARG
1	C	386	ASP
1	C	390	PRO
1	C	412	GLN
1	D	92	LEU
1	D	221	LEU
1	D	239	LYS
1	D	298	LEU
1	D	390	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	HIS
1	A	127	GLN
1	A	210	GLN
1	A	216	ASN
1	A	245	ASN
1	A	278	ASN
1	A	302	ASN
1	A	308	GLN
1	A	327	GLN
1	B	245	ASN
1	B	258	GLN
1	B	412	GLN
1	C	245	ASN
1	C	278	ASN

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Mol	Chain	Res	Type
1	C	308	GLN
1	C	407	GLN
1	D	127	GLN
1	D	245	ASN
1	D	250	GLN
1	D	308	GLN
1	D	312	ASN
1	D	389	HIS
1	D	412	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)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 for Mogul analysis.

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	IHM	A	1	-	39,43,43	2.81	21 (53%)	50,60,60	0.99	3 (6%)
2	IHM	B	1	-	39,43,43	2.78	22 (56%)	50,60,60	1.00	4 (8%)
2	IHM	C	1	-	39,43,43	2.80	21 (53%)	50,60,60	1.00	2 (4%)
2	IHM	D	1	-	39,43,43	2.80	20 (51%)	50,60,60	1.04	4 (8%)

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	IHM	A	1	-	-	0/23/31/31	0/4/5/5
2	IHM	B	1	-	-	0/23/31/31	0/4/5/5
2	IHM	C	1	-	-	0/23/31/31	0/4/5/5
2	IHM	D	1	-	-	0/23/31/31	0/4/5/5

