wwPDB EM Map/Model Validation Report (i)

May 2, 2016 – 05:34 PM EDT

PDB ID	:	3JCZ
EMDB ID:	:	EMD-6630
Title	:	Structure of bovine glutamate dehydrogenase in the unliganded state
Authors	:	Borgnia, M.J.; Banerjee, S.; Merk, A.; Matthies, D.; Bartesaghi, A.; Rao, P.; Pierson, J.; Earl, L.A.; Falconieri, V.; Subramaniam, S.; Milne, J.L.S.
Deposited on	:	2016-03-27
Resolution	:	3.26 Å(reported)
Based on PDB ID	:	3MW9

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/EMValidationReportHelp

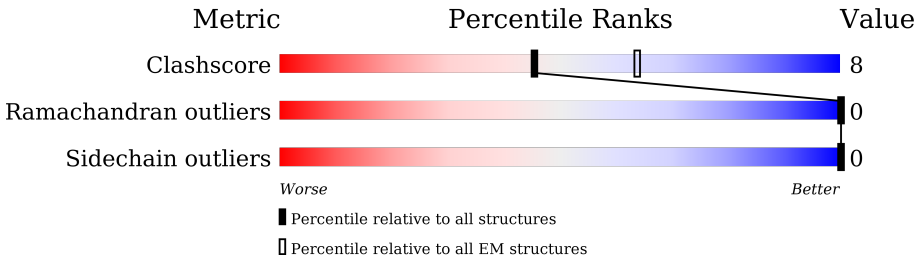
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027457

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.26 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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726
Sidechain outliers	111093	686

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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%

Mol	Chain	Length	Quality of chain
1	A	501	78% 21% .
1	B	501	78% 21% .
1	C	501	79% 20% .
1	D	501	78% 21% .
1	E	501	78% 21% .
1	F	501	78% 21% .

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 23286 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Glutamate dehydrogenase 1, mitochondrial.

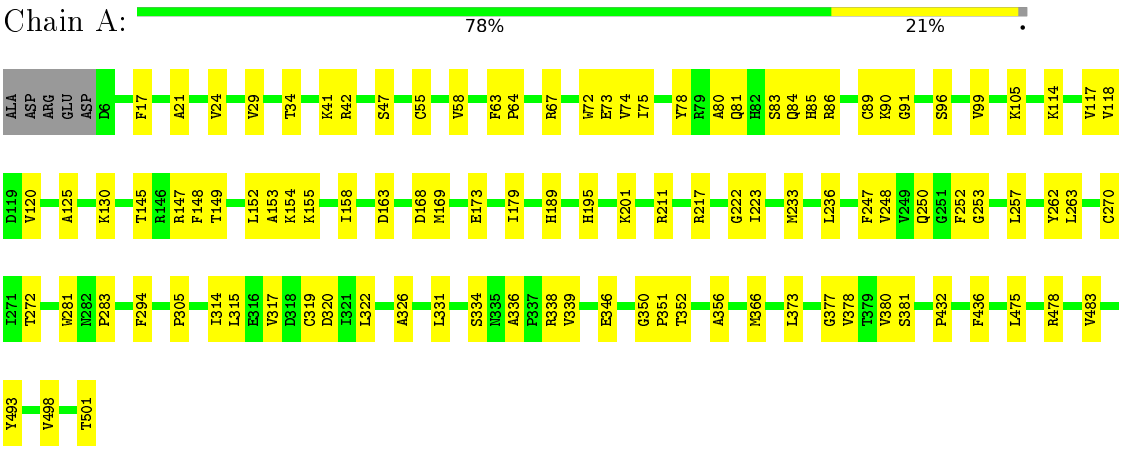
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	496	Total	C	N	O	S	0	0
			3881	2454	679	729	19		
1	B	496	Total	C	N	O	S	0	0
			3881	2454	679	729	19		
1	C	496	Total	C	N	O	S	0	0
			3881	2454	679	729	19		
1	D	496	Total	C	N	O	S	0	0
			3881	2454	679	729	19		
1	E	496	Total	C	N	O	S	0	0
			3881	2454	679	729	19		
1	F	496	Total	C	N	O	S	0	0
			3881	2454	679	729	19		

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. 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. 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.

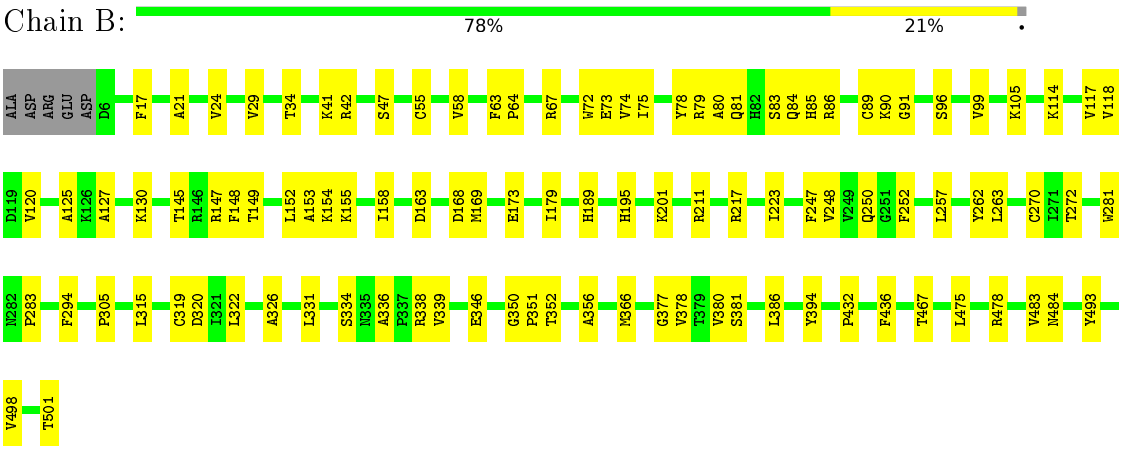
- Molecule 1: Glutamate dehydrogenase 1, mitochondrial

