Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 06:09 AM GMT

PDB ID	:	2W2C
Title	:	STRUCTURE OF THE TETRADECAMERIC OLIGOMERISATION DOMAIN OF CALCIUM-CALMODULIN DEPENDENT PROTEIN KINASE II DELTA
Authors	:	Pike, A.C.W.; Rellos, P.; Sethi, R.; Salah, E.; Burgess-Brown, N.; Shrestha, L.; Roos, A.; Murray, J.W.; Von Delft, F.; Edwards, A.; Arrowsmith, C.H.; Weigelt, J.; Bountra, C.; Knapp, S.
Deposited on	:	2008-10-28
Resolution	:	2.70 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:

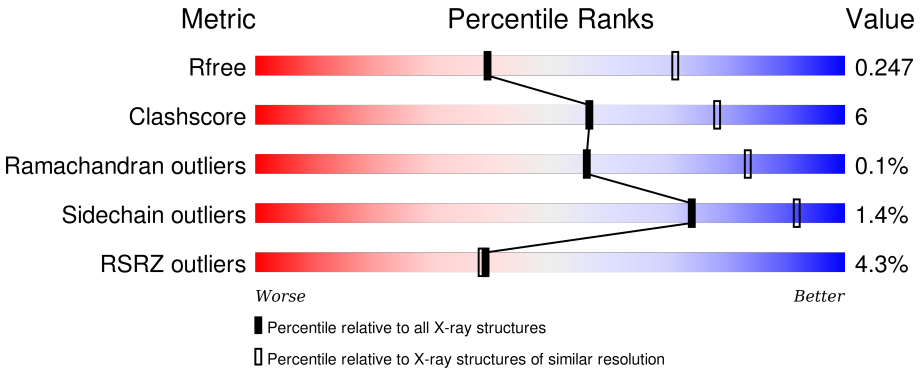
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.70 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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	144	3% 81% 8% • 11%
1	B	144	2% 75% 13% • 11%
1	C	144	3% 74% 13% • 12%
1	D	144	5% 76% 10% • 13%
1	E	144	4% 79% 10% 10%

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Mol	Chain	Length	Quality of chain
1	F	144	5% 78% 10% 13%
1	G	144	3% 75% 13% 12%
1	H	144	4% 76% 13% 9%
1	I	144	7% 77% 11% 11%
1	J	144	2% 75% 11% 13%
1	K	144	4% 81% 8% 12%
1	L	144	3% 82% 8% 10%
1	M	144	3% 72% 15% 13%
1	N	144	4% 78% 13% 9%

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	ACT	A	632	-	-	-	X
2	ACT	B	632	-	-	-	X
2	ACT	C	632	-	-	-	X
2	ACT	D	632	-	-	-	X
2	ACT	E	632	-	-	-	X
2	ACT	I	632	-	-	-	X
2	ACT	K	632	-	-	-	X

2 Entry composition (i)

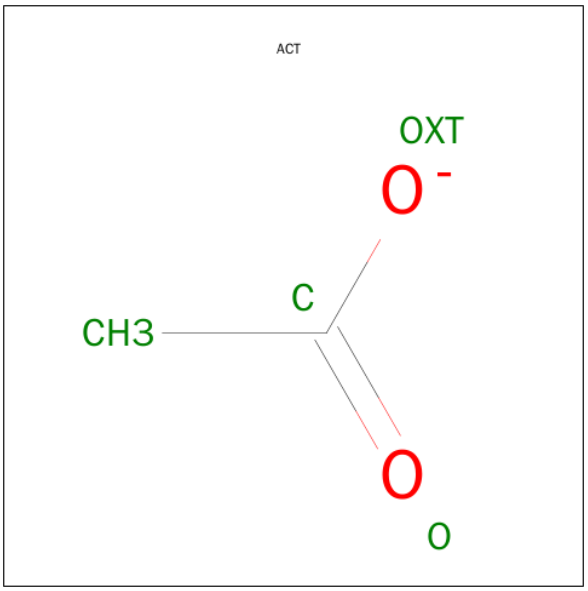
There are 4 unique types of molecules in this entry. The entry contains 14067 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	128	Total	C	N	O	S	0	0	0
			996	630	174	186	6			
1	B	128	Total	C	N	O	S	0	0	0
			1011	640	175	190	6			
1	C	127	Total	C	N	O	S	0	0	0
			992	628	174	184	6			
1	D	125	Total	C	N	O	S	0	0	0
			988	626	173	183	6			
1	E	129	Total	C	N	O	S	0	0	0
			994	627	175	187	5			
1	F	126	Total	C	N	O	S	0	0	0
			986	623	173	184	6			
1	G	127	Total	C	N	O	S	0	0	0
			991	625	175	186	5			
1	H	131	Total	C	N	O	S	0	0	0
			1010	636	178	191	5			
1	I	128	Total	C	N	O	S	0	0	0
			985	625	171	184	5			
1	J	125	Total	C	N	O	S	0	0	0
			972	617	168	181	6			
1	K	127	Total	C	N	O	S	0	0	0
			983	624	174	179	6			
1	L	130	Total	C	N	O	S	0	0	0
			1014	640	177	191	6			
1	M	125	Total	C	N	O	S	0	0	0
			975	620	171	179	5			
1	N	131	Total	C	N	O	S	0	0	0
			1015	644	175	190	6			

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	C	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	E	1	Total C O 4 2 2	0	0
2	F	1	Total C O 4 2 2	0	0
2	G	1	Total C O 4 2 2	0	0
2	H	1	Total C O 4 2 2	0	0
2	I	1	Total C O 4 2 2	0	0
2	J	1	Total C O 4 2 2	0	0
2	K	1	Total C O 4 2 2	0	0
2	L	1	Total C O 4 2 2	0	0
2	M	1	Total C O 4 2 2	0	0
2	N	1	Total C O 4 2 2	0	0

- Molecule 3 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	H	1	Total Cd 1 1	0	0
3	B	1	Total Cd 1 1	0	0
3	J	3	Total Cd 3 3	0	0
3	F	1	Total Cd 1 1	0	0

- Molecule 4 is water.