All (84) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	IHM	O17-N37	-3.77	1.23	1.32
2	A	1	IHM	O17-N37	-3.72	1.23	1.32
2	B	1	IHM	O17-N37	-3.61	1.24	1.32
2	D	1	IHM	O17-N37	-3.56	1.24	1.32
2	B	1	IHM	C01-C06	2.01	1.44	1.40
2	B	1	IHM	C36-C35	2.07	1.42	1.38
2	B	1	IHM	C02-C03	2.09	1.42	1.38
2	D	1	IHM	C36-C35	2.17	1.42	1.38
2	D	1	IHM	C18-C19	2.20	1.40	1.37
2	C	1	IHM	C18-C19	2.28	1.40	1.37
2	A	1	IHM	C02-C03	2.28	1.42	1.38
2	B	1	IHM	C18-C19	2.31	1.41	1.37
2	B	1	IHM	C05-C06	2.32	1.43	1.38
2	C	1	IHM	C02-C03	2.34	1.43	1.38
2	C	1	IHM	C01-C06	2.35	1.45	1.40
2	A	1	IHM	C01-C06	2.37	1.45	1.40
2	D	1	IHM	C02-C03	2.37	1.43	1.38
2	A	1	IHM	C18-C19	2.38	1.41	1.37
2	C	1	IHM	C05-C06	2.41	1.43	1.38
2	A	1	IHM	C05-C06	2.43	1.43	1.38
2	D	1	IHM	C30-N29	2.48	1.40	1.36
2	A	1	IHM	C05-C04	2.63	1.43	1.39
2	A	1	IHM	C24-C23	2.66	1.44	1.39
2	B	1	IHM	C24-C23	2.68	1.44	1.39
2	B	1	IHM	C05-C04	2.69	1.43	1.39
2	D	1	IHM	C24-C23	2.70	1.44	1.39
2	C	1	IHM	C05-C04	2.70	1.43	1.39
2	B	1	IHM	C30-N29	2.76	1.40	1.36
2	C	1	IHM	C39-C34	2.77	1.44	1.38
2	C	1	IHM	C24-C23	2.81	1.44	1.39
2	D	1	IHM	C39-C34	2.85	1.44	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1	IHM	C05-C04	2.88	1.43	1.39
2	A	1	IHM	C39-C34	2.88	1.44	1.38
2	A	1	IHM	C30-N29	2.93	1.41	1.36
2	B	1	IHM	C03-C04	2.94	1.43	1.39
2	B	1	IHM	C39-C34	3.03	1.45	1.38
2	B	1	IHM	C28-C23	3.05	1.45	1.39
2	C	1	IHM	C27-C28	3.06	1.45	1.38
2	D	1	IHM	C27-C28	3.08	1.45	1.38
2	D	1	IHM	C03-C04	3.10	1.44	1.39
2	B	1	IHM	C35-C34	3.10	1.45	1.38
2	C	1	IHM	C35-C34	3.13	1.45	1.38
2	B	1	IHM	C27-C28	3.16	1.45	1.38
2	A	1	IHM	C27-C28	3.21	1.45	1.38
2	B	1	IHM	C27-C26	3.21	1.45	1.38
2	D	1	IHM	C28-C23	3.21	1.46	1.39
2	D	1	IHM	C27-C26	3.25	1.45	1.38
2	C	1	IHM	C30-N29	3.26	1.41	1.36
2	C	1	IHM	C28-C23	3.27	1.46	1.39
2	A	1	IHM	C27-C26	3.31	1.45	1.38
2	D	1	IHM	C35-C34	3.35	1.45	1.38
2	A	1	IHM	C35-C34	3.38	1.46	1.38
2	C	1	IHM	C03-C04	3.39	1.44	1.39
2	A	1	IHM	C28-C23	3.41	1.46	1.39
2	C	1	IHM	C27-C26	3.41	1.45	1.38
2	A	1	IHM	C03-C04	3.52	1.44	1.39
2	A	1	IHM	C24-C25	4.08	1.46	1.39
2	D	1	IHM	C24-C25	4.26	1.46	1.39
2	A	1	IHM	C02-C01	4.29	1.48	1.39
2	B	1	IHM	C24-C25	4.31	1.46	1.39
2	C	1	IHM	C19-C20	4.32	1.46	1.40
2	D	1	IHM	C02-C01	4.34	1.48	1.39
2	C	1	IHM	C02-C01	4.35	1.48	1.39
2	B	1	IHM	C02-C01	4.38	1.48	1.39
2	C	1	IHM	C24-C25	4.49	1.47	1.39
2	A	1	IHM	C19-C20	4.71	1.46	1.40
2	C	1	IHM	C26-C25	4.73	1.47	1.39
2	B	1	IHM	C26-C25	4.74	1.47	1.39
2	B	1	IHM	C19-C20	4.76	1.46	1.40
2	D	1	IHM	C19-C20	4.78	1.46	1.40
2	D	1	IHM	C26-C25	4.78	1.47	1.39
2	A	1	IHM	C26-C25	4.80	1.47	1.39
2	A	1	IHM	C18-N22	4.87	1.41	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	IHM	C18-N22	4.88	1.41	1.35
2	C	1	IHM	C18-N22	4.92	1.41	1.35
2	B	1	IHM	C38-N37	5.18	1.43	1.35
2	C	1	IHM	C38-N37	5.24	1.43	1.35
2	D	1	IHM	C18-N22	5.35	1.42	1.35
2	A	1	IHM	C36-N37	5.44	1.43	1.35
2	D	1	IHM	C36-N37	5.56	1.44	1.35
2	C	1	IHM	C36-N37	5.57	1.44	1.35
2	D	1	IHM	C38-N37	5.63	1.44	1.35
2	A	1	IHM	C38-N37	5.74	1.44	1.35
2	B	1	IHM	C36-N37	5.95	1.44	1.35

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1	IHM	C34-C32-C16	-2.92	107.47	114.31
2	D	1	IHM	C34-C32-C16	-2.88	107.57	114.31
2	C	1	IHM	C34-C32-C16	-2.86	107.61	114.31
2	B	1	IHM	C34-C32-C16	-2.58	108.27	114.31
2	D	1	IHM	C24-C23-C20	-2.31	117.52	120.54
2	B	1	IHM	C24-C23-C20	-2.28	117.56	120.54
2	D	1	IHM	C02-C03-C04	-2.22	118.92	121.20
2	A	1	IHM	C24-C23-C20	-2.11	117.78	120.54
2	B	1	IHM	C02-C03-C04	-2.00	119.15	121.20
2	D	1	IHM	C15-C13-C12	2.82	135.67	119.95
2	C	1	IHM	C15-C13-C12	2.83	135.73	119.95
2	A	1	IHM	C15-C13-C12	2.85	135.82	119.95
2	B	1	IHM	C15-C13-C12	2.85	135.85	119.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	IHM	1	0
2	B	1	IHM	1	0
2	C	1	IHM	2	0
2	D	1	IHM	1	0