Chain A:



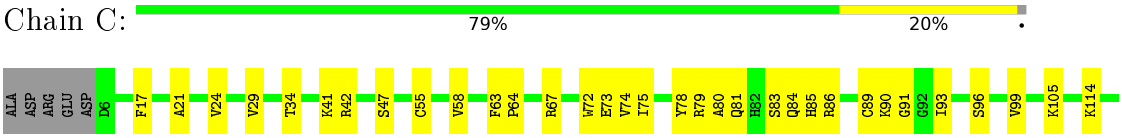
- Molecule 1: Glutamate dehydrogenase 1, mitochondrial

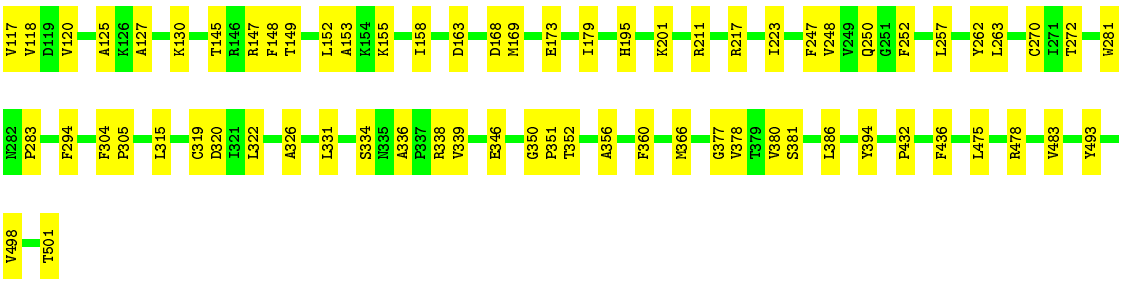
Chain B:



- Molecule 1: Glutamate dehydrogenase 1, mitochondrial

Chain C:





• Molecule 1: Glutamate dehydrogenase 1, mitochondrial

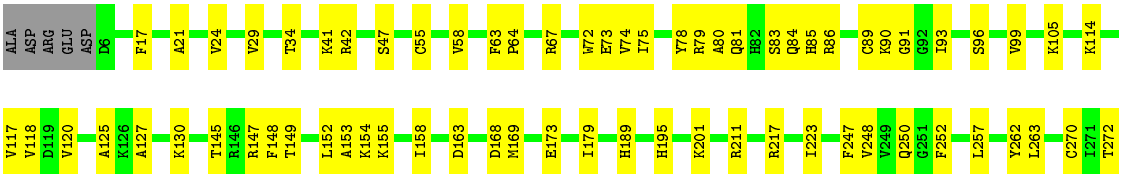
Chain D:

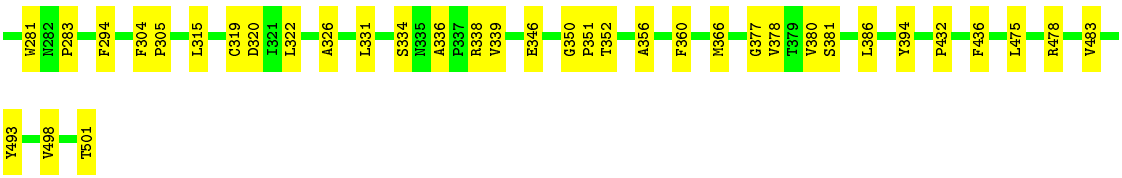
• Molecule 1: Glutamate dehydrogenase 1, mitochondrial

Chain E:

• Molecule 1: Glutamate dehydrogenase 1, mitochondrial

Chain F:




W281
N282
P283
F294
F304
P305
L315
C319
D320
T321
L322
A326
L331
S334
N335
A336
P337
R338
V339
E346
G350
P351
T352
A356
F360
M366
G377
V378
T379
Y380
S381
L386
Y394
P432
F436
L475
R478
V483
Y493
V498
T501

4 Experimental information (i)

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	Each micrograph	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	45	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality

5.1 Standard geometry

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	$\#\|Z\| > 2$	RMSZ	$\#\|Z\| > 2$
1	A	0.41	0/3964	0.48	0/5351
1	B	0.41	0/3964	0.48	0/5351
1	C	0.41	0/3964	0.48	0/5351
1	D	0.41	0/3964	0.48	0/5351
1	E	0.41	0/3964	0.48	0/5351
1	F	0.41	0/3964	0.48	0/5351
All	All	0.41	0/23784	0.48	0/32106