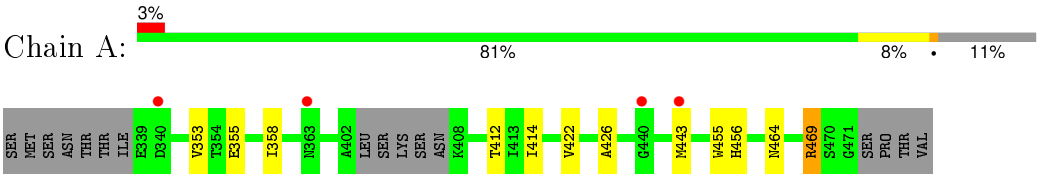
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	7	Total O 7 7	0	0
4	B	10	Total O 10 10	0	0
4	C	5	Total O 5 5	0	0
4	D	8	Total O 8 8	0	0
4	E	5	Total O 5 5	0	0
4	F	5	Total O 5 5	0	0
4	G	9	Total O 9 9	0	0
4	H	6	Total O 6 6	0	0
4	I	9	Total O 9 9	0	0
4	J	8	Total O 8 8	0	0
4	K	4	Total O 4 4	0	0
4	L	5	Total O 5 5	0	0
4	M	4	Total O 4 4	0	0
4	N	8	Total O 8 8	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.

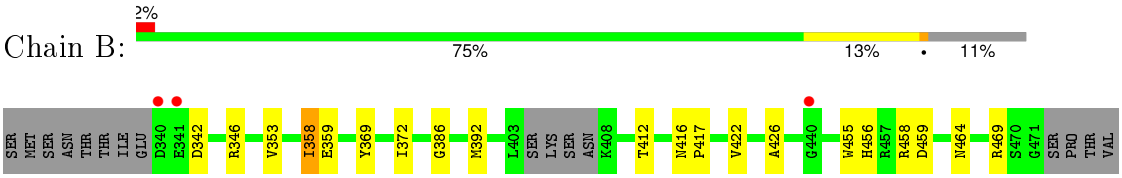
• Molecule 1: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN

Chain A:



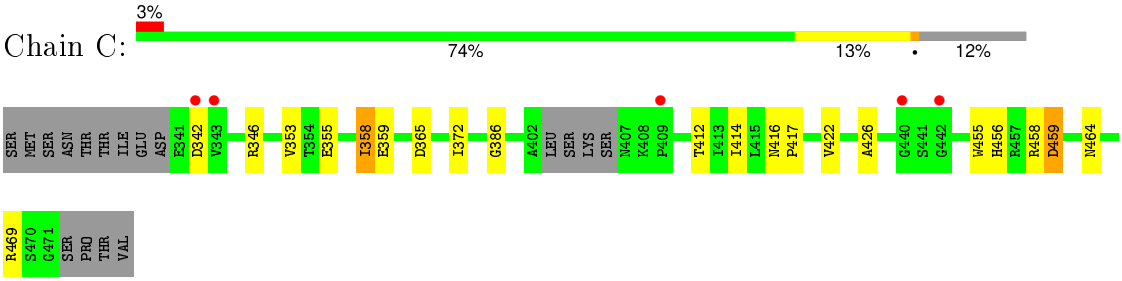
• Molecule 1: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN

Chain B:



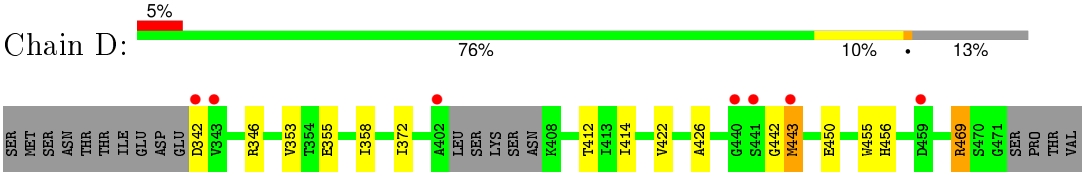
• Molecule 1: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN

Chain C:



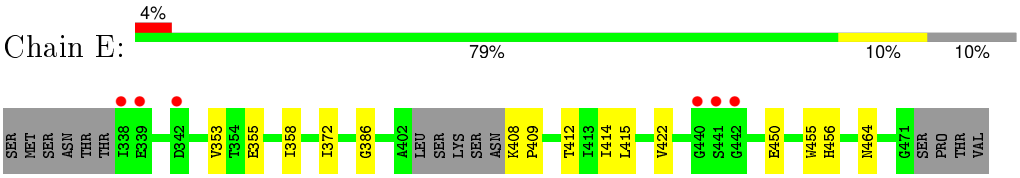
• Molecule 1: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN

Chain D:



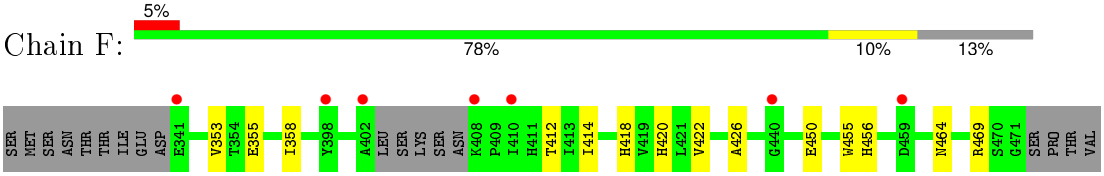
• Molecule 1: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN

Chain E:



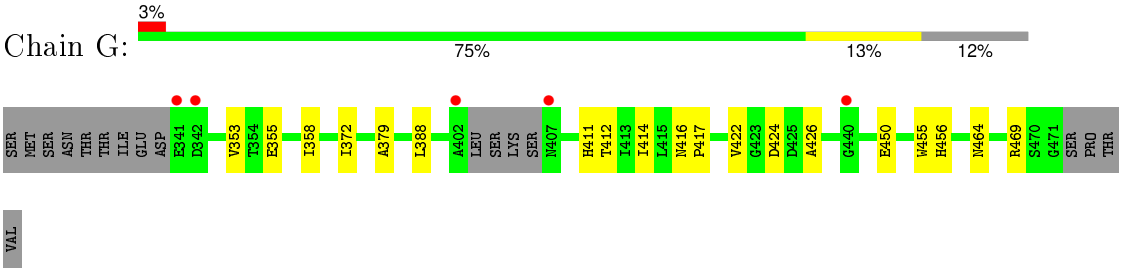
• Molecule 1: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN

