Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 12:11 AM GMT

PDB ID	:	1ZZH
Title	:	Structure of the fully oxidized di-heme cytochrome c peroxidase from R. capsulatus
Authors	:	De Smet, L.; Savvides, S.N.; Van Horen, E.; Pettigrew, G.; Van Beeumen, J.J.
Deposited on	:	2005-06-14
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:

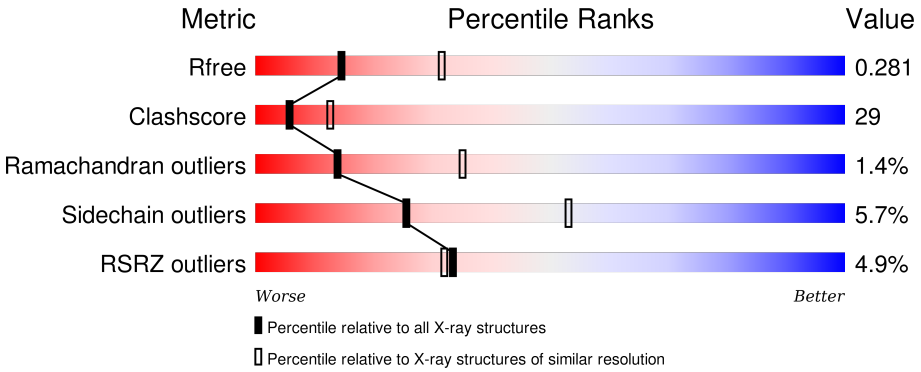
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance

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	328	5%, 54%, 33%, •, 9%
1	B	328	6%, 54%, 37%, •, 6%
1	C	328	3%, 55%, 35%, •, 6%
1	D	328	4%, 53%, 34%, •, 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	CA	B	501	-	-	-	X
2	CA	C	601	-	-	-	X

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 9290 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 cytochrome c peroxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	297	Total 2172	C 1382	N 367	O 412	S 11	0	0	0
1	B	308	Total 2277	C 1446	N 388	O 432	S 11	0	0	0
1	C	307	Total 2251	C 1429	N 384	O 427	S 11	0	0	0
1	D	298	Total 2198	C 1396	N 375	O 416	S 11	0	0	0

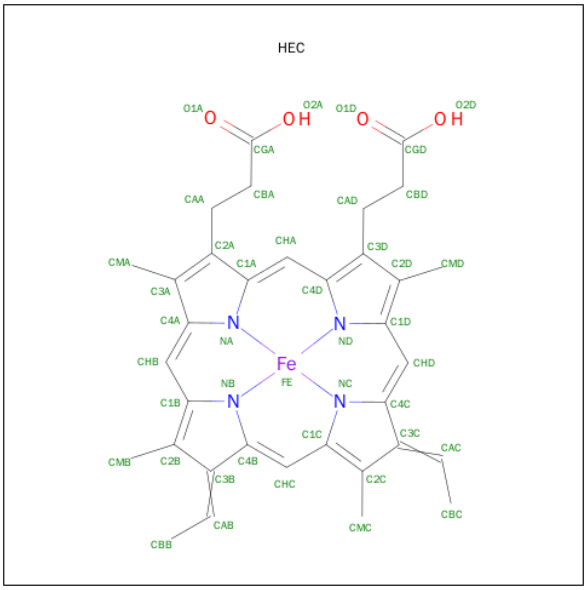
- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total 1	Ca 1	0	0
2	A	1	Total 1	Ca 1	0	0
2	D	1	Total 1	Ca 1	0	0
2	C	1	Total 1	Ca 1	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	4	Total 4	Zn 4	0	0
3	A	2	Total 2	Zn 2	0	0
3	D	1	Total 1	Zn 1	0	0
3	C	1	Total 1	Zn 1	0	0

- Molecule 4 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	9	Total	O	0	0
			9	9		
5	B	5	Total	O	0	0
			5	5		
5	C	15	Total	O	0	0
			15	15		

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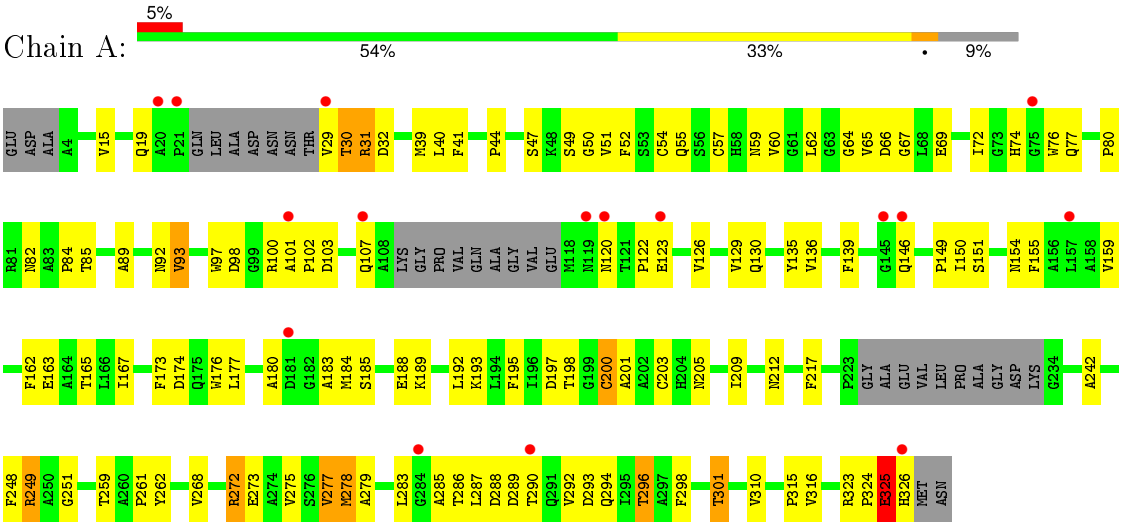
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	D	7	Total O 7 7	0	0

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.

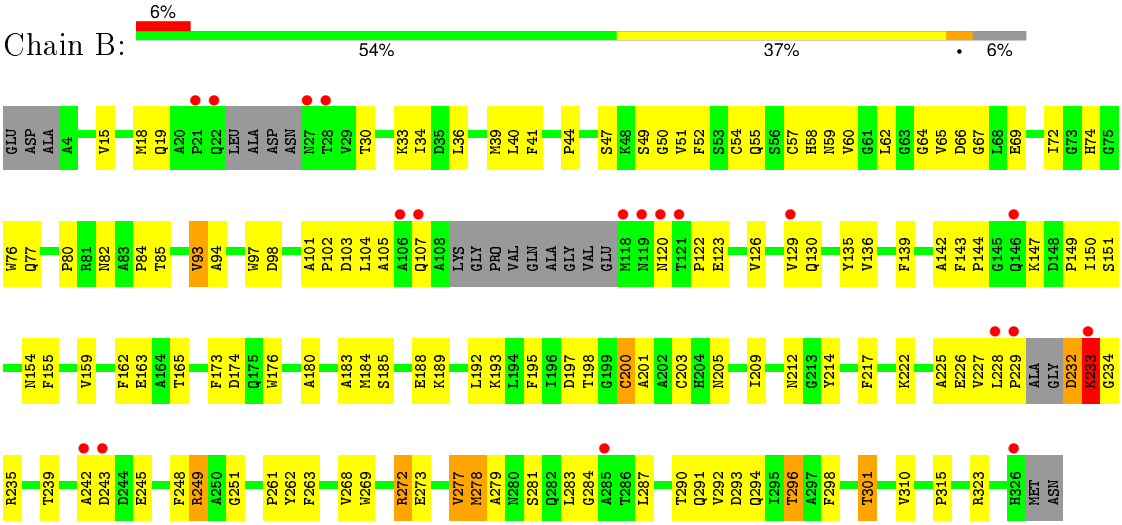
- Molecule 1: cytochrome c peroxidase

Chain A:



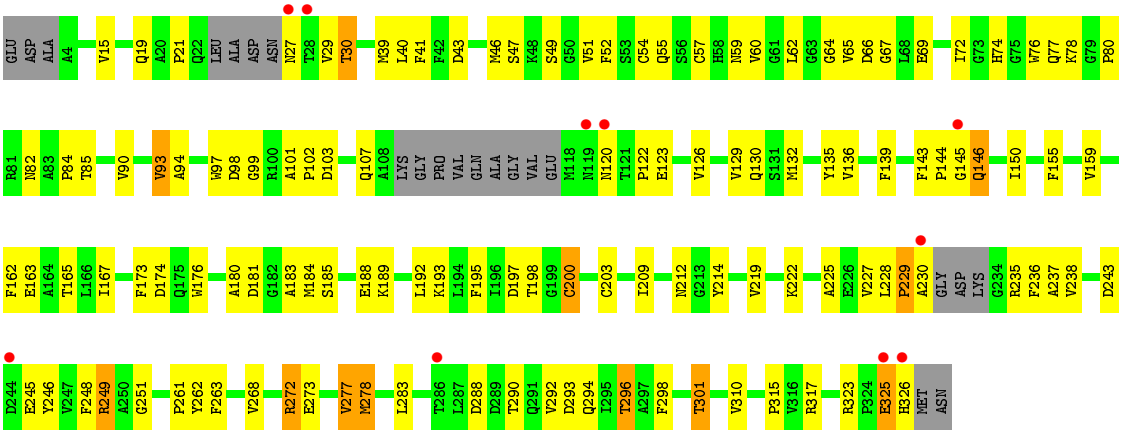
- Molecule 1: cytochrome c peroxidase

Chain B:



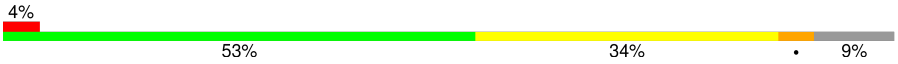
- Molecule 1: cytochrome c peroxidase

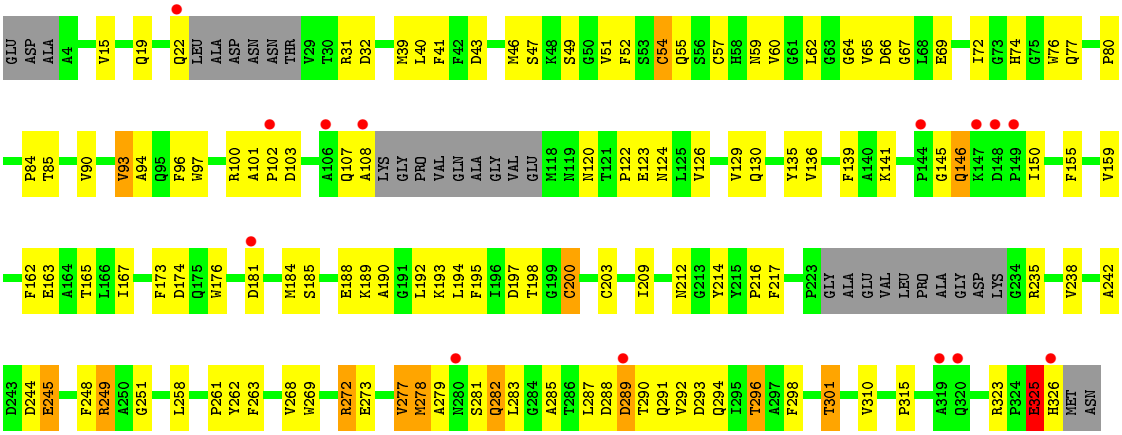
Chain C:



- Molecule 1: cytochrome c peroxidase

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	64.63Å 132.47Å 163.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.70 15.01 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.0 (30.00-2.70) 96.1 (15.01-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.37 (at 2.69Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.249 , 0.278 0.253 , 0.281	Depositor DCC
R_{free} test set	1877 reflections (5.26%)	DCC
Wilson B-factor (Å^2)	50.6	Xtriage
Anisotropy	0.281	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 56.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.35$	Xtriage
Outliers	2 of 37558 reflections (0.005%)	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	9290	wwPDB-VP
Average B, all atoms (Å^2)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 29.27 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.5940e-03.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 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, CA, HEC

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.43	0/2225	0.65	1/3035 (0.0%)
1	B	0.45	0/2330	0.69	1/3174 (0.0%)
1	C	0.44	0/2304	0.66	1/3141 (0.0%)
1	D	0.48	1/2250 (0.0%)	0.72	2/3066 (0.1%)
All	All	0.45	1/9109 (0.0%)	0.68	5/12416 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	325	GLU	C-N	5.25	1.46	1.34

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	289	ASP	CB-CG-OD2	12.28	129.35	118.30
1	B	233	LYS	N-CA-C	8.55	134.08	111.00
1	D	181	ASP	CB-CG-OD1	7.17	124.76	118.30
1	C	181	ASP	CB-CG-OD1	6.79	124.42	118.30
1	A	325	GLU	O-C-N	-6.69	111.99	122.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	325	GLU	Mainchain
1	C	325	GLU	Mainchain

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	2172	0	2040	130	0
1	B	2277	0	2175	131	0
1	C	2251	0	2127	131	0
1	D	2198	0	2084	138	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	2	0	0	0	0
3	B	4	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	86	0	64	17	0
4	B	86	0	64	17	0
4	C	86	0	64	19	0
4	D	86	0	64	21	0
5	A	9	0	0	0	0
5	B	5	0	0	0	0
5	C	15	0	0	1	0
5	D	7	0	0	1	0
All	All	9290	0	8682	519	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 29.