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	3881	0	3848	68	0
1	B	3881	0	3848	66	0
1	C	3881	0	3848	67	0
1	D	3881	0	3848	68	0
1	E	3881	0	3848	66	0
1	F	3881	0	3848	69	0
All	All	23286	0	23088	376	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (376) 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:72:TRP:HB2	1:E:47:SER:HB2	1.54	0.90
1:B:47:SER:HB2	1:D:72:TRP:HB2	1.54	0.89
1:C:47:SER:HB2	1:F:72:TRP:HB2	1.53	0.88
1:A:47:SER:HB2	1:E:72:TRP:HB2	1.54	0.88
1:B:72:TRP:HB2	1:D:47:SER:HB2	1.54	0.88
1:C:72:TRP:HB2	1:F:47:SER:HB2	1.55	0.86
1:C:319:CYS:SG	1:C:320:ASP:N	2.64	0.71
1:F:319:CYS:SG	1:F:320:ASP:N	2.64	0.71
1:E:319:CYS:SG	1:E:320:ASP:N	2.64	0.71
1:B:319:CYS:SG	1:B:320:ASP:N	2.64	0.71
1:A:319:CYS:SG	1:A:320:ASP:N	2.64	0.70
1:D:319:CYS:SG	1:D:320:ASP:N	2.64	0.70
1:D:81:GLN:NE2	1:D:163:ASP:OD2	2.26	0.68
1:A:81:GLN:NE2	1:A:163:ASP:OD2	2.26	0.68
1:D:83:SER:OG	1:D:85:HIS:ND1	2.24	0.65
1:B:83:SER:OG	1:B:85:HIS:ND1	2.25	0.64
1:C:83:SER:OG	1:C:85:HIS:ND1	2.24	0.64
1:F:81:GLN:NE2	1:F:163:ASP:OD2	2.26	0.64
1:F:83:SER:OG	1:F:85:HIS:ND1	2.24	0.64
1:B:195:HIS:O	1:B:201:LYS:NZ	2.30	0.63
1:C:81:GLN:NE2	1:C:163:ASP:OD2	2.26	0.63
1:E:195:HIS:O	1:E:201:LYS:NZ	2.30	0.63
1:A:195:HIS:O	1:A:201:LYS:NZ	2.30	0.62
1:B:432:PRO:HB3	1:B:436:PHE:HD2	1.65	0.62
1:E:432:PRO:HB3	1:E:436:PHE:HD2	1.65	0.62
1:A:432:PRO:HB3	1:A:436:PHE:HD2	1.65	0.61
1:D:195:HIS:O	1:D:201:LYS:NZ	2.30	0.61
1:E:83:SER:OG	1:E:85:HIS:ND1	2.25	0.61
1:A:58:VAL:HG21	1:A:105:LYS:HE2	1.82	0.61
1:A:223:ILE:HD11	1:A:263:LEU:HD21	1.82	0.61
1:D:58:VAL:HG21	1:D:105:LYS:HE2	1.82	0.61
1:A:81:GLN:OE1	1:A:84:GLN:NE2	2.33	0.61
1:D:223:ILE:HD11	1:D:263:LEU:HD21	1.82	0.61
1:D:81:GLN:OE1	1:D:84:GLN:NE2	2.33	0.61
1:D:432:PRO:HB3	1:D:436:PHE:HD2	1.65	0.61
1:F:58:VAL:HG21	1:F:105:LYS:HE2	1.82	0.61
1:C:58:VAL:HG21	1:C:105:LYS:HE2	1.82	0.61
1:C:432:PRO:HB3	1:C:436:PHE:HD2	1.65	0.61
1:F:223:ILE:HD11	1:F:263:LEU:HD21	1.82	0.61
1:F:432:PRO:HB3	1:F:436:PHE:HD2	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:81:GLN:NE2	1:E:163:ASP:OD2	2.26	0.61
1:B:81:GLN:NE2	1:B:163:ASP:OD2	2.26	0.61
1:C:223:ILE:HD11	1:C:263:LEU:HD21	1.82	0.61
1:C:81:GLN:OE1	1:C:84:GLN:NE2	2.33	0.60
1:F:81:GLN:OE1	1:F:84:GLN:NE2	2.33	0.60
1:C:195:HIS:O	1:C:201:LYS:NZ	2.30	0.60
1:A:83:SER:OG	1:A:85:HIS:ND1	2.24	0.60
1:F:195:HIS:O	1:F:201:LYS:NZ	2.30	0.60
1:E:58:VAL:HG21	1:E:105:LYS:HE2	1.82	0.59
1:B:58:VAL:HG21	1:B:105:LYS:HE2	1.82	0.59
1:B:223:ILE:HD11	1:B:263:LEU:HD21	1.82	0.59
1:B:81:GLN:OE1	1:B:84:GLN:NE2	2.33	0.59
1:D:83:SER:HG	1:D:85:HIS:HD1	1.47	0.59
1:E:223:ILE:HD11	1:E:263:LEU:HD21	1.82	0.59
1:A:85:HIS:CD2	1:A:86:ARG:HG3	2.38	0.59
1:E:81:GLN:OE1	1:E:84:GLN:NE2	2.33	0.59
1:C:85:HIS:CD2	1:C:86:ARG:HG3	2.38	0.59
1:D:85:HIS:CD2	1:D:86:ARG:HG3	2.38	0.59
1:F:85:HIS:CD2	1:F:86:ARG:HG3	2.38	0.59
1:B:168:ASP:OD1	1:B:169:MET:N	2.36	0.59
1:B:85:HIS:CD2	1:B:86:ARG:HG3	2.38	0.59
1:C:114:LYS:HE3	1:C:378:VAL:HG21	1.85	0.59
1:D:114:LYS:HE3	1:D:378:VAL:HG21	1.85	0.59
1:D:78:TYR:HE2	1:D:130:LYS:HE3	1.68	0.59
1:A:114:LYS:HE3	1:A:378:VAL:HG21	1.85	0.59
1:E:168:ASP:OD1	1:E:169:MET:N	2.36	0.59
1:E:85:HIS:CD2	1:E:86:ARG:HG3	2.38	0.59
1:A:78:TYR:HE2	1:A:130:LYS:HE3	1.68	0.58
1:F:114:LYS:HE3	1:F:378:VAL:HG21	1.85	0.58
1:B:114:LYS:HE3	1:B:378:VAL:HG21	1.85	0.58
1:E:114:LYS:HE3	1:E:378:VAL:HG21	1.85	0.58