Chain F:



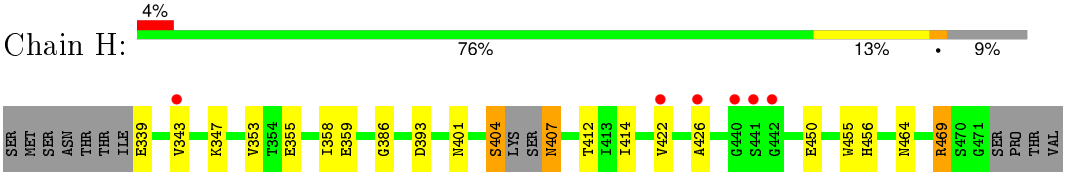
• Molecule 1: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN

Chain G:



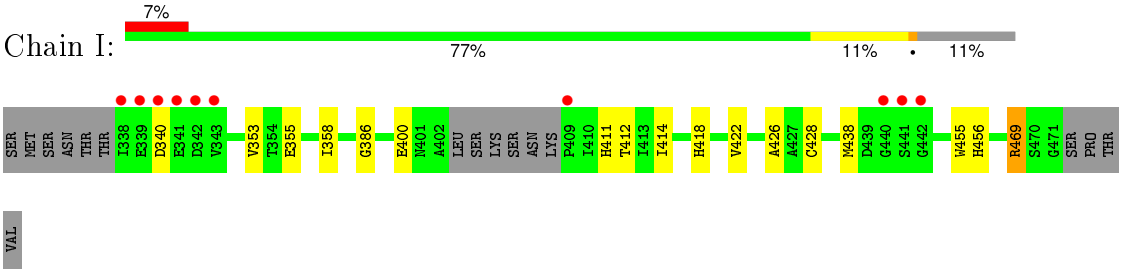
• Molecule 1: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN

Chain H:



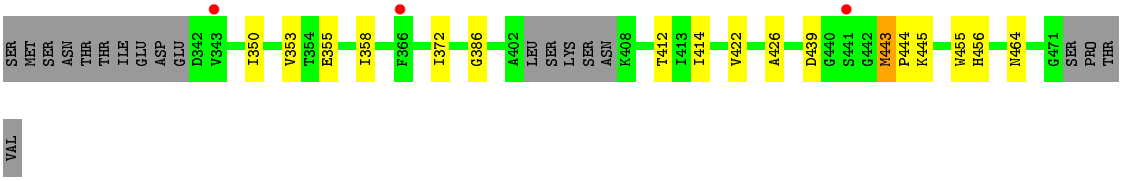
• Molecule 1: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN

Chain I:



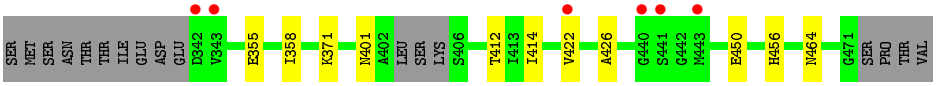
• Molecule 1: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN

Chain J:



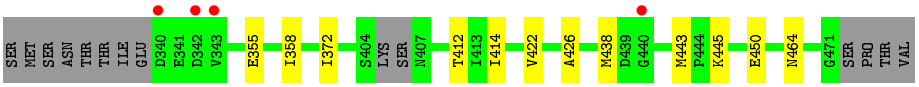
• Molecule 1: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN

Chain K:



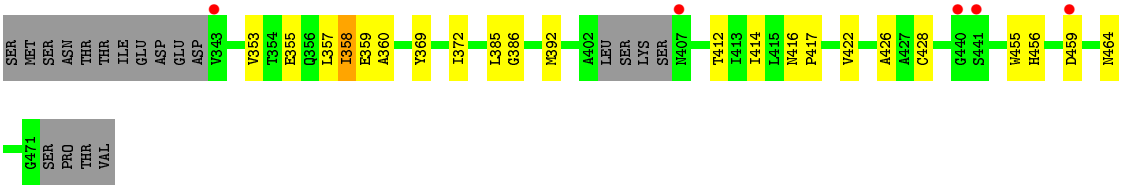
• Molecule 1: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN

Chain L:



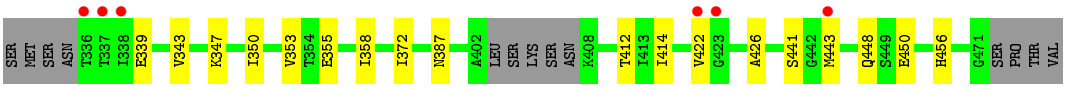
• Molecule 1: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN

Chain M:



• Molecule 1: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN

Chain N:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	149.55Å 117.80Å 160.76Å 90.00° 111.92° 90.00°	Depositor
Resolution (Å)	44.80 – 2.70 43.37 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.5 (44.80-2.70) 99.6 (43.37-2.70)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.06 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0055	Depositor
R, R_{free}	0.211 , 0.245 0.218 , 0.247	Depositor DCC
R_{free} test set	2134 reflections (3.11%)	DCC
Wilson B-factor (Å^2)	70.9	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 67.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Outliers	3 of 70678 reflections (0.004%)	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	14067	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% 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: CD, ACT