All (519) 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:200:CYS:SG	4:C:402:HEC:HAB	1.88	1.14
1:D:200:CYS:SG	4:D:402:HEC:HAB	1.92	1.09
1:B:200:CYS:SG	4:B:402:HEC:HAB	1.94	1.06
1:A:200:CYS:SG	4:A:803:HEC:HAB	1.95	1.06
1:C:54:CYS:SG	4:C:401:HEC:HAB	1.98	1.03
1:B:54:CYS:SG	4:B:401:HEC:HAB	2.00	1.02
1:A:325:GLU:O	1:A:326:HIS:HB3	1.59	1.01
1:B:54:CYS:SG	4:B:401:HEC:CAB	2.49	1.00
1:B:173:PHE:HB2	1:B:301:THR:HG23	1.45	0.99
1:A:173:PHE:HB2	1:A:301:THR:HG23	1.45	0.98
1:D:54:CYS:SG	4:D:401:HEC:HAB	2.03	0.97
1:D:173:PHE:HB2	1:D:301:THR:HG23	1.44	0.97
1:B:103:ASP:O	1:B:107:GLN:HB2	1.65	0.96
1:C:173:PHE:HB2	1:C:301:THR:HG23	1.47	0.95
1:A:72:ILE:HD11	1:A:80:PRO:HG3	1.49	0.95
1:C:54:CYS:SG	4:C:401:HEC:CAB	2.55	0.94
1:C:55:GLN:HE22	1:C:60:VAL:H	1.15	0.94
1:C:200:CYS:SG	4:C:402:HEC:CAB	2.55	0.93
1:A:54:CYS:SG	4:A:802:HEC:CAB	2.57	0.92
1:D:200:CYS:SG	4:D:402:HEC:CAB	2.57	0.92
1:A:54:CYS:SG	4:A:802:HEC:HAB	2.09	0.92
1:D:282:GLN:H	1:D:282:GLN:HE21	0.96	0.90
1:B:200:CYS:SG	4:B:402:HEC:CAB	2.60	0.89
1:D:54:CYS:SG	4:D:401:HEC:CAB	2.60	0.89
1:D:72:ILE:HD11	1:D:80:PRO:HG3	1.56	0.88
1:C:143:PHE:HB3	1:C:146:GLN:HG3	1.56	0.88
1:D:282:GLN:H	1:D:282:GLN:NE2	1.70	0.87
1:A:200:CYS:SG	4:A:803:HEC:CAB	2.61	0.87
1:B:72:ILE:HD11	1:B:80:PRO:HG3	1.54	0.87
1:A:325:GLU:O	1:A:326:HIS:CB	2.17	0.87
1:B:228:LEU:O	1:B:235:ARG:HD3	1.74	0.86
1:B:55:GLN:HE22	1:B:60:VAL:H	1.21	0.86
1:A:55:GLN:HE22	1:A:60:VAL:H	1.22	0.85
1:A:40:LEU:HD22	1:A:155:PHE:CE1	2.12	0.85
1:C:72:ILE:HD11	1:C:80:PRO:HG3	1.59	0.85
1:B:40:LEU:HD22	1:B:155:PHE:CE1	2.13	0.84
1:D:40:LEU:HD22	1:D:155:PHE:CE1	2.12	0.84
1:B:323:ARG:HH11	1:B:323:ARG:HG2	1.43	0.83
1:A:279:ALA:HB1	1:A:287:LEU:HD12	1.58	0.83
1:D:282:GLN:N	1:D:282:GLN:HE21	1.76	0.83
1:C:65:VAL:HG12	1:C:66:ASP:H	1.43	0.83
1:D:325:GLU:O	1:D:326:HIS:CB	2.27	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:173:PHE:HB2	1:D:301:THR:CG2	2.09	0.82
1:B:65:VAL:HG12	1:B:66:ASP:H	1.42	0.82
1:D:323:ARG:HH11	1:D:323:ARG:HG2	1.45	0.82
1:D:65:VAL:HG12	1:D:66:ASP:H	1.45	0.81
1:A:323:ARG:HG2	1:A:323:ARG:HH11	1.43	0.81
1:C:40:LEU:HD22	1:C:155:PHE:CE1	2.16	0.81
1:A:173:PHE:HB2	1:A:301:THR:CG2	2.11	0.80
1:D:55:GLN:HE22	1:D:60:VAL:H	1.28	0.80
1:D:90:VAL:HG13	5:D:1013:HOH:O	1.81	0.80
1:B:65:VAL:HG12	1:B:66:ASP:N	1.96	0.80
1:A:292:VAL:O	1:A:296:THR:HG22	1.82	0.79
1:C:93:VAL:HG13	1:C:212:ASN:HA	1.65	0.79
1:B:173:PHE:HB2	1:B:301:THR:CG2	2.12	0.79
1:C:65:VAL:HG12	1:C:66:ASP:N	1.98	0.79
1:B:162:PHE:O	1:B:165:THR:HB	1.81	0.79
1:D:162:PHE:O	1:D:165:THR:HB	1.83	0.79
1:C:41:PHE:HA	1:C:54:CYS:SG	2.23	0.78
1:B:93:VAL:HG13	1:B:212:ASN:HA	1.65	0.78
1:A:162:PHE:O	1:A:165:THR:HB	1.83	0.78
1:C:323:ARG:HH11	1:C:323:ARG:HG2	1.48	0.78
1:D:41:PHE:HA	1:D:54:CYS:SG	2.25	0.77
1:A:93:VAL:HG13	1:A:212:ASN:HA	1.66	0.77
1:D:93:VAL:HG13	1:D:212:ASN:HA	1.66	0.77
1:C:162:PHE:O	1:C:165:THR:HB	1.85	0.76
1:D:65:VAL:HG12	1:D:66:ASP:N	1.99	0.76
1:A:41:PHE:HA	1:A:54:CYS:SG	2.25	0.76
1:C:173:PHE:HB2	1:C:301:THR:CG2	2.15	0.75
1:D:19:GLN:NE2	1:D:22:GLN:HE22	1.85	0.74
1:A:65:VAL:HG12	1:A:66:ASP:N	2.04	0.73
1:A:65:VAL:HG12	1:A:66:ASP:H	1.54	0.73
1:D:122:PRO:O	1:D:126:VAL:HG23	1.89	0.73
1:A:324:PRO:HD2	1:D:269:TRP:CH2	2.24	0.72
1:D:100:ARG:CZ	1:D:245:GLU:HG2	2.18	0.72
1:C:222:LYS:HE3	1:C:237:ALA:HB2	1.73	0.71
1:D:129:VAL:HG11	1:D:139:PHE:CE1	2.26	0.71
1:D:283:LEU:HD22	4:D:402:HEC:HBC2	1.73	0.71
1:A:283:LEU:HD22	4:A:803:HEC:HBC2	1.73	0.71
1:C:203:CYS:SG	4:C:402:HEC:CAC	2.79	0.70
1:D:272:ARG:NH2	1:D:289:ASP:OD1	2.22	0.70
1:B:129:VAL:HG21	1:B:155:PHE:CE1	2.26	0.70
1:B:209:ILE:HD12	1:B:209:ILE:N	2.07	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:129:VAL:HG11	1:B:139:PHE:CE1	2.27	0.69
1:C:15:VAL:HG23	1:C:174:ASP:HB3	1.74	0.69
1:B:41:PHE:HA	1:B:54:CYS:SG	2.31	0.69
1:A:57:CYS:HA	1:A:66:ASP:HB3	1.74	0.69
1:D:203:CYS:SG	4:D:402:HEC:CAC	2.81	0.69
1:B:292:VAL:O	1:B:296:THR:HG22	1.92	0.69
1:C:129:VAL:HG21	1:C:155:PHE:CE1	2.28	0.68
1:B:57:CYS:SG	4:B:401:HEC:CAC	2.82	0.68
1:A:310:VAL:HA	1:D:310:VAL:HA	1.76	0.68
1:A:129:VAL:HG11	1:A:139:PHE:CE1	2.28	0.68
1:B:101:ALA:HB3	1:B:102:PRO:HD3	1.74	0.68
1:D:290:THR:O	1:D:294:GLN:HG3	1.94	0.68
1:C:283:LEU:HD13	4:C:402:HEC:HBC2	1.75	0.68
1:D:235:ARG:HH11	1:D:235:ARG:HG3	1.59	0.67
1:B:65:VAL:CG1	1:B:66:ASP:H	2.07	0.67
1:A:203:CYS:SG	4:A:803:HEC:CAC	2.82	0.67
1:A:129:VAL:HG21	1:A:155:PHE:CE1	2.28	0.67
1:C:227:VAL:HG11	1:D:100:ARG:NH1	2.10	0.67
1:D:292:VAL:O	1:D:296:THR:HG22	1.94	0.67
1:C:122:PRO:O	1:C:126:VAL:HG23	1.94	0.67
1:D:15:VAL:HG23	1:D:174:ASP:HB3	1.77	0.67
1:D:273:GLU:O	1:D:277:VAL:HG13	1.95	0.66
1:C:209:ILE:N	1:C:209:ILE:HD12	2.11	0.66
1:A:273:GLU:O	1:A:277:VAL:HG13	1.95	0.66
1:D:298:PHE:O	1:D:301:THR:HB	1.96	0.65
1:D:57:CYS:HA	1:D:66:ASP:HB3	1.77	0.65
1:C:57:CYS:SG	4:C:401:HEC:CAC	2.84	0.65
1:C:65:VAL:CG1	1:C:66:ASP:H	2.09	0.65
1:B:15:VAL:HG23	1:B:174:ASP:HB3	1.79	0.65
1:D:57:CYS:SG	4:D:401:HEC:CAC	2.84	0.64
1:B:273:GLU:O	1:B:277:VAL:HG13	1.96	0.64
1:B:159:VAL:O	1:B:163:GLU:HG3	1.97	0.64
1:A:209:ILE:N	1:A:209:ILE:HD12	2.13	0.64
1:B:203:CYS:SG	4:B:402:HEC:CAC	2.85	0.64
1:D:101:ALA:HB3	1:D:102:PRO:HD3	1.79	0.64
1:D:129:VAL:HG21	1:D:155:PHE:CE1	2.32	0.64
1:A:122:PRO:O	1:A:126:VAL:HG23	1.98	0.64
1:C:101:ALA:HB3	1:C:102:PRO:HD3	1.78	0.64
1:C:143:PHE:CB	1:C:146:GLN:HG3	2.27	0.64
1:C:290:THR:O	1:C:294:GLN:HG3	1.98	0.64
1:B:122:PRO:O	1:B:126:VAL:HG23	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:209:ILE:N	1:D:209:ILE:HD12	2.13	0.63
1:C:273:GLU:O	1:C:277:VAL:HG13	1.98	0.63
1:B:57:CYS:HA	1:B:66:ASP:HB3	1.79	0.63
1:A:159:VAL:O	1:A:163:GLU:HG3	1.99	0.63
1:D:65:VAL:CG1	1:D:66:ASP:H	2.11	0.62
1:C:57:CYS:HA	1:C:66:ASP:HB3	1.81	0.62