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	331/360 (91%)	0.10	19 (5%)	27	35	12, 24, 56, 82	0
1	B	327/360 (90%)	-0.00	11 (3%)	49	58	14, 28, 50, 102	0
1	C	325/360 (90%)	0.13	23 (7%)	19	26	13, 25, 68, 86	0
1	D	326/360 (90%)	-0.11	11 (3%)	49	58	12, 21, 48, 88	0
All	All	1309/1440 (90%)	0.03	64 (4%)	33	42	12, 25, 59, 102	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	412	GLN	8.0
1	D	87	GLU	7.4
1	C	412	GLN	7.3
1	A	295	SER	7.0
1	C	294	SER	6.8
1	A	411	PRO	6.3
1	B	86	THR	6.3
1	C	411	PRO	5.7
1	C	356	PRO	5.5
1	B	87	GLU	5.4
1	C	354	ILE	5.0
1	C	351	GLY	4.8
1	C	292	VAL	4.5
1	C	362	ASN	4.1
1	C	295	SER	4.1
1	C	375	TYR	3.9
1	D	356	PRO	3.9
1	A	293	THR	3.8
1	D	354	ILE	3.8
1	A	294	SER	3.8
1	D	90	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	353	GLU	3.7
1	D	89	GLU	3.6
1	A	362	ASN	3.6
1	D	412	GLN	3.6
1	A	296	GLY	3.6
1	A	292	VAL	3.6
1	C	353	GLU	3.5
1	C	296	GLY	3.5
1	C	293	THR	3.2
1	B	356	PRO	3.2
1	D	355	SER	3.1
1	A	356	PRO	3.1
1	C	301	ASP	3.1
1	B	362	ASN	3.1
1	A	353	GLU	3.0
1	B	412	GLN	2.9
1	A	299	LEU	2.8
1	C	355	SER	2.8
1	A	291	LYS	2.8
1	D	88	GLN	2.8
1	C	299	LEU	2.7
1	D	362	ASN	2.7
1	A	82	PHE	2.7
1	C	357	MET	2.7
1	C	352	MET	2.7
1	A	298	LEU	2.6
1	B	88	GLN	2.5
1	C	89	GLU	2.5
1	A	375	TYR	2.5
1	B	222	MET	2.5
1	B	355	SER	2.4
1	C	298	LEU	2.4
1	A	354	ILE	2.3
1	D	357	MET	2.3
1	C	361	HIS	2.3
1	C	88	GLN	2.3
1	A	83	GLY	2.3
1	C	348	ARG	2.3
1	A	301	ASP	2.2
1	B	91	VAL	2.2
1	B	136	LYS	2.0
1	A	363	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	353	GLU	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)

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	IHM	B	1	39/39	0.93	0.13	1.91	20,24,28,33	0
2	IHM	A	1	39/39	0.94	0.13	1.71	22,26,30,38	0
2	IHM	D	1	39/39	0.93	0.15	1.08	18,21,31,32	0
2	IHM	C	1	39/39	0.93	0.13	0.53	26,28,32,36	0
3	ZN	B	503	1/1	1.00	0.09	0.51	23,23,23,23	0
3	ZN	D	507	1/1	1.00	0.11	-0.11	20,20,20,20	0
3	ZN	C	505	1/1	1.00	0.09	-0.61	25,25,25,25	0
3	ZN	A	501	1/1	1.00	0.09	-0.72	23,23,23,23	0
3	ZN	B	504	1/1	0.98	0.06	-2.22	46,46,46,46	0
3	ZN	D	508	1/1	0.99	0.06	-2.63	43,43,43,43	0
3	ZN	C	506	1/1	0.97	0.06	-3.45	46,46,46,46	0
3	ZN	A	502	1/1	0.99	0.05	-3.47	42,42,42,42	0

6.5 Other polymers (i)

There are no such residues in this entry.