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	0.75	0/1020	0.72	2/1385 (0.1%)
1	B	0.85	0/1035	0.76	1/1403 (0.1%)
1	C	0.73	0/1016	0.77	2/1380 (0.1%)
1	D	0.77	0/1012	0.76	2/1372 (0.1%)
1	E	0.66	0/1018	0.72	0/1386
1	F	0.66	0/1010	0.72	1/1371 (0.1%)
1	G	0.69	0/1015	0.71	0/1379
1	H	0.64	0/1034	0.70	1/1407 (0.1%)
1	I	0.67	1/1009 (0.1%)	0.69	1/1372 (0.1%)
1	J	0.65	0/996	0.71	0/1354
1	K	0.67	1/1007 (0.1%)	0.73	0/1368
1	L	0.75	0/1038	0.72	0/1409
1	M	0.75	1/999 (0.1%)	0.73	0/1357
1	N	0.67	0/1039	0.72	0/1412
All	All	0.71	3/14248 (0.0%)	0.73	10/19355 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	M	428	CYS	CB-SG	-7.37	1.69	1.82
1	I	428	CYS	CB-SG	-5.22	1.73	1.81
1	K	450	GLU	CG-CD	5.12	1.59	1.51

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	I	469	ARG	NE-CZ-NH2	5.60	123.10	120.30
1	C	469	ARG	NE-CZ-NH1	-5.58	117.51	120.30
1	H	469	ARG	NE-CZ-NH2	5.55	123.08	120.30
1	D	469	ARG	NE-CZ-NH2	5.54	123.07	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	469	ARG	NE-CZ-NH2	5.37	122.99	120.30
1	F	469	ARG	NE-CZ-NH2	5.32	122.96	120.30
1	C	469	ARG	NE-CZ-NH2	5.19	122.90	120.30
1	A	469	ARG	NE-CZ-NH1	-5.09	117.75	120.30
1	D	443	MET	CG-SD-CE	5.05	108.29	100.20
1	A	469	ARG	NE-CZ-NH2	5.04	122.82	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	996	0	903	12	0
1	B	1011	0	931	16	0
1	C	992	0	908	16	1
1	D	988	0	920	20	0
1	E	994	0	893	12	0
1	F	986	0	902	13	0
1	G	991	0	901	18	0
1	H	1010	0	908	16	1
1	I	985	0	889	15	1
1	J	972	0	887	15	0
1	K	983	0	903	10	1
1	L	1014	0	926	15	0
1	M	975	0	895	16	0
1	N	1015	0	928	17	0
2	A	4	0	3	1	0
2	B	4	0	3	0	0
2	C	4	0	3	0	0
2	D	4	0	3	1	0
2	E	4	0	3	0	0
2	F	4	0	3	0	0
2	G	4	0	3	1	0
2	H	4	0	3	1	0
2	I	4	0	3	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	J	4	0	3	0	0
2	K	4	0	3	0	0
2	L	4	0	3	0	0
2	M	4	0	3	0	0
2	N	4	0	3	0	0
3	B	1	0	0	0	0
3	F	1	0	0	0	0
3	H	1	0	0	0	0
3	J	3	0	0	0	0
4	A	7	0	0	0	0
4	B	10	0	0	0	0
4	C	5	0	0	0	0
4	D	8	0	0	0	0
4	E	5	0	0	0	0
4	F	5	0	0	2	0
4	G	9	0	0	0	0
4	H	6	0	0	0	0
4	I	9	0	0	3	0
4	J	8	0	0	0	0
4	K	4	0	0	0	0
4	L	5	0	0	0	0
4	M	4	0	0	0	0
4	N	8	0	0	0	0
All	All	14067	0	12736	163	2

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 6.