1:C:159:VAL:O	1:C:163:GLU:HG3	2.00	0.62
1:C:185:SER:OG	1:C:188:GLU:HG3	1.98	0.62
1:C:129:VAL:HG11	1:C:139:PHE:CE1	2.33	0.62
1:C:292:VAL:O	1:C:296:THR:HG22	1.99	0.62
1:B:193:LYS:HE2	1:B:197:ASP:OD1	2.00	0.62
1:C:228:LEU:O	1:C:235:ARG:HD3	1.99	0.62
1:C:193:LYS:HE2	1:C:197:ASP:OD1	2.00	0.62
1:B:49:SER:OG	1:B:51:VAL:HG13	2.01	0.61
1:C:249:ARG:HH22	4:C:401:HEC:CGA	2.14	0.61
1:B:65:VAL:CG1	1:B:66:ASP:N	2.63	0.60
1:D:249:ARG:HH22	4:D:401:HEC:CGA	2.13	0.60
1:D:193:LYS:HE2	1:D:197:ASP:OD1	2.01	0.60
1:A:310:VAL:HG22	1:D:310:VAL:HG22	1.84	0.60
1:A:193:LYS:HE2	1:A:197:ASP:OD1	2.02	0.60
1:D:100:ARG:NH2	1:D:245:GLU:HG2	2.17	0.59
1:C:227:VAL:HG11	1:D:100:ARG:HH12	1.67	0.59
1:B:243:ASP:OD2	1:B:245:GLU:HB2	2.02	0.59
1:C:65:VAL:CG1	1:C:66:ASP:N	2.65	0.59
1:B:225:ALA:HB1	1:B:235:ARG:HB3	1.84	0.59
1:B:129:VAL:HG21	1:B:155:PHE:CD1	2.36	0.59
1:D:159:VAL:O	1:D:163:GLU:HG3	2.03	0.59
1:B:278:MET:HG2	4:B:402:HEC:NB	2.17	0.59
1:A:129:VAL:HG21	1:A:155:PHE:CD1	2.38	0.59
1:A:290:THR:O	1:A:294:GLN:HG3	2.03	0.59
1:A:15:VAL:HG23	1:A:174:ASP:HB3	1.84	0.59
1:A:249:ARG:HH22	4:A:802:HEC:CGA	2.15	0.59
1:B:287:LEU:HD22	1:B:291:GLN:HB3	1.84	0.59
1:B:249:ARG:HH22	4:B:401:HEC:CGA	2.16	0.59
1:C:298:PHE:O	1:C:301:THR:HB	2.03	0.59
1:C:323:ARG:HH11	1:C:323:ARG:CG	2.16	0.59
1:B:323:ARG:HH11	1:B:323:ARG:CG	2.13	0.58
1:A:65:VAL:CG1	1:A:66:ASP:H	2.16	0.58
1:B:209:ILE:O	1:B:209:ILE:HG22	2.04	0.58
1:C:272:ARG:HH11	1:C:272:ARG:HG3	1.68	0.58
1:A:185:SER:OG	1:A:188:GLU:HG3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:CYS:SG	4:A:802:HEC:CAC	2.92	0.58
1:D:19:GLN:HE22	1:D:22:GLN:HE22	1.50	0.58
1:B:278:MET:HG2	4:B:402:HEC:C4B	2.34	0.58
1:D:192:LEU:HD13	1:D:298:PHE:CE1	2.38	0.58
1:C:27:ASN:CB	1:C:30:THR:HG22	2.33	0.58
1:A:65:VAL:HG12	1:A:67:GLY:H	1.69	0.58
1:B:39:MET:CE	1:B:315:PRO:HD3	2.34	0.58
1:D:103:ASP:O	1:D:107:GLN:HB2	2.04	0.58
1:D:65:VAL:HG12	1:D:67:GLY:H	1.70	0.57
1:B:298:PHE:O	1:B:301:THR:HB	2.04	0.57
1:A:298:PHE:O	1:A:301:THR:HB	2.05	0.57
1:A:323:ARG:HH11	1:A:323:ARG:CG	2.14	0.57
1:D:279:ALA:HB1	1:D:287:LEU:HD12	1.85	0.57
1:D:283:LEU:HD22	4:D:402:HEC:CBC	2.33	0.57
1:B:147:LYS:O	1:B:149:PRO:HD3	2.05	0.57
1:A:101:ALA:HB3	1:A:102:PRO:HD3	1.85	0.57
1:D:272:ARG:HG3	1:D:272:ARG:HH11	1.70	0.57
1:B:290:THR:O	1:B:294:GLN:HG3	2.05	0.57
1:A:285:ALA:O	1:A:287:LEU:HG	2.04	0.57
1:D:190:ALA:O	1:D:194:LEU:HG	2.04	0.57
1:B:195:PHE:O	1:B:200:CYS:SG	2.62	0.56
1:B:129:VAL:CG2	1:B:155:PHE:CE1	2.88	0.56
1:C:129:VAL:HG21	1:C:155:PHE:CD1	2.41	0.56
1:D:65:VAL:CG1	1:D:66:ASP:N	2.67	0.56
1:B:69:GLU:HA	1:B:261:PRO:HG3	1.88	0.56
1:D:198:THR:HG23	1:D:285:ALA:HB3	1.88	0.56
1:A:129:VAL:CG2	1:A:155:PHE:CE1	2.89	0.56
1:B:195:PHE:HA	1:B:200:CYS:SG	2.46	0.56
1:C:278:MET:HG2	4:C:402:HEC:C4B	2.36	0.55
1:D:209:ILE:HG22	1:D:209:ILE:O	2.06	0.55
1:B:292:VAL:O	1:B:296:THR:CG2	2.54	0.55
1:C:278:MET:HG2	4:C:402:HEC:NB	2.22	0.55
1:D:49:SER:HA	1:D:325:GLU:CB	2.36	0.55
1:C:15:VAL:HG23	1:C:174:ASP:CB	2.36	0.55
1:B:65:VAL:HG12	1:B:67:GLY:H	1.71	0.55
1:A:278:MET:HG2	4:A:803:HEC:NB	2.22	0.55
1:B:228:LEU:HD12	1:B:229:PRO:HD2	1.89	0.55
1:D:15:VAL:HG23	1:D:174:ASP:CG	2.27	0.55
1:A:65:VAL:CG1	1:A:66:ASP:N	2.70	0.55
1:A:100:ARG:NH1	1:B:227:VAL:HG11	2.22	0.54
1:B:176:TRP:HB2	1:B:184:MET:HG3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:195:PHE:HA	1:D:200:CYS:SG	2.48	0.54
1:D:15:VAL:HG23	1:D:174:ASP:CB	2.37	0.54
1:B:279:ALA:HB1	1:B:287:LEU:HD12	1.88	0.54
1:C:203:CYS:SG	4:C:402:HEC:HAC	2.48	0.54
1:D:323:ARG:HH11	1:D:323:ARG:CG	2.16	0.54
1:A:316:VAL:HG22	1:D:258:LEU:HD22	1.89	0.54
1:D:129:VAL:HG21	1:D:155:PHE:CD1	2.41	0.54
1:D:185:SER:O	1:D:189:LYS:HG3	2.06	0.54
1:A:278:MET:HG2	4:A:803:HEC:C4B	2.37	0.54
1:A:103:ASP:O	1:A:107:GLN:HB2	2.08	0.54
1:A:262:TYR:HB2	1:A:268:VAL:CG2	2.38	0.54
1:B:268:VAL:HG23	1:B:268:VAL:O	2.07	0.54
1:C:65:VAL:HG12	1:C:67:GLY:H	1.74	0.53
1:C:145:GLY:O	1:C:146:GLN:HG2	2.08	0.53
1:C:129:VAL:CG2	1:C:155:PHE:CE1	2.91	0.53
1:B:129:VAL:CG2	1:B:155:PHE:HE1	2.21	0.53
1:D:292:VAL:O	1:D:296:THR:CG2	2.55	0.53
1:A:272:ARG:HG3	1:A:272:ARG:HH11	1.72	0.53
1:A:209:ILE:O	1:A:209:ILE:HG22	2.08	0.53
1:D:126:VAL:O	1:D:130:GLN:HB2	2.09	0.53
1:A:126:VAL:O	1:A:130:GLN:HB2	2.09	0.53
1:C:129:VAL:CG2	1:C:155:PHE:HE1	2.22	0.53
1:A:47:SER:HB3	1:A:52:PHE:O	2.09	0.53
1:D:216:PRO:HB3	1:D:244:ASP:HA	1.91	0.53
1:A:129:VAL:CG2	1:A:155:PHE:HE1	2.22	0.53
1:C:15:VAL:HG23	1:C:174:ASP:CG	2.29	0.53
1:C:55:GLN:NE2	1:C:60:VAL:H	1.96	0.52
1:D:195:PHE:O	1:D:200:CYS:SG	2.66	0.52
1:D:129:VAL:CG2	1:D:155:PHE:CE1	2.92	0.52
1:C:292:VAL:O	1:C:296:THR:CG2	2.57	0.52
1:A:185:SER:O	1:A:189:LYS:HG3	2.09	0.52
1:D:59:ASN:HB3	1:D:62:LEU:HB2	1.91	0.52
1:B:272:ARG:HH11	1:B:272:ARG:HG3	1.75	0.52
1:C:268:VAL:O	1:C:268:VAL:HG23	2.09	0.52
1:B:209:ILE:CD1	1:B:209:ILE:N	2.73	0.52
1:A:195:PHE:HA	1:A:200:CYS:SG	2.49	0.52
1:A:49:SER:OG	1:A:51:VAL:HG13	2.10	0.52
1:B:126:VAL:O	1:B:130:GLN:HB2	2.10	0.51
1:C:126:VAL:O	1:C:130:GLN:HB2	2.10	0.51
1:C:209:ILE:HG22	1:C:209:ILE:O	2.10	0.51
1:A:195:PHE:O	1:A:200:CYS:SG	2.65	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:262:TYR:HB2	1:C:268:VAL:CG2	2.40	0.51
1:A:69:GLU:HA	1:A:261:PRO:HG3	1.93	0.51
1:B:151:SER:OG	1:B:154:ASN:ND2	2.44	0.51
1:D:74:HIS:O	1:D:77:GLN:HB2	2.11	0.51
1:D:278:MET:HG2	4:D:402:HEC:C4B	2.40	0.51
1:D:200:CYS:CB	4:D:402:HEC:HAB	2.39	0.51
1:D:129:VAL:HG13	1:D:135:TYR:HB3	1.92	0.51
1:B:15:VAL:HG23	1:B:174:ASP:CB	2.40	0.51
1:D:268:VAL:HG23	1:D:268:VAL:O	2.11	0.51
1:C:103:ASP:O	1:C:107:GLN:HB2	2.11	0.51
1:B:185:SER:OG	1:B:188:GLU:HG3	2.10	0.51
1:B:104:LEU:O	1:B:107:GLN:HB3	2.11	0.50
1:D:49:SER:OG	1:D:51:VAL:HG13	2.11	0.50
1:A:323:ARG:HG2	1:A:323:ARG:NH1	2.22	0.50
1:B:262:TYR:HB2	1:B:268:VAL:CG2	2.41	0.50