1:B:89:CYS:HB2	1:B:163:ASP:OD1	2.04	0.58
1:C:117:VAL:HG23	1:C:118:VAL:HG13	1.85	0.58
1:E:89:CYS:HB2	1:E:163:ASP:OD1	2.04	0.58
1:F:117:VAL:HG23	1:F:118:VAL:HG13	1.85	0.57
1:B:334:SER:O	1:B:338:ARG:NH2	2.37	0.57
1:E:334:SER:O	1:E:338:ARG:NH2	2.37	0.57
1:D:117:VAL:HG23	1:D:118:VAL:HG13	1.85	0.57
1:E:117:VAL:HG23	1:E:118:VAL:HG13	1.85	0.57
1:A:117:VAL:HG23	1:A:118:VAL:HG13	1.85	0.57
1:B:117:VAL:HG23	1:B:118:VAL:HG13	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:78:TYR:HE2	1:B:130:LYS:HE3	1.68	0.57
1:F:334:SER:O	1:F:338:ARG:NH2	2.37	0.57
1:A:89:CYS:HB2	1:A:163:ASP:OD1	2.04	0.57
1:C:334:SER:O	1:C:338:ARG:NH2	2.37	0.57
1:C:89:CYS:HB2	1:C:163:ASP:OD1	2.04	0.57
1:F:89:CYS:HB2	1:F:163:ASP:OD1	2.04	0.57
1:D:89:CYS:HB2	1:D:163:ASP:OD1	2.04	0.57
1:E:78:TYR:HE2	1:E:130:LYS:HE3	1.68	0.57
1:A:334:SER:O	1:A:338:ARG:NH2	2.37	0.57
1:F:78:TYR:HE2	1:F:130:LYS:HE3	1.68	0.57
1:A:346:GLU:OE2	1:A:478:ARG:NH2	2.38	0.57
1:D:346:GLU:OE2	1:D:478:ARG:NH2	2.38	0.57
1:D:334:SER:O	1:D:338:ARG:NH2	2.37	0.57
1:F:346:GLU:OE2	1:F:478:ARG:NH2	2.38	0.57
1:C:78:TYR:HE2	1:C:130:LYS:HE3	1.68	0.56
1:C:346:GLU:OE2	1:C:478:ARG:NH2	2.38	0.56
1:B:346:GLU:OE2	1:B:478:ARG:NH2	2.38	0.56
1:E:346:GLU:OE2	1:E:478:ARG:NH2	2.38	0.56
1:F:432:PRO:HB3	1:F:436:PHE:CD2	2.41	0.56
1:C:432:PRO:HB3	1:C:436:PHE:CD2	2.41	0.56
1:C:168:ASP:OD1	1:C:169:MET:N	2.36	0.56
1:F:168:ASP:OD1	1:F:169:MET:N	2.36	0.55
1:A:432:PRO:HB3	1:A:436:PHE:CD2	2.41	0.55
1:D:432:PRO:HB3	1:D:436:PHE:CD2	2.41	0.55
1:A:168:ASP:OD1	1:A:169:MET:N	2.36	0.54
1:F:366:MET:HB2	1:F:475:LEU:HD22	1.89	0.54
1:C:366:MET:HB2	1:C:475:LEU:HD22	1.89	0.54
1:F:83:SER:HG	1:F:85:HIS:HD1	1.51	0.54
1:D:168:ASP:OD1	1:D:169:MET:N	2.36	0.54
1:E:64:PRO:HD2	1:E:147:ARG:HE	1.73	0.54
1:B:64:PRO:HD2	1:B:147:ARG:HE	1.72	0.54
1:E:432:PRO:HB3	1:E:436:PHE:CD2	2.41	0.54
1:B:432:PRO:HB3	1:B:436:PHE:CD2	2.41	0.54
1:A:64:PRO:HD2	1:A:147:ARG:HE	1.73	0.54
1:D:64:PRO:HD2	1:D:147:ARG:HE	1.73	0.54
1:F:64:PRO:HD2	1:F:147:ARG:HE	1.72	0.53
1:C:64:PRO:HD2	1:C:147:ARG:HE	1.73	0.53
1:D:366:MET:HB2	1:D:475:LEU:HD22	1.89	0.53
1:A:366:MET:HB2	1:A:475:LEU:HD22	1.89	0.53
1:C:83:SER:HG	1:C:85:HIS:HD1	1.52	0.53
1:B:366:MET:HB2	1:B:475:LEU:HD22	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:366:MET:HB2	1:E:475:LEU:HD22	1.89	0.52
1:C:315:LEU:HD13	1:C:331:LEU:HD13	1.91	0.52
1:F:315:LEU:HD13	1:F:331:LEU:HD13	1.91	0.52
1:B:149:THR:O	1:B:153:ALA:N	2.40	0.52
1:E:149:THR:O	1:E:153:ALA:N	2.40	0.52
1:A:281:TRP:CE2	1:A:283:PRO:HD3	2.45	0.52
1:B:315:LEU:HD13	1:B:331:LEU:HD13	1.91	0.52
1:D:315:LEU:HD13	1:D:331:LEU:HD13	1.91	0.52
1:E:315:LEU:HD13	1:E:331:LEU:HD13	1.91	0.52
1:A:315:LEU:HD13	1:A:331:LEU:HD13	1.91	0.52
1:C:281:TRP:CE2	1:C:283:PRO:HD3	2.45	0.52
1:F:281:TRP:CE2	1:F:283:PRO:HD3	2.45	0.52
1:B:281:TRP:CE2	1:B:283:PRO:HD3	2.45	0.52
1:C:149:THR:O	1:C:153:ALA:N	2.40	0.52
1:D:281:TRP:CE2	1:D:283:PRO:HD3	2.45	0.52
1:F:149:THR:O	1:F:153:ALA:N	2.40	0.52
1:E:281:TRP:CE2	1:E:283:PRO:HD3	2.45	0.52
1:D:352:THR:HG23	1:D:356:ALA:HB3	1.92	0.51
1:A:352:THR:HG23	1:A:356:ALA:HB3	1.92	0.51
1:B:352:THR:HG23	1:B:356:ALA:HB3	1.92	0.51
1:F:90:LYS:HD2	1:F:381:SER:OG	2.11	0.51
1:C:352:THR:HG23	1:C:356:ALA:HB3	1.92	0.51
1:C:90:LYS:HD2	1:C:381:SER:OG	2.11	0.51
1:E:352:THR:HG23	1:E:356:ALA:HB3	1.92	0.51
1:F:352:THR:HG23	1:F:356:ALA:HB3	1.92	0.51