All (163) 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:D:443:MET:HE2	1:D:443:MET:HA	1.31	1.12
1:G:411:HIS:CE1	4:I:2003:HOH:O	2.23	0.91
1:B:422:VAL:HG12	1:L:426:ALA:HB2	1.62	0.81
1:G:411:HIS:HE1	4:I:2003:HOH:O	1.62	0.81
1:N:441:SER:O	1:N:443:MET:HE2	1.85	0.76
1:D:443:MET:CE	1:D:443:MET:HA	2.12	0.75
1:J:443:MET:HE3	1:J:444:PRO:HD2	1.66	0.75
1:A:422:VAL:HG12	1:K:426:ALA:HB2	1.68	0.74
1:J:439:ASP:HB3	1:J:445:LYS:CD	2.18	0.73
1:B:422:VAL:HG12	1:L:426:ALA:CB	2.20	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:422:VAL:HG13	1:H:456:HIS:HB2	1.74	0.69
1:D:442:GLY:O	1:D:443:MET:CE	2.43	0.66
1:C:422:VAL:HG12	1:D:426:ALA:HB2	1.78	0.65
1:E:456:HIS:HB2	1:H:422:VAL:HG13	1.77	0.65
1:B:426:ALA:HB2	1:L:422:VAL:HG12	1.81	0.63
1:B:359:GLU:OE1	1:B:359:GLU:HA	1.99	0.62
1:A:426:ALA:HB2	1:K:422:VAL:HG12	1.80	0.62
1:F:426:ALA:HB2	1:J:422:VAL:HG12	1.82	0.62
1:I:426:ALA:HB2	1:N:422:VAL:HG12	1.82	0.61
1:A:422:VAL:HG12	1:K:426:ALA:CB	2.30	0.61
1:D:442:GLY:O	1:D:443:MET:HE3	2.00	0.60
1:I:456:HIS:HB2	1:N:422:VAL:HG13	1.85	0.59
1:I:422:VAL:HG12	1:N:426:ALA:HB2	1.84	0.59
1:D:358:ILE:HG21	1:D:412:THR:HG21	1.85	0.58
1:A:358:ILE:HG21	1:A:412:THR:HG21	1.85	0.58
1:C:456:HIS:HB2	1:D:422:VAL:HG13	1.86	0.57
1:C:422:VAL:HG12	1:D:426:ALA:CB	2.35	0.57
1:H:358:ILE:HG21	1:H:412:THR:HG21	1.87	0.57
1:E:422:VAL:HG12	1:H:426:ALA:HB2	1.87	0.57
1:A:355:GLU:HG2	1:A:414:ILE:HD12	1.86	0.57
1:F:418:HIS:NE2	4:F:2002:HOH:O	2.33	0.57
1:I:469:ARG:HH12	2:I:632:ACT:H3	1.69	0.57
1:A:456:HIS:HB2	1:K:422:VAL:HG13	1.86	0.56
1:G:358:ILE:HG21	1:G:412:THR:HG21	1.88	0.56
1:F:355:GLU:HG2	1:F:414:ILE:HD12	1.87	0.56
1:G:426:ALA:HB2	1:M:422:VAL:HG12	1.87	0.56
1:L:355:GLU:HG2	1:L:414:ILE:HD12	1.88	0.56
1:B:353:VAL:HG13	1:B:455:TRP:CZ2	2.41	0.56
1:A:355:GLU:CG	1:A:414:ILE:HD12	2.37	0.55
1:F:422:VAL:HG12	1:J:426:ALA:HB2	1.87	0.55
1:L:443:MET:CE	1:L:445:LYS:NZ	2.70	0.55
1:D:443:MET:CA	1:D:443:MET:HE2	2.22	0.54
1:M:359:GLU:HA	1:M:359:GLU:OE1	2.07	0.54
1:B:369:TYR:CD2	1:B:392:MET:HE1	2.43	0.54
1:D:442:GLY:O	1:D:443:MET:HE2	2.08	0.54
1:C:422:VAL:HG13	1:D:456:HIS:HB2	1.89	0.54
1:N:339:GLU:O	1:N:343:VAL:HG23	2.08	0.53
1:F:456:HIS:HB2	1:J:422:VAL:HG13	1.89	0.53
1:K:358:ILE:HG21	1:K:412:THR:HG21	1.91	0.53
1:F:422:VAL:HG13	1:J:456:HIS:HB2	1.91	0.53
1:C:359:GLU:OE1	1:C:359:GLU:HA	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:422:VAL:HG13	1:K:456:HIS:HB2	1.92	0.52
1:I:422:VAL:HG13	1:N:456:HIS:HB2	1.90	0.52
1:D:469:ARG:NH1	2:D:632:ACT:OXT	2.42	0.52
1:H:393:ASP:CG	1:I:411:HIS:HE2	2.12	0.52
1:C:358:ILE:HG21	1:C:412:THR:HG21	1.91	0.52
1:H:355:GLU:HG2	1:H:414:ILE:HD12	1.91	0.52
1:C:426:ALA:HB2	1:D:422:VAL:HG12	1.92	0.52
1:G:422:VAL:HG13	1:M:456:HIS:HB2	1.92	0.52
1:B:358:ILE:HG21	1:B:412:THR:HG21	1.92	0.52
1:B:342:ASP:OD1	1:B:346:ARG:HD2	2.09	0.51
1:F:355:GLU:CG	1:F:414:ILE:HD12	2.40	0.51
1:N:355:GLU:HG2	1:N:414:ILE:HD12	1.91	0.51
1:L:355:GLU:CG	1:L:414:ILE:HD12	2.41	0.51
1:E:358:ILE:HG21	1:E:412:THR:HG21	1.93	0.51
1:B:422:VAL:O	1:L:426:ALA:HB2	2.10	0.51
1:C:353:VAL:HG13	1:C:455:TRP:CZ2	2.46	0.51
1:E:415:LEU:HD21	1:N:387:ASN:HB3	1.93	0.50
1:H:339:GLU:O	1:H:343:VAL:HG23	2.11	0.50
1:J:358:ILE:HG21	1:J:412:THR:HG21	1.93	0.50
1:G:456:HIS:HB2	1:M:422:VAL:HG13	1.94	0.49
1:J:355:GLU:HG2	1:J:414:ILE:HD12	1.93	0.49
1:M:353:VAL:HG13	1:M:455:TRP:CZ2	2.47	0.49
1:N:372:ILE:O	1:N:372:ILE:HG22	2.12	0.49
1:K:355:GLU:HG2	1:K:414:ILE:HD12	1.94	0.49
1:D:372:ILE:O	1:D:372:ILE:HG22	2.13	0.49
1:I:355:GLU:HG2	1:I:414:ILE:HD12	1.94	0.49
1:N:355:GLU:CG	1:N:414:ILE:HD12	2.43	0.49
1:G:372:ILE:O	1:G:372:ILE:HG22	2.14	0.48
1:B:372:ILE:O	1:B:372:ILE:HG22	2.13	0.48
1:C:386:GLY:HA2	1:D:450:GLU:OE2	2.13	0.48
1:E:355:GLU:HG2	1:E:414:ILE:HD12	1.94	0.48
1:B:353:VAL:HG13	1:B:455:TRP:CH2	2.49	0.48
1:I:355:GLU:CG	1:I:414:ILE:HD12	2.44	0.48
1:L:443:MET:HE1	1:L:445:LYS:NZ	2.29	0.48
1:C:458:ARG:O	1:C:459:ASP:C	2.52	0.48
1:F:358:ILE:HG21	1:F:412:THR:HG21	1.96	0.48
1:H:355:GLU:CG	1:H:414:ILE:HD12	2.44	0.48
1:K:355:GLU:CG	1:K:414:ILE:HD12	2.44	0.47
1:D:355:GLU:HG2	1:D:414:ILE:HD12	1.95	0.47
1:G:422:VAL:HG12	1:M:426:ALA:HB2	1.96	0.47
1:I:358:ILE:HG21	1:I:412:THR:HG21	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:426:ALA:CB	1:K:422:VAL:HG12	2.44	0.47
1:J:355:GLU:CG	1:J:414:ILE:HD12	2.45	0.47
1:C:355:GLU:HG3	1:C:414:ILE:HD12	1.97	0.47
1:B:342:ASP:O	1:B:346:ARG:HG3	2.15	0.47
1:H:404:SER:O	1:H:407:ASN:N	2.48	0.46
1:L:443:MET:CE	1:L:445:LYS:HZ3	2.27	0.46
1:N:358:ILE:HG21	1:N:412:THR:HG21	1.96	0.46
1:E:408:LYS:CB	1:E:409:PRO:HD2	2.45	0.46
1:B:456:HIS:HB2	1:L:422:VAL:HG13	1.97	0.46
1:M:369:TYR:CD2	1:M:392:MET:HE1	2.51	0.46
1:G:426:ALA:CB	1:M:422:VAL:HG12	2.45	0.46
1:D:355:GLU:CG	1:D:414:ILE:HD12	2.45	0.46
1:H:469:ARG:HH12	2:H:632:ACT:H3	1.81	0.46
1:D:342:ASP:OD1	1:D:346:ARG:HG3	2.15	0.46
1:F:426:ALA:CB	1:J:422:VAL:HG12	2.46	0.46
1:J:372:ILE:O	1:J:372:ILE:HG22	2.15	0.46
1:I:426:ALA:CB	1:N:422:VAL:HG12	2.46	0.45
1:I:418:HIS:NE2	4:I:2007:HOH:O	2.36	0.45
1:E:372:ILE:HG22	1:E:372:ILE:O	2.16	0.45
1:M:355:GLU:HG3	1:M:414:ILE:HD12	1.98	0.45
1:D:443:MET:CA	1:D:443:MET:CE	2.91	0.45
1:M:358:ILE:HG21	1:M:412:THR:HG21	1.98	0.45
1:L:443:MET:HE2	1:L:445:LYS:NZ	2.32	0.44
1:M:353:VAL:HG13	1:M:455:TRP:CH2	2.52	0.44
1:E:355:GLU:CG	1:E:414:ILE:HD12	2.48	0.44
1:H:353:VAL:HG13	1:H:455:TRP:CZ2	2.52	0.44
1:G:355:GLU:HG2	1:G:414:ILE:HD12	2.00	0.44
1:H:401:ASN:HB3	1:I:438:MET:SD	2.57	0.44
1:B:386:GLY:HA2	1:L:450:GLU:OE2	2.18	0.44
1:I:386:GLY:HA2	1:N:450:GLU:OE2	2.18	0.43
1:G:469:ARG:NH1	2:G:632:ACT:OXT	2.51	0.43
1:H:353:VAL:HG13	1:H:455:TRP:CH2	2.53	0.43
1:G:355:GLU:CG	1:G:414:ILE:HD12	2.49	0.43
1:F:422:VAL:HG12	1:J:426:ALA:CB	2.49	0.43
1:N:350:ILE:O	1:N:353:VAL:HG12	2.18	0.43
1:C:422:VAL:O	1:C:426:ALA:HB3	2.19	0.43
1:F:420:HIS:ND1	4:F:2003:HOH:O	2.12	0.43
1:E:386:GLY:HA2	1:H:450:GLU:OE2	2.18	0.43
1:M:357:LEU:O	1:M:360:ALA:HB3	2.18	0.42
1:B:458:ARG:O	1:B:459:ASP:C	2.58	0.42
1:L:358:ILE:HG21	1:L:412:THR:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:416:ASN:N	1:C:417:PRO:CD	2.83	0.42
1:L:372:ILE:O	1:L:372:ILE:HG22	2.19	0.42
1:F:353:VAL:HG13	1:F:455:TRP:CZ2	2.55	0.42
1:J:353:VAL:HG13	1:J:455:TRP:CZ2	2.55	0.42
1:M:372:ILE:HG22	1:M:372:ILE:O	2.20	0.42
1:C:372:ILE:O	1:C:372:ILE:HG22	2.20	0.41
1:I:422:VAL:HG12	1:N:426:ALA:CB	2.49	0.41
1:J:350:ILE:O	1:J:353:VAL:HG12	2.20	0.41
1:A:469:ARG:HH12	2:A:632:ACT:H3	1.84	0.41
1:C:342:ASP:O	1:C:346:ARG:HG3	2.20	0.41
1:G:353:VAL:HG13	1:G:455:TRP:CZ2	2.55	0.41
1:G:353:VAL:HG13	1:G:455:TRP:CH2	2.55	0.41
1:M:385:LEU:HB3	1:N:448:GLN:NE2	2.36	0.41
1:A:422:VAL:O	1:A:426:ALA:HB3	2.20	0.41
1:G:424:ASP:N	1:G:424:ASP:OD1	2.52	0.41
1:C:353:VAL:HG13	1:C:455:TRP:CH2	2.55	0.41
1:N:343:VAL:CG1	1:N:347:LYS:HE3	2.50	0.41
1:M:416:ASN:N	1:M:417:PRO:CD	2.83	0.41
1:B:416:ASN:N	1:B:417:PRO:CD	2.84	0.41
1:D:353:VAL:HG13	1:D:455:TRP:CZ2	2.56	0.41
1:E:450:GLU:OE2	1:H:386:GLY:HA2	2.21	0.41
1:I:353:VAL:HG13	1:I:455:TRP:CZ2	2.56	0.41
1:E:353:VAL:HG13	1:E:455:TRP:CZ2	2.56	0.40
1:H:343:VAL:HG12	1:H:347:LYS:HE3	2.03	0.40
1:A:353:VAL:HG13	1:A:455:TRP:CH2	2.55	0.40
1:G:416:ASN:N	1:G:417:PRO:CD	2.85	0.40
1:G:450:GLU:OE2	1:M:386:GLY:HA2	2.21	0.40
1:G:379:ALA:O	1:G:388:LEU:HD12	2.21	0.40
1:K:401:ASN:HB3	1:L:438:MET:SD	2.61	0.40
1:F:450:GLU:OE2	1:J:386:GLY:HA2	2.21	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:365:ASP:OD2	1:H:359:GLU:OE2[3_445]	2.11	0.09
1:I:400:GLU:O	1:K:371:LYS:NZ[3_545]	2.19	0.01