1:B:249:ARG:O	4:B:402:HEC:HAD1	2.11	0.50
1:B:129:VAL:HG13	1:B:135:TYR:HB3	1.94	0.50
1:A:39:MET:CE	1:A:315:PRO:HD3	2.41	0.50
1:B:143:PHE:N	1:B:144:PRO:HD3	2.27	0.50
1:A:129:VAL:HG13	1:A:135:TYR:HB3	1.93	0.50
1:C:69:GLU:HA	1:C:261:PRO:HG3	1.93	0.50
1:C:195:PHE:HA	1:C:200:CYS:SG	2.52	0.50
1:C:27:ASN:C	1:C:29:VAL:H	2.15	0.50
1:D:283:LEU:HD13	4:D:402:HEC:HBC2	1.94	0.50
1:D:40:LEU:HD22	1:D:155:PHE:CZ	2.47	0.50
1:A:324:PRO:CD	1:D:269:TRP:CH2	2.95	0.50
1:C:185:SER:O	1:C:189:LYS:HG3	2.12	0.49
1:D:129:VAL:CG2	1:D:155:PHE:HE1	2.24	0.49
1:C:249:ARG:O	4:C:402:HEC:HAD1	2.12	0.49
1:B:15:VAL:HG23	1:B:174:ASP:CG	2.32	0.49
1:B:47:SER:HB3	1:B:52:PHE:O	2.13	0.49
1:B:200:CYS:CB	4:B:402:HEC:HAB	2.42	0.49
1:C:184:MET:HE3	1:C:189:LYS:HG2	1.95	0.49
1:A:184:MET:HE3	1:A:189:LYS:HG2	1.94	0.49
1:C:99:GLY:HA2	1:C:246:TYR:CE1	2.48	0.49
1:C:229:PRO:O	1:C:230:ALA:C	2.51	0.49
1:D:278:MET:HG2	4:D:402:HEC:NB	2.27	0.49
1:A:200:CYS:CB	4:A:803:HEC:HAB	2.42	0.49
1:C:209:ILE:CD1	1:C:209:ILE:N	2.76	0.49
1:B:279:ALA:O	1:B:284:GLY:HA3	2.13	0.49
1:D:69:GLU:HA	1:D:261:PRO:HG3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:200:CYS:CB	4:C:402:HEC:HAB	2.43	0.49
1:C:135:TYR:O	1:C:139:PHE:HD1	1.96	0.49
1:C:15:VAL:CG2	1:C:174:ASP:HB3	2.41	0.49
1:B:185:SER:O	1:B:189:LYS:HG3	2.13	0.49
1:D:185:SER:OG	1:D:188:GLU:HG3	2.11	0.49
1:D:100:ARG:NH2	1:D:245:GLU:OE2	2.46	0.49
1:B:193:LYS:HE2	1:B:197:ASP:CG	2.33	0.49
1:C:235:ARG:NH2	1:C:236:PHE:HE1	2.11	0.49
1:A:15:VAL:HG23	1:A:174:ASP:CG	2.33	0.49
1:D:203:CYS:SG	4:D:402:HEC:HAC	2.51	0.49
1:B:323:ARG:NH1	1:B:323:ARG:CG	2.74	0.49
1:C:176:TRP:HB2	1:C:184:MET:HG3	1.95	0.49
1:C:39:MET:CE	1:C:315:PRO:HD3	2.43	0.49
1:A:323:ARG:HD3	1:D:269:TRP:CD1	2.48	0.48
1:D:193:LYS:HG3	1:D:197:ASP:OD2	2.13	0.48
1:A:192:LEU:HD13	1:A:298:PHE:CE1	2.48	0.48
1:C:193:LYS:HE2	1:C:197:ASP:CG	2.34	0.48
1:C:195:PHE:O	1:C:200:CYS:SG	2.69	0.48
1:B:203:CYS:SG	4:B:402:HEC:HAC	2.53	0.48
1:A:176:TRP:HB2	1:A:184:MET:HG3	1.95	0.48
1:B:222:LYS:O	1:B:225:ALA:HB2	2.13	0.48
1:A:40:LEU:HD22	1:A:155:PHE:CZ	2.49	0.48
1:C:47:SER:HB3	1:C:52:PHE:O	2.14	0.48
1:B:281:SER:C	1:B:283:LEU:H	2.15	0.48
1:B:59:ASN:HB3	1:B:62:LEU:HB2	1.94	0.48
1:C:84:PRO:HD3	4:C:401:HEC:HAD1	1.95	0.48
1:C:55:GLN:NE2	1:C:60:VAL:HG13	2.28	0.48
1:C:143:PHE:HB3	1:C:146:GLN:CG	2.38	0.48
1:B:40:LEU:HD22	1:B:155:PHE:CZ	2.48	0.48
1:B:233:LYS:CB	1:B:233:LYS:NZ	2.77	0.48
1:A:203:CYS:SG	4:A:803:HEC:HAC	2.53	0.48
1:B:228:LEU:HG	1:B:232:ASP:CG	2.34	0.48
1:A:279:ALA:CB	1:A:287:LEU:HD12	2.38	0.48
1:C:129:VAL:HG13	1:C:135:TYR:HB3	1.95	0.48
1:A:268:VAL:O	1:A:268:VAL:HG23	2.13	0.48
1:D:262:TYR:HB2	1:D:268:VAL:CG2	2.44	0.48
1:A:323:ARG:CG	1:A:323:ARG:NH1	2.75	0.47
1:D:209:ILE:N	1:D:209:ILE:CD1	2.77	0.47
1:B:193:LYS:HE2	1:B:197:ASP:OD2	2.15	0.47
1:B:82:ASN:ND2	1:B:261:PRO:HG2	2.27	0.47
1:B:272:ARG:NH1	1:B:293:ASP:OD1	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:135:TYR:O	1:D:139:PHE:HD1	1.97	0.47
1:A:74:HIS:O	1:A:77:GLN:HB2	2.14	0.47
1:A:84:PRO:HD3	4:A:802:HEC:HAD1	1.97	0.47
1:C:19:GLN:HA	1:C:167:ILE:HD11	1.96	0.47
1:A:242:ALA:CB	1:B:225:ALA:HA	2.44	0.47
1:D:323:ARG:NH1	1:D:323:ARG:CG	2.77	0.47
1:B:269:TRP:NE1	1:C:323:ARG:HD3	2.28	0.47
1:C:225:ALA:O	1:C:235:ARG:HD2	2.15	0.47
1:B:310:VAL:HA	1:C:310:VAL:HA	1.97	0.47
1:A:30:THR:O	1:A:31:ARG:CB	2.62	0.47
1:C:283:LEU:HD22	4:C:402:HEC:HBC2	1.97	0.47
1:A:59:ASN:HB3	1:A:62:LEU:HB2	1.97	0.47
1:D:176:TRP:HB2	1:D:184:MET:HG3	1.95	0.47
4:C:401:HEC:HMC1	4:C:401:HEC:HBC3	1.96	0.47
1:C:78:LYS:HG3	1:C:246:TYR:OH	2.15	0.47
1:A:249:ARG:O	4:A:803:HEC:HAD1	2.15	0.47
1:D:272:ARG:NH1	1:D:293:ASP:OD1	2.48	0.47
1:D:15:VAL:CG2	1:D:174:ASP:HB3	2.43	0.47
1:C:27:ASN:N	1:C:30:THR:CG2	2.78	0.47
1:C:198:THR:O	1:C:198:THR:HG22	2.16	0.46
1:D:40:LEU:CD2	1:D:155:PHE:CE1	2.93	0.46
1:A:15:VAL:HG23	1:A:174:ASP:CB	2.44	0.46
1:C:76:TRP:C	1:C:76:TRP:CD1	2.89	0.46
1:C:84:PRO:CD	4:C:401:HEC:HAD1	2.46	0.46
1:C:193:LYS:HE2	1:C:197:ASP:OD2	2.16	0.46
1:D:262:TYR:O	1:D:263:PHE:HB2	2.15	0.46
1:A:180:ALA:HB3	1:A:183:ALA:HB2	1.97	0.46
1:C:55:GLN:HE22	1:C:60:VAL:HG13	1.80	0.46
1:A:272:ARG:NH1	1:A:293:ASP:OD1	2.48	0.46
1:C:272:ARG:NH1	1:C:293:ASP:OD1	2.49	0.46
1:B:262:TYR:O	1:B:263:PHE:HB2	2.15	0.46
1:C:59:ASN:HB3	1:C:62:LEU:HB2	1.97	0.46
1:A:209:ILE:N	1:A:209:ILE:CD1	2.77	0.46
1:B:84:PRO:HG2	4:B:401:HEC:HBA1	1.98	0.46
1:C:225:ALA:HA	1:D:242:ALA:CB	2.46	0.46
1:A:193:LYS:HE2	1:A:197:ASP:CG	2.36	0.46
1:A:184:MET:CE	1:A:189:LYS:HG2	2.46	0.46
1:C:49:SER:OG	1:C:51:VAL:HG13	2.16	0.46
1:B:193:LYS:HG3	1:B:197:ASP:OD2	2.16	0.46
1:D:76:TRP:C	1:D:76:TRP:CD1	2.89	0.46
1:B:198:THR:HG22	1:B:198:THR:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:84:PRO:HD3	4:B:401:HEC:HAD1	1.97	0.46
1:A:316:VAL:HG22	1:D:258:LEU:CD2	2.46	0.46
1:A:262:TYR:HB2	1:A:268:VAL:HG23	1.98	0.46
1:A:29:VAL:O	1:A:30:THR:C	2.55	0.46
1:A:217:PHE:O	1:A:248:PHE:HB2	2.17	0.45
1:A:29:VAL:O	1:A:31:ARG:N	2.49	0.45
1:B:33:LYS:HB2	1:B:33:LYS:HE3	1.84	0.45
1:A:136:VAL:HA	1:A:150:ILE:HD11	1.99	0.45
1:A:129:VAL:CG1	1:A:139:PHE:CE1	3.00	0.45
1:A:64:GLY:O	1:A:85:THR:HA	2.16	0.45
1:D:84:PRO:HG2	4:D:401:HEC:HBA1	1.99	0.45
1:B:249:ARG:HD3	1:B:251:GLY:HA2	1.98	0.45
1:C:136:VAL:HA	1:C:150:ILE:HD11	1.98	0.45
1:D:84:PRO:HD3	4:D:401:HEC:HAD1	1.97	0.45
1:A:146:GLN:O	1:A:149:PRO:HD3	2.17	0.45
1:A:151:SER:OG	1:A:154:ASN:ND2	2.49	0.45
1:C:288:ASP:OD1	1:C:290:THR:N	2.50	0.45
1:A:49:SER:HA	1:A:325:GLU:CB	2.46	0.45
1:B:129:VAL:CG1	1:B:139:PHE:CE1	2.98	0.45
1:B:287:LEU:HA	1:B:291:GLN:OE1	2.17	0.45
1:A:29:VAL:O	1:A:32:ASP:N	2.49	0.45
1:C:219:VAL:HG22	1:C:238:VAL:HG22	1.99	0.45
1:A:249:ARG:HD3	1:A:251:GLY:HA2	1.99	0.44
1:D:129:VAL:CG1	1:D:139:PHE:CE1	2.98	0.44