1:B:90:LYS:HD2	1:B:381:SER:OG	2.11	0.51
1:A:63:PHE:CZ	1:A:148:PHE:HD1	2.29	0.51
1:D:63:PHE:CZ	1:D:148:PHE:HD1	2.29	0.51
1:E:90:LYS:HD2	1:E:381:SER:OG	2.11	0.50
1:B:24:VAL:HB	1:B:483:VAL:HG13	1.93	0.50
1:D:24:VAL:HB	1:D:483:VAL:HG13	1.93	0.50
1:A:24:VAL:HB	1:A:483:VAL:HG13	1.93	0.50
1:E:24:VAL:HB	1:E:483:VAL:HG13	1.93	0.50
1:F:24:VAL:HB	1:F:483:VAL:HG13	1.93	0.50
1:F:63:PHE:CZ	1:F:148:PHE:HD1	2.29	0.50
1:C:24:VAL:HB	1:C:483:VAL:HG13	1.94	0.50
1:C:63:PHE:CZ	1:C:148:PHE:HD1	2.29	0.50
1:B:63:PHE:CZ	1:B:148:PHE:HD1	2.29	0.49
1:A:90:LYS:HD2	1:A:381:SER:OG	2.11	0.49
1:B:34:THR:HG22	1:B:41:LYS:HE2	1.95	0.49
1:D:90:LYS:HD2	1:D:381:SER:OG	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:63:PHE:CZ	1:E:148:PHE:HD1	2.29	0.49
1:E:34:THR:HG22	1:E:41:LYS:HE2	1.95	0.49
1:D:217:ARG:HD3	1:D:262:TYR:CZ	2.48	0.49
1:A:217:ARG:HD3	1:A:262:TYR:CZ	2.48	0.49
1:E:217:ARG:HD3	1:E:262:TYR:CZ	2.48	0.49
1:B:217:ARG:HD3	1:B:262:TYR:CZ	2.48	0.49
1:A:63:PHE:HB2	1:A:75:ILE:HB	1.95	0.49
1:D:63:PHE:HB2	1:D:75:ILE:HB	1.95	0.49
1:A:34:THR:HG22	1:A:41:LYS:HE2	1.94	0.48
1:A:377:GLY:HA2	1:A:380:VAL:HG22	1.96	0.48
1:C:34:THR:HG22	1:C:41:LYS:HE2	1.95	0.48
1:D:377:GLY:HA2	1:D:380:VAL:HG22	1.96	0.48
1:D:34:THR:HG22	1:D:41:LYS:HE2	1.94	0.48
1:F:34:THR:HG22	1:F:41:LYS:HE2	1.94	0.48
1:C:377:GLY:HA2	1:C:380:VAL:HG22	1.96	0.48
1:F:377:GLY:HA2	1:F:380:VAL:HG22	1.96	0.48
1:C:217:ARG:HD3	1:C:262:TYR:CZ	2.48	0.48
1:F:217:ARG:HD3	1:F:262:TYR:CZ	2.48	0.48
1:C:63:PHE:HB2	1:C:75:ILE:HB	1.95	0.48
1:F:17:PHE:O	1:F:21:ALA:N	2.45	0.48
1:F:63:PHE:HB2	1:F:75:ILE:HB	1.95	0.48
1:C:17:PHE:O	1:C:21:ALA:N	2.45	0.48
1:E:29:VAL:HG21	1:E:42:ARG:HD3	1.96	0.48
1:B:29:VAL:HG21	1:B:42:ARG:HD3	1.96	0.48
1:C:29:VAL:HG21	1:C:42:ARG:HD3	1.96	0.48
1:F:29:VAL:HG21	1:F:42:ARG:HD3	1.96	0.48
1:A:29:VAL:HG21	1:A:42:ARG:HD3	1.96	0.47
1:B:63:PHE:HB2	1:B:75:ILE:HB	1.95	0.47
1:D:29:VAL:HG21	1:D:42:ARG:HD3	1.96	0.47
1:E:63:PHE:HB2	1:E:75:ILE:HB	1.95	0.47
1:B:377:GLY:HA2	1:B:380:VAL:HG22	1.96	0.47
1:E:377:GLY:HA2	1:E:380:VAL:HG22	1.96	0.47
1:C:493:TYR:HB3	1:C:498:VAL:HG22	1.97	0.47
1:C:498:VAL:HB	1:F:72:TRP:CH2	2.49	0.47
1:B:294:PHE:CE1	1:B:305:PRO:HD3	2.51	0.46
1:E:294:PHE:CE1	1:E:305:PRO:HD3	2.51	0.46
1:F:493:TYR:HB3	1:F:498:VAL:HG22	1.97	0.46
1:A:498:VAL:HB	1:E:72:TRP:CH2	2.50	0.46
1:B:72:TRP:CH2	1:D:498:VAL:HB	2.50	0.46
1:A:72:TRP:CH2	1:E:498:VAL:HB	2.50	0.46
1:E:17:PHE:O	1:E:21:ALA:N	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:THR:HG21	1:A:179:ILE:HG23	1.98	0.46
1:D:149:THR:HG21	1:D:179:ILE:HG23	1.98	0.46
1:B:498:VAL:HB	1:D:72:TRP:CH2	2.50	0.46
1:F:294:PHE:CE1	1:F:305:PRO:HD3	2.51	0.46
1:A:294:PHE:CE1	1:A:305:PRO:HD3	2.51	0.46
1:B:17:PHE:O	1:B:21:ALA:N	2.45	0.46
1:C:294:PHE:CE1	1:C:305:PRO:HD3	2.51	0.46
1:B:149:THR:HG21	1:B:179:ILE:HG23	1.98	0.46
1:D:294:PHE:CE1	1:D:305:PRO:HD3	2.51	0.46
1:E:149:THR:HG21	1:E:179:ILE:HG23	1.98	0.46
1:D:493:TYR:HB3	1:D:498:VAL:HG22	1.97	0.45
1:A:493:TYR:HB3	1:A:498:VAL:HG22	1.97	0.45
1:C:63:PHE:HZ	1:C:148:PHE:HD1	1.65	0.45
1:D:17:PHE:O	1:D:21:ALA:N	2.45	0.45
1:F:63:PHE:HZ	1:F:148:PHE:HD1	1.65	0.45
1:A:149:THR:O	1:A:153:ALA:N	2.40	0.45
1:B:493:TYR:HB3	1:B:498:VAL:HG22	1.97	0.45
1:C:149:THR:HG21	1:C:179:ILE:HG23	1.98	0.45
1:D:63:PHE:HZ	1:D:148:PHE:HD1	1.65	0.45
1:E:493:TYR:HB3	1:E:498:VAL:HG22	1.97	0.45
1:F:149:THR:HG21	1:F:179:ILE:HG23	1.98	0.45