5.3 Torsion angles

5.3.1 Protein backbone

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	124/144 (86%)	120 (97%)	4 (3%)	0	100	100
1	B	124/144 (86%)	119 (96%)	5 (4%)	0	100	100
1	C	123/144 (85%)	119 (97%)	3 (2%)	1 (1%)	24	51
1	D	121/144 (84%)	118 (98%)	3 (2%)	0	100	100
1	E	125/144 (87%)	123 (98%)	2 (2%)	0	100	100
1	F	122/144 (85%)	117 (96%)	5 (4%)	0	100	100
1	G	123/144 (85%)	119 (97%)	4 (3%)	0	100	100
1	H	127/144 (88%)	123 (97%)	4 (3%)	0	100	100
1	I	124/144 (86%)	119 (96%)	5 (4%)	0	100	100
1	J	121/144 (84%)	118 (98%)	3 (2%)	0	100	100
1	K	123/144 (85%)	118 (96%)	5 (4%)	0	100	100
1	L	126/144 (88%)	120 (95%)	6 (5%)	0	100	100
1	M	121/144 (84%)	116 (96%)	4 (3%)	1 (1%)	24	51
1	N	127/144 (88%)	123 (97%)	4 (3%)	0	100	100
All	All	1731/2016 (86%)	1672 (97%)	57 (3%)	2 (0%)	56	83