1:C:193:LYS:HG3	1:C:197:ASP:OD2	2.17	0.44
1:D:193:LYS:HE2	1:D:197:ASP:CG	2.37	0.44
1:D:249:ARG:O	4:D:402:HEC:HAD1	2.17	0.44
1:A:40:LEU:HD22	1:A:155:PHE:HE1	1.75	0.44
1:A:198:THR:HG22	1:A:198:THR:O	2.18	0.44
1:D:323:ARG:NH1	1:D:323:ARG:HG2	2.22	0.44
1:D:41:PHE:HA	1:D:54:CYS:HG	1.79	0.44
4:A:802:HEC:HBC3	4:A:802:HEC:HMC1	1.99	0.44
1:D:198:THR:HG22	1:D:198:THR:O	2.18	0.44
1:C:82:ASN:ND2	1:C:261:PRO:HG2	2.32	0.44
1:C:40:LEU:HD22	1:C:155:PHE:CZ	2.50	0.44
1:C:272:ARG:HG3	1:C:272:ARG:NH1	2.32	0.44
1:A:76:TRP:C	1:A:76:TRP:CD1	2.89	0.44
1:D:136:VAL:HA	1:D:150:ILE:HD11	2.00	0.44
1:C:74:HIS:O	1:C:77:GLN:HB2	2.16	0.44
1:C:132:MET:HG2	1:C:317:ARG:HA	1.99	0.44
1:C:84:PRO:HG2	4:C:401:HEC:HBA1	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:19:GLN:HA	1:A:167:ILE:HD11	1.99	0.44
1:C:192:LEU:HD13	1:C:298:PHE:CE1	2.54	0.43
1:B:39:MET:HE2	1:B:315:PRO:HD3	2.00	0.43
1:C:243:ASP:OD1	1:C:245:GLU:CD	2.57	0.43
1:D:39:MET:CE	1:D:315:PRO:HD3	2.47	0.43
1:B:74:HIS:O	1:B:77:GLN:HB2	2.18	0.43
1:B:233:LYS:HE3	1:B:233:LYS:HB2	1.73	0.43
1:D:145:GLY:O	1:D:146:GLN:CB	2.67	0.43
1:C:98:ASP:HB3	1:C:248:PHE:CD2	2.52	0.43
1:B:102:PRO:C	1:B:104:LEU:N	2.70	0.43
1:D:40:LEU:HD22	1:D:155:PHE:HE1	1.76	0.43
1:D:22:GLN:OE1	1:D:22:GLN:N	2.51	0.43
1:B:102:PRO:O	1:B:105:ALA:N	2.51	0.43
1:D:288:ASP:OD1	1:D:288:ASP:C	2.56	0.43
1:C:262:TYR:O	1:C:263:PHE:HB2	2.18	0.43
1:C:64:GLY:O	1:C:85:THR:HA	2.19	0.43
1:D:47:SER:HB3	1:D:52:PHE:O	2.19	0.43
1:A:84:PRO:CD	4:A:802:HEC:HAD1	2.49	0.43
1:B:84:PRO:CD	4:B:401:HEC:HAD1	2.49	0.43
1:B:44:PRO:O	1:B:50:GLY:HA2	2.19	0.43
1:B:228:LEU:O	1:B:232:ASP:HB2	2.19	0.43
1:B:40:LEU:HD22	1:B:155:PHE:HE1	1.76	0.43
1:D:19:GLN:HA	1:D:167:ILE:HD11	2.01	0.43
1:D:235:ARG:CG	1:D:235:ARG:HH11	2.26	0.43
1:B:142:ALA:C	1:B:144:PRO:HD3	2.39	0.43
1:D:288:ASP:OD1	1:D:291:GLN:HG3	2.19	0.43
1:C:94:ALA:HB1	1:C:214:TYR:CZ	2.54	0.43
4:B:401:HEC:HMC1	4:B:401:HEC:HBC3	2.01	0.42
1:D:283:LEU:CD2	4:D:402:HEC:HBC2	2.46	0.42
1:D:84:PRO:CD	4:D:401:HEC:HAD1	2.49	0.42
1:B:192:LEU:HD13	1:B:298:PHE:CE1	2.55	0.42
1:B:222:LYS:HA	1:B:222:LYS:HD3	1.85	0.42
1:B:15:VAL:CG2	1:B:174:ASP:HB3	2.46	0.42
1:B:30:THR:O	1:B:34:ILE:HG13	2.19	0.42
1:D:96:PHE:O	1:D:214:TYR:HE2	2.02	0.42
1:A:217:PHE:CD2	1:A:283:LEU:HD21	2.54	0.42
1:B:58:HIS:HA	1:B:64:GLY:O	2.20	0.42
1:C:325:GLU:O	1:C:326:HIS:CB	2.65	0.42
1:D:238:VAL:HG11	1:D:283:LEU:HG	2.01	0.42
1:D:217:PHE:O	1:D:248:PHE:HB2	2.20	0.42
1:B:180:ALA:HB3	1:B:183:ALA:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:201:ALA:O	1:B:205:ASN:HB3	2.20	0.42
1:C:84:PRO:HD2	4:C:401:HEC:C3D	2.49	0.42
1:C:184:MET:CE	1:C:189:LYS:HG2	2.49	0.42
1:A:324:PRO:HD2	1:D:269:TRP:CZ2	2.55	0.42
1:B:176:TRP:CB	1:B:184:MET:HG3	2.50	0.42
1:A:76:TRP:HB2	1:A:107:GLN:NE2	2.35	0.42
1:A:288:ASP:CG	1:A:289:ASP:N	2.73	0.42
1:A:44:PRO:O	1:A:50:GLY:HA2	2.19	0.42
1:D:214:TYR:CD2	1:D:249:ARG:HB2	2.54	0.42
1:A:65:VAL:HG21	1:A:259:THR:HB	2.02	0.42
1:B:301:THR:HG23	1:B:301:THR:O	2.18	0.42
1:B:262:TYR:HB2	1:B:268:VAL:HG23	2.02	0.42
1:B:98:ASP:HB3	1:B:248:PHE:CD2	2.55	0.42
4:D:401:HEC:HMC1	4:D:401:HEC:HBC3	2.02	0.42
1:C:43:ASP:HB3	1:C:46:MET:HG2	2.01	0.42
1:C:249:ARG:HD3	1:C:251:GLY:HA2	2.02	0.41
1:A:293:ASP:O	1:A:296:THR:HG23	2.20	0.41
1:B:184:MET:CE	1:B:189:LYS:HG2	2.50	0.41
1:D:84:PRO:HD2	4:D:401:HEC:C3D	2.50	0.41
1:A:275:VAL:HG21	1:A:296:THR:HB	2.02	0.41
1:B:268:VAL:CG2	1:B:268:VAL:O	2.68	0.41
1:B:136:VAL:HA	1:B:150:ILE:HD11	2.02	0.41
1:D:96:PHE:HE1	1:D:108:ALA:HB2	1.84	0.41
1:A:135:TYR:O	1:A:139:PHE:HD1	2.03	0.41
1:A:193:LYS:HE2	1:A:197:ASP:OD2	2.21	0.41
1:A:193:LYS:HG3	1:A:197:ASP:OD2	2.20	0.41
1:B:36:LEU:HD11	1:B:139:PHE:CE1	2.56	0.41
1:A:198:THR:HG21	1:A:287:LEU:HD11	2.02	0.41
1:B:217:PHE:O	1:B:248:PHE:HB2	2.19	0.41
1:A:201:ALA:O	1:A:205:ASN:HB3	2.21	0.41
1:B:76:TRP:CD1	1:B:76:TRP:C	2.93	0.41
1:D:43:ASP:HB3	1:D:46:MET:HG2	2.02	0.41
1:C:41:PHE:HA	1:C:54:CYS:HG	1.82	0.41
1:D:214:TYR:CE2	1:D:249:ARG:HB2	2.55	0.41
1:A:98:ASP:HB3	1:A:248:PHE:CD2	2.55	0.41
1:D:192:LEU:HD13	1:D:298:PHE:CZ	2.54	0.41
1:D:32:ASP:OD2	1:D:141:LYS:HB3	2.20	0.41
1:D:94:ALA:HB1	1:D:214:TYR:CZ	2.55	0.41
1:D:235:ARG:CG	1:D:235:ARG:NH1	2.84	0.41
1:A:40:LEU:CD2	1:A:155:PHE:CE1	2.95	0.41
1:B:64:GLY:O	1:B:85:THR:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:249:ARG:HD3	1:D:251:GLY:HA2	2.03	0.41
1:B:283:LEU:HD13	4:B:402:HEC:HBC2	2.03	0.41
1:B:40:LEU:CD2	1:B:155:PHE:CE1	2.95	0.41
1:A:82:ASN:ND2	1:A:261:PRO:HG2	2.35	0.41
1:C:40:LEU:CD2	1:C:155:PHE:CE1	2.98	0.41
1:A:292:VAL:O	1:A:296:THR:CG2	2.61	0.41
1:C:272:ARG:C	1:C:272:ARG:HD3	2.41	0.40
1:C:262:TYR:HB2	1:C:268:VAL:HG23	2.03	0.40
1:C:243:ASP:C	1:C:245:GLU:H	2.24	0.40
1:C:90:VAL:HG13	5:C:1017:HOH:O	2.21	0.40
1:A:84:PRO:HD2	4:A:802:HEC:C3D	2.51	0.40
1:C:301:THR:O	1:C:301:THR:HG23	2.21	0.40
1:C:146:GLN:HE21	1:C:146:GLN:HA	1.85	0.40
1:A:55:GLN:HE22	1:A:60:VAL:HG13	1.87	0.40
1:A:55:GLN:NE2	1:A:60:VAL:HG13	2.36	0.40
1:D:64:GLY:O	1:D:85:THR:HA	2.20	0.40
1:B:135:TYR:O	1:B:139:PHE:HD1	2.04	0.40
1:B:18:MET:O	1:B:19:GLN:HG3	2.21	0.40
1:C:180:ALA:HB3	1:C:183:ALA:HB2	2.04	0.40
1:A:177:LEU:HD23	1:A:177:LEU:HA	1.96	0.40
1:B:94:ALA:HB1	1:B:214:TYR:CZ	2.55	0.40
1:A:217:PHE:CG	1:A:283:LEU:HD21	2.56	0.40
1:C:323:ARG:NH1	1:C:323:ARG:CG	2.77	0.40
1:D:238:VAL:HB	1:D:281:SER:HB2	2.03	0.40
1:C:129:VAL:CG1	1:C:139:PHE:CE1	3.03	0.40
1:A:89:ALA:HA	1:A:92:ASN:ND2	2.36	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	289/328 (88%)	272 (94%)	14 (5%)	3 (1%)	19	45
1	B	300/328 (92%)	276 (92%)	19 (6%)	5 (2%)	11	29
1	C	299/328 (91%)	278 (93%)	17 (6%)	4 (1%)	15	37
1	D	290/328 (88%)	272 (94%)	14 (5%)	4 (1%)	14	35
All	All	1178/1312 (90%)	1098 (93%)	64 (5%)	16 (1%)	14	35