1:A:17:PHE:O	1:A:21:ALA:N	2.45	0.45
1:A:63:PHE:HZ	1:A:148:PHE:HD1	1.65	0.45
1:C:72:TRP:CH2	1:F:498:VAL:HB	2.51	0.45
1:D:149:THR:O	1:D:153:ALA:N	2.40	0.45
1:D:117:VAL:O	1:D:460:SER:OG	2.31	0.44
1:D:252:PHE:CZ	1:D:257:LEU:HD13	2.52	0.44
1:A:252:PHE:CZ	1:A:257:LEU:HD13	2.52	0.44
1:E:252:PHE:CZ	1:E:257:LEU:HD13	2.52	0.44
1:A:152:LEU:HD23	1:A:158:ILE:HD11	2.00	0.44
1:B:252:PHE:CZ	1:B:257:LEU:HD13	2.52	0.44
1:E:217:ARG:HD3	1:E:262:TYR:CE1	2.53	0.44
1:F:152:LEU:HD23	1:F:158:ILE:HD11	2.00	0.44
1:F:252:PHE:CZ	1:F:257:LEU:HD13	2.52	0.44
1:C:252:PHE:CZ	1:C:257:LEU:HD13	2.52	0.44
1:D:152:LEU:HD23	1:D:158:ILE:HD11	2.00	0.44
1:B:217:ARG:HD3	1:B:262:TYR:CE1	2.53	0.44
1:E:63:PHE:HZ	1:E:148:PHE:HD1	1.65	0.44
1:F:217:ARG:HD3	1:F:262:TYR:CE1	2.53	0.44
1:C:152:LEU:HD23	1:C:158:ILE:HD11	2.00	0.44
1:C:217:ARG:HD3	1:C:262:TYR:CE1	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:ARG:HD3	1:A:262:TYR:CE1	2.53	0.44
1:B:63:PHE:HZ	1:B:148:PHE:HD1	1.65	0.44
1:D:217:ARG:HD3	1:D:262:TYR:CE1	2.53	0.44
1:B:152:LEU:HD23	1:B:158:ILE:HD11	2.00	0.43
1:B:67:ARG:HD3	1:B:73:GLU:OE2	2.18	0.43
1:C:67:ARG:HD3	1:C:73:GLU:OE2	2.18	0.43
1:D:67:ARG:HD3	1:D:73:GLU:OE2	2.18	0.43
1:E:152:LEU:HD23	1:E:158:ILE:HD11	2.00	0.43
1:F:67:ARG:HD3	1:F:73:GLU:OE2	2.18	0.43
1:A:67:ARG:HD3	1:A:73:GLU:OE2	2.18	0.43
1:E:67:ARG:HD3	1:E:73:GLU:OE2	2.18	0.43
1:A:173:GLU:OE2	1:A:211:ARG:NH2	2.52	0.43
1:A:233:MET:HE1	1:A:236:LEU:HD12	2.01	0.43
1:D:173:GLU:OE2	1:D:211:ARG:NH2	2.52	0.43
1:D:233:MET:HE1	1:D:236:LEU:HD12	2.01	0.43
1:E:173:GLU:OE2	1:E:211:ARG:NH2	2.52	0.43
1:B:173:GLU:OE2	1:B:211:ARG:NH2	2.52	0.43
1:F:96:SER:HB3	1:F:99:VAL:HG23	2.01	0.43
1:B:55:CYS:SG	1:B:80:ALA:HB1	2.59	0.43
1:C:96:SER:HB3	1:C:99:VAL:HG23	2.01	0.43
1:D:55:CYS:SG	1:D:80:ALA:HB1	2.59	0.43
1:E:55:CYS:SG	1:E:80:ALA:HB1	2.59	0.43
1:F:350:GLY:N	1:F:351:PRO:HD3	2.34	0.43
1:F:55:CYS:SG	1:F:80:ALA:HB1	2.59	0.43
1:A:55:CYS:SG	1:A:80:ALA:HB1	2.59	0.42
1:C:250:GLN:HG2	1:C:326:ALA:HB2	2.01	0.42
1:C:350:GLY:N	1:C:351:PRO:HD3	2.34	0.42
1:C:55:CYS:SG	1:C:80:ALA:HB1	2.59	0.42
1:F:250:GLN:HG2	1:F:326:ALA:HB2	2.01	0.42
1:D:350:GLY:N	1:D:351:PRO:HD3	2.34	0.42
1:F:173:GLU:OE2	1:F:211:ARG:NH2	2.52	0.42
1:A:350:GLY:N	1:A:351:PRO:HD3	2.34	0.42
1:B:91:GLY:HA3	1:B:125:ALA:O	2.20	0.42
1:B:155:LYS:NZ	1:D:81:GLN:HE22	2.17	0.42
1:B:350:GLY:N	1:B:351:PRO:HD3	2.34	0.42
1:C:173:GLU:OE2	1:C:211:ARG:NH2	2.52	0.42
1:E:91:GLY:HA3	1:E:125:ALA:O	2.20	0.42
1:A:118:VAL:HG23	1:A:120:VAL:HG23	2.02	0.42
1:A:81:GLN:HE22	1:E:155:LYS:NZ	2.18	0.42
1:C:118:VAL:HG23	1:C:120:VAL:HG23	2.02	0.42
1:E:350:GLY:N	1:E:351:PRO:HD3	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:118:VAL:HG23	1:F:120:VAL:HG23	2.02	0.42
1:B:96:SER:HB3	1:B:99:VAL:HG23	2.01	0.42
1:D:118:VAL:HG23	1:D:120:VAL:HG23	2.02	0.42
1:D:253:GLY:O	1:D:257:LEU:N	2.40	0.42
1:E:250:GLN:HG2	1:E:326:ALA:HB2	2.01	0.42
1:E:96:SER:HB3	1:E:99:VAL:HG23	2.01	0.42
1:A:78:TYR:CE2	1:A:130:LYS:HE3	2.53	0.42
1:A:96:SER:HB3	1:A:99:VAL:HG23	2.01	0.42
1:B:250:GLN:HG2	1:B:326:ALA:HB2	2.01	0.42
1:C:81:GLN:HE22	1:F:155:LYS:NZ	2.18	0.42
1:D:78:TYR:CE2	1:D:130:LYS:HE3	2.53	0.42
1:F:145:THR:O	1:F:149:THR:HG23	2.20	0.42
1:A:253:GLY:O	1:A:257:LEU:N	2.40	0.41
1:A:91:GLY:HA3	1:A:125:ALA:O	2.20	0.41
1:C:272:THR:HG22	1:C:281:TRP:HD1	1.85	0.41
1:D:96:SER:HB3	1:D:99:VAL:HG23	2.01	0.41