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	459	ASP
1	C	459	ASP

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	97/126 (77%)	95 (98%)	2 (2%)	61	87
1	B	101/126 (80%)	99 (98%)	2 (2%)	63	87
1	C	98/126 (78%)	96 (98%)	2 (2%)	63	87
1	D	100/126 (79%)	100 (100%)	0	100	100
1	E	97/126 (77%)	96 (99%)	1 (1%)	82	94
1	F	98/126 (78%)	97 (99%)	1 (1%)	82	94
1	G	98/126 (78%)	97 (99%)	1 (1%)	82	94
1	H	99/126 (79%)	96 (97%)	3 (3%)	48	79
1	I	95/126 (75%)	94 (99%)	1 (1%)	80	94
1	J	96/126 (76%)	94 (98%)	2 (2%)	61	87
1	K	96/126 (76%)	95 (99%)	1 (1%)	82	94
1	L	101/126 (80%)	100 (99%)	1 (1%)	82	94
1	M	95/126 (75%)	93 (98%)	2 (2%)	61	87
1	N	100/126 (79%)	100 (100%)	0	100	100
All	All	1371/1764 (78%)	1352 (99%)	19 (1%)	74	92

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	443	MET
1	A	464	ASN
1	B	358	ILE
1	B	464	ASN
1	C	358	ILE
1	C	464	ASN
1	E	464	ASN
1	F	464	ASN
1	G	464	ASN
1	H	404	SER
1	H	407	ASN
1	H	464	ASN
1	I	340	ASP
1	J	443	MET
1	J	464	ASN
1	K	464	ASN

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Mol	Chain	Res	Type
1	L	464	ASN
1	M	358	ILE
1	M	464	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	387	ASN
1	G	411	HIS
1	H	387	ASN
1	H	407	ASN
1	I	448	GLN
1	M	387	ASN
1	M	448	GLN
1	N	448	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 20 ligands modelled in this entry, 6 are monoatomic - leaving 14 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	ACT	A	632	-	1,3,3	2.54	1 (100%)	0,3,3	0.00	-
2	ACT	B	632	-	1,3,3	5.20	1 (100%)	0,3,3	0.00	-
2	ACT	C	632	-	1,3,3	4.75	1 (100%)	0,3,3	0.00	-
2	ACT	D	632	-	1,3,3	4.73	1 (100%)	0,3,3	0.00	-
2	ACT	E	632	-	1,3,3	3.23	1 (100%)	0,3,3	0.00	-
2	ACT	F	632	-	1,3,3	2.06	1 (100%)	0,3,3	0.00	-
2	ACT	G	632	-	1,3,3	3.48	1 (100%)	0,3,3	0.00	-
2	ACT	H	632	-	1,3,3	5.01	1 (100%)	0,3,3	0.00	-
2	ACT	I	632	-	1,3,3	3.85	1 (100%)	0,3,3	0.00	-
2	ACT	J	632	-	1,3,3	4.44	1 (100%)	0,3,3	0.00	-
2	ACT	K	632	-	1,3,3	5.21	1 (100%)	0,3,3	0.00	-
2	ACT	L	632	-	1,3,3	4.11	1 (100%)	0,3,3	0.00	-
2	ACT	M	632	-	1,3,3	3.42	1 (100%)	0,3,3	0.00	-
2	ACT	N	632	-	1,3,3	2.32	1 (100%)	0,3,3	0.00	-

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	ACT	A	632	-	-	0/0/0/0	0/0/0/0
2	ACT	B	632	-	-	0/0/0/0	0/0/0/0
2	ACT	C	632	-	-	0/0/0/0	0/0/0/0
2	ACT	D	632	-	-	0/0/0/0	0/0/0/0
2	ACT	E	632	-	-	0/0/0/0	0/0/0/0
2	ACT	F	632	-	-	0/0/0/0	0/0/0/0
2	ACT	G	632	-	-	0/0/0/0	0/0/0/0
2	ACT	H	632	-	-	0/0/0/0	0/0/0/0
2	ACT	I	632	-	-	0/0/0/0	0/0/0/0
2	ACT	J	632	-	-	0/0/0/0	0/0/0/0
2	ACT	K	632	-	-	0/0/0/0	0/0/0/0
2	ACT	L	632	-	-	0/0/0/0	0/0/0/0
2	ACT	M	632	-	-	0/0/0/0	0/0/0/0
2	ACT	N	632	-	-	0/0/0/0	0/0/0/0

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	632	ACT	CH3-C	2.06	1.51	1.48
2	N	632	ACT	CH3-C	2.32	1.52	1.48
2	A	632	ACT	CH3-C	2.54	1.52	1.48
2	E	632	ACT	CH3-C	3.23	1.53	1.48
2	M	632	ACT	CH3-C	3.42	1.53	1.48
2	G	632	ACT	CH3-C	3.48	1.53	1.48
2	I	632	ACT	CH3-C	3.85	1.54	1.48
2	L	632	ACT	CH3-C	4.11	1.54	1.48
2	J	632	ACT	CH3-C	4.44	1.55	1.48
2	D	632	ACT	CH3-C	4.73	1.55	1.48
2	C	632	ACT	CH3-C	4.75	1.55	1.48
2	H	632	ACT	CH3-C	5.01	1.55	1.48
2	B	632	ACT	CH3-C	5.20	1.56	1.48
2	K	632	ACT	CH3-C	5.21	1.56	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	632	ACT	1	0
2	D	632	ACT	1	0
2	G	632	ACT	1	0
2	H	632	ACT	1	0
2	I	632	ACT	1	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