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	31	ARG
1	B	233	LYS
1	D	325	GLU
1	A	120	ASN
1	B	120	ASN
1	B	242	ALA
1	C	120	ASN
1	D	31	ARG
1	D	120	ASN
1	D	146	GLN
1	A	30	THR
1	B	226	GLU
1	C	144	PRO
1	B	234	GLY
1	C	21	PRO
1	C	229	PRO

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	214/254 (84%)	203 (95%)	11 (5%)	29	59
1	B	229/254 (90%)	216 (94%)	13 (6%)	25	53
1	C	222/254 (87%)	210 (95%)	12 (5%)	27	56
1	D	219/254 (86%)	205 (94%)	14 (6%)	22	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	884/1016 (87%)	834 (94%)	50 (6%)	25 53

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	93	VAL
1	A	97	TRP
1	A	123	GLU
1	A	200	CYS
1	A	249	ARG
1	A	272	ARG
1	A	277	VAL
1	A	278	MET
1	A	286	THR
1	A	296	THR
1	A	301	THR
1	B	93	VAL
1	B	97	TRP
1	B	123	GLU
1	B	200	CYS
1	B	232	ASP
1	B	233	LYS
1	B	239	THR
1	B	249	ARG
1	B	272	ARG
1	B	277	VAL
1	B	278	MET
1	B	296	THR
1	B	301	THR
1	C	30	THR
1	C	93	VAL
1	C	97	TRP
1	C	123	GLU
1	C	146	GLN
1	C	200	CYS
1	C	249	ARG
1	C	272	ARG
1	C	277	VAL
1	C	278	MET
1	C	296	THR
1	C	301	THR
1	D	54	CYS