1:F:272:THR:HG22	1:F:281:TRP:HD1	1.85	0.41
1:C:145:THR:O	1:C:149:THR:HG23	2.20	0.41
1:C:63:PHE:O	1:C:74:VAL:HA	2.21	0.41
1:D:272:THR:HG22	1:D:281:TRP:HD1	1.85	0.41
1:D:91:GLY:HA3	1:D:125:ALA:O	2.20	0.41
1:E:248:VAL:HG23	1:E:322:LEU:HD23	2.02	0.41
1:B:272:THR:HG22	1:B:281:TRP:HD1	1.85	0.41
1:F:63:PHE:O	1:F:74:VAL:HA	2.21	0.41
1:A:250:GLN:HG2	1:A:326:ALA:HB2	2.01	0.41
1:A:272:THR:HG22	1:A:281:TRP:HD1	1.85	0.41
1:B:248:VAL:HG23	1:B:322:LEU:HD23	2.02	0.41
1:D:145:THR:O	1:D:149:THR:HG23	2.20	0.41
1:A:501:THR:HG23	1:D:501:THR:O	2.21	0.41
1:C:336:ALA:O	1:C:339:VAL:HG23	2.20	0.41
1:D:250:GLN:HG2	1:D:326:ALA:HB2	2.01	0.41
1:E:272:THR:HG22	1:E:281:TRP:HD1	1.86	0.41
1:C:501:THR:O	1:E:501:THR:HG23	2.21	0.41
1:A:145:THR:O	1:A:149:THR:HG23	2.20	0.41
1:C:386:LEU:HB2	1:C:394:TYR:OH	2.21	0.41
1:C:501:THR:HG23	1:E:501:THR:O	2.20	0.41
1:A:501:THR:O	1:D:501:THR:HG23	2.21	0.41
1:F:336:ALA:O	1:F:339:VAL:HG23	2.21	0.41
1:B:386:LEU:HB2	1:B:394:TYR:OH	2.21	0.41
1:B:467:THR:OG1	1:B:484:ASN:OD1	2.35	0.41
1:B:81:GLN:HE22	1:D:155:LYS:NZ	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:386:LEU:HB2	1:E:394:TYR:OH	2.21	0.41
1:A:155:LYS:NZ	1:E:81:GLN:HE22	2.18	0.41
1:F:386:LEU:HB2	1:F:394:TYR:OH	2.21	0.41
1:B:501:THR:O	1:F:501:THR:HG23	2.21	0.41
1:C:155:LYS:NZ	1:F:81:GLN:HE22	2.19	0.41
1:A:154:LYS:HD2	1:F:189:HIS:CE1	2.56	0.41
1:A:248:VAL:HG23	1:A:322:LEU:HD23	2.02	0.41
1:A:314:ILE:HA	1:A:317:VAL:HG23	2.02	0.41
1:B:501:THR:HG23	1:F:501:THR:O	2.21	0.41
1:D:248:VAL:HG23	1:D:322:LEU:HD23	2.02	0.41
1:E:118:VAL:HG23	1:E:120:VAL:HG23	2.02	0.41
1:B:118:VAL:HG23	1:B:120:VAL:HG23	2.02	0.41
1:C:79:ARG:HH11	1:C:127:ALA:HB2	1.86	0.41
1:C:356:ALA:O	1:C:360:PHE:N	2.52	0.41
1:D:247:PHE:CZ	1:D:270:CYS:HB2	2.56	0.41
1:E:79:ARG:HH11	1:E:127:ALA:HB2	1.86	0.41
1:F:79:ARG:HH11	1:F:127:ALA:HB2	1.85	0.41
1:A:247:PHE:CZ	1:A:270:CYS:HB2	2.56	0.41
1:A:63:PHE:O	1:A:74:VAL:HA	2.21	0.41
1:B:79:ARG:HH11	1:B:127:ALA:HB2	1.86	0.41
1:B:63:PHE:O	1:B:74:VAL:HA	2.21	0.41
1:D:314:ILE:HA	1:D:317:VAL:HG23	2.02	0.41
1:D:63:PHE:O	1:D:74:VAL:HA	2.21	0.41
1:C:247:PHE:CZ	1:C:270:CYS:HB2	2.56	0.41
1:C:93:ILE:HG12	1:C:127:ALA:HB3	2.03	0.41
1:E:63:PHE:O	1:E:74:VAL:HA	2.21	0.41
1:F:93:ILE:HG12	1:F:127:ALA:HB3	2.03	0.41
1:F:247:PHE:CZ	1:F:270:CYS:HB2	2.56	0.41
1:F:356:ALA:O	1:F:360:PHE:N	2.52	0.41
1:B:145:THR:O	1:B:149:THR:HG23	2.20	0.40
1:B:336:ALA:O	1:B:339:VAL:HG23	2.20	0.40
1:C:248:VAL:HG23	1:C:322:LEU:HD23	2.02	0.40
1:B:189:HIS:CE1	1:E:154:LYS:HD2	2.56	0.40
1:A:222:GLY:HA3	1:A:373:LEU:HD23	2.03	0.40
1:B:154:LYS:HD2	1:E:189:HIS:CE1	2.56	0.40
1:C:91:GLY:HA3	1:C:125:ALA:O	2.20	0.40
1:E:145:THR:O	1:E:149:THR:HG23	2.20	0.40
1:F:248:VAL:HG23	1:F:322:LEU:HD23	2.02	0.40
1:F:91:GLY:HA3	1:F:125:ALA:O	2.20	0.40
1:A:336:ALA:O	1:A:339:VAL:HG23	2.20	0.40
1:C:304:PHE:HA	1:C:305:PRO:HD3	1.97	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:336:ALA:O	1:E:339:VAL:HG23	2.20	0.40
1:F:304:PHE:HA	1:F:305:PRO:HD3	1.97	0.40
1:B:247:PHE:CZ	1:B:270:CYS:HB2	2.56	0.40
1:D:222:GLY:HA3	1:D:373:LEU:HD23	2.03	0.40
1:D:336:ALA:O	1:D:339:VAL:HG23	2.21	0.40
1:E:247:PHE:CZ	1:E:270:CYS:HB2	2.56	0.40
1:E:314:ILE:HA	1:E:317:VAL:HG23	2.02	0.40
1:A:189:HIS:CE1	1:F:154:LYS:HD2	2.56	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 PDB entries followed by that with respect to all EM entries.