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	128/144 (88%)	0.32	4 (3%)	52	52	36, 42, 52, 55	0
1	B	128/144 (88%)	0.06	3 (2%)	64	64	34, 41, 52, 66	0
1	C	127/144 (88%)	0.16	5 (3%)	43	43	33, 41, 50, 58	0
1	D	125/144 (86%)	0.33	7 (5%)	28	26	36, 42, 51, 55	0
1	E	129/144 (89%)	0.25	6 (4%)	35	34	38, 45, 52, 56	0
1	F	126/144 (87%)	0.20	7 (5%)	28	26	40, 45, 52, 56	0
1	G	127/144 (88%)	0.15	5 (3%)	43	43	38, 44, 52, 55	0
1	H	131/144 (90%)	0.24	6 (4%)	36	35	36, 44, 52, 59	0
1	I	128/144 (88%)	0.45	10 (7%)	16	14	37, 44, 52, 54	0
1	J	125/144 (86%)	0.13	3 (2%)	62	62	39, 45, 51, 53	0
1	K	127/144 (88%)	0.32	6 (4%)	35	34	35, 42, 51, 54	0
1	L	130/144 (90%)	0.28	4 (3%)	52	52	35, 42, 52, 57	0
1	M	125/144 (86%)	0.07	5 (4%)	42	41	36, 43, 51, 57	0
1	N	131/144 (90%)	0.33	6 (4%)	36	35	38, 45, 51, 55	0
All	All	1787/2016 (88%)	0.24	77 (4%)	39	38	33, 44, 52, 66	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	341	GLU	5.1
1	K	443	MET	5.0
1	K	441	SER	4.9
1	N	336	THR	4.8
1	D	343	VAL	4.6
1	L	343	VAL	4.6
1	F	459	ASP	4.6
1	D	342	ASP	4.4

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Mol	Chain	Res	Type	RSRZ
1	I	440	GLY	4.3
1	I	338	ILE	4.3
1	G	341	GLU	4.2
1	E	441	SER	4.2
1	F	402	ALA	4.1
1	A	440	GLY	4.0
1	L	340	ASP	3.9
1	E	440	GLY	3.8
1	F	440	GLY	3.7
1	M	459	ASP	3.6
1	D	440	GLY	3.4
1	I	341	GLU	3.4
1	H	440	GLY	3.4
1	H	422	VAL	3.4
1	J	343	VAL	3.3
1	H	343	VAL	3.2
1	I	342	ASP	3.2
1	B	340	ASP	3.2
1	N	423	GLY	3.2
1	G	440	GLY	3.1
1	I	442	GLY	3.1
1	M	407	ASN	3.0
1	M	343	VAL	3.0
1	D	459	ASP	3.0
1	J	441	SER	2.9
1	G	342	ASP	2.9
1	F	410	ILE	2.9
1	B	440	GLY	2.9
1	C	343	VAL	2.8
1	C	440	GLY	2.8
1	N	338	ILE	2.8
1	D	443	MET	2.7
1	E	338	ILE	2.7
1	B	341	GLU	2.7
1	I	340	ASP	2.7
1	N	337	THR	2.7
1	F	408	LYS	2.6
1	K	440	GLY	2.6
1	L	440	GLY	2.6
1	A	443	MET	2.6
1	D	441	SER	2.5
1	J	366	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	402	ALA	2.5
1	K	342	ASP	2.4
1	N	422	VAL	2.4
1	F	398	TYR	2.4
1	I	441	SER	2.3
1	M	441	SER	2.3
1	H	441	SER	2.3
1	A	363	ASN	2.2
1	N	443	MET	2.2
1	C	409	PRO	2.2
1	I	339	GLU	2.2
1	A	340	ASP	2.2
1	C	342	ASP	2.2
1	L	342	ASP	2.2
1	G	407	ASN	2.2
1	E	342	ASP	2.2
1	G	402	ALA	2.2
1	I	409	PRO	2.1
1	C	442	GLY	2.1
1	H	426	ALA	2.1
1	K	422	VAL	2.1
1	K	343	VAL	2.1
1	H	442	GLY	2.0
1	E	339	GLU	2.0
1	I	343	VAL	2.0
1	E	442	GLY	2.0
1	M	440	GLY	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	ACT	K	632	4/4	0.79	0.30	3.93	45,48,48,48	0
2	ACT	C	632	4/4	0.76	0.30	3.66	55,58,58,58	0
2	ACT	E	632	4/4	0.76	0.30	3.42	63,65,65,65	0
2	ACT	B	632	4/4	0.76	0.21	3.17	48,51,51,51	0
2	ACT	I	632	4/4	0.68	0.27	2.70	65,67,67,68	0
2	ACT	D	632	4/4	0.77	0.29	2.36	52,55,55,55	0
2	ACT	A	632	4/4	0.90	0.26	2.07	50,51,52,53	0
2	ACT	M	632	4/4	0.89	0.21	1.71	67,67,68,68	0
2	ACT	L	632	4/4	0.87	0.20	1.59	56,57,57,58	0
2	ACT	N	632	4/4	0.87	0.21	1.04	74,76,76,76	0
2	ACT	J	632	4/4	0.88	0.20	0.76	60,62,62,62	0
2	ACT	H	632	4/4	0.76	0.20	0.70	54,56,56,57	0
2	ACT	F	632	4/4	0.87	0.17	-0.37	67,68,68,68	0
2	ACT	G	632	4/4	0.90	0.16	-0.72	58,58,59,59	0
3	CD	H	1472	1/1	0.90	0.14	-	78,78,78,78	1
3	CD	F	1472	1/1	0.74	0.13	-	96,96,96,96	1
3	CD	J	1474	1/1	0.81	0.13	-	94,94,94,94	1
3	CD	B	1472	1/1	0.87	0.18	-	82,82,82,82	1
3	CD	J	1472	1/1	0.72	0.17	-	79,79,79,79	1
3	CD	J	1473	1/1	0.94	0.11	-	77,77,77,77	1

6.5 Other polymers (i)

There are no such residues in this entry.