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	494/501 (99%)	460 (93%)	34 (7%)	0	100	100
1	B	494/501 (99%)	459 (93%)	35 (7%)	0	100	100
1	C	494/501 (99%)	459 (93%)	35 (7%)	0	100	100
1	D	494/501 (99%)	460 (93%)	34 (7%)	0	100	100
1	E	494/501 (99%)	459 (93%)	35 (7%)	0	100	100
1	F	494/501 (99%)	459 (93%)	35 (7%)	0	100	100
All	All	2964/3006 (99%)	2756 (93%)	208 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	416/420 (99%)	416 (100%)	0	100	100
1	B	416/420 (99%)	416 (100%)	0	100	100
1	C	416/420 (99%)	416 (100%)	0	100	100
1	D	416/420 (99%)	416 (100%)	0	100	100
1	E	416/420 (99%)	416 (100%)	0	100	100
1	F	416/420 (99%)	416 (100%)	0	100	100
All	All	2496/2520 (99%)	2496 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	330	GLN
1	A	391	HIS
1	B	330	GLN
1	B	391	HIS
1	C	330	GLN
1	C	391	HIS
1	D	330	GLN
1	D	391	HIS
1	E	330	GLN
1	E	391	HIS
1	F	330	GLN
1	F	391	HIS

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

There are no carbohydrates in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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.