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Mol	Chain	Res	Type
1	D	93	VAL
1	D	97	TRP
1	D	123	GLU
1	D	124	ASN
1	D	200	CYS
1	D	245	GLU
1	D	249	ARG
1	D	272	ARG
1	D	277	VAL
1	D	278	MET
1	D	282	GLN
1	D	296	THR
1	D	301	THR

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

Mol	Chain	Res	Type
1	A	55	GLN
1	A	107	GLN
1	A	154	ASN
1	A	311	HIS
1	B	55	GLN
1	B	154	ASN
1	B	311	HIS
1	C	55	GLN
1	C	107	GLN
1	C	146	GLN
1	C	154	ASN
1	C	311	HIS
1	D	19	GLN
1	D	55	GLN
1	D	107	GLN
1	D	124	ASN
1	D	154	ASN
1	D	282	GLN
1	D	311	HIS

5.3.3 RNA

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, 12 are monoatomic - leaving 8 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	$\#\|Z\| > 2$
4	HEC	A	802	1	24,50,50	1.32	2 (8%)	19,82,82	1.99	6 (31%)
4	HEC	A	803	1	24,50,50	1.37	1 (4%)	19,82,82	1.79	2 (10%)
4	HEC	B	401	1	24,50,50	1.32	3 (12%)	19,82,82	2.05	6 (31%)
4	HEC	B	402	1	24,50,50	1.38	1 (4%)	19,82,82	1.87	3 (15%)
4	HEC	C	401	1	24,50,50	1.41	2 (8%)	19,82,82	1.95	6 (31%)
4	HEC	C	402	1	24,50,50	1.37	2 (8%)	19,82,82	1.86	3 (15%)
4	HEC	D	401	1	24,50,50	1.40	3 (12%)	19,82,82	2.08	6 (31%)
4	HEC	D	402	1	24,50,50	1.29	1 (4%)	19,82,82	1.72	2 (10%)

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
4	HEC	A	802	1	-	0/6/54/54	0/0/8/8
4	HEC	A	803	1	-	0/6/54/54	0/0/8/8
4	HEC	B	401	1	-	0/6/54/54	0/0/8/8
4	HEC	B	402	1	-	0/6/54/54	0/0/8/8
4	HEC	C	401	1	-	0/6/54/54	0/0/8/8

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	HEC	C	402	1	-	0/6/54/54	0/0/8/8
4	HEC	D	401	1	-	0/6/54/54	0/0/8/8
4	HEC	D	402	1	-	0/6/54/54	0/0/8/8

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	402	HEC	C3C-C2C	-4.75	1.35	1.40
4	A	803	HEC	C3C-C2C	-4.48	1.36	1.40
4	D	402	HEC	C3C-C2C	-4.43	1.36	1.40
4	C	402	HEC	C3C-C2C	-4.39	1.36	1.40
4	C	401	HEC	C3C-C2C	-3.67	1.36	1.40
4	D	401	HEC	C3C-C2C	-3.39	1.37	1.40
4	A	802	HEC	C3C-C2C	-3.13	1.37	1.40
4	B	401	HEC	C3C-C2C	-2.63	1.38	1.40
4	D	401	HEC	C3B-C2B	-2.49	1.38	1.40
4	B	401	HEC	C3B-C2B	-2.14	1.38	1.40
4	C	401	HEC	C3B-C2B	-2.08	1.38	1.40
4	C	402	HEC	CMB-C2B	2.02	1.56	1.51
4	A	802	HEC	CAD-C3D	2.23	1.55	1.52
4	D	401	HEC	CAD-C3D	2.41	1.56	1.52
4	B	401	HEC	CAD-C3D	2.41	1.56	1.52

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	D	401	HEC	CBB-CAB-C3B	-5.85	114.36	127.35
4	B	401	HEC	CBB-CAB-C3B	-5.80	114.47	127.35
4	B	402	HEC	CBB-CAB-C3B	-5.50	115.13	127.35
4	C	401	HEC	CBB-CAB-C3B	-5.48	115.17	127.35
4	A	802	HEC	CBB-CAB-C3B	-5.48	115.18	127.35
4	C	402	HEC	CBB-CAB-C3B	-5.43	115.28	127.35
4	A	803	HEC	CBB-CAB-C3B	-5.10	116.02	127.35
4	D	402	HEC	CBB-CAB-C3B	-5.00	116.25	127.35
4	B	402	HEC	CBC-CAC-C3C	-3.54	119.48	127.35
4	C	402	HEC	CBC-CAC-C3C	-3.48	119.62	127.35
4	A	803	HEC	CBC-CAC-C3C	-3.48	119.63	127.35
4	D	402	HEC	CBC-CAC-C3C	-3.21	120.22	127.35
4	A	802	HEC	CMC-C2C-C1C	-2.61	124.05	128.36
4	D	401	HEC	CMC-C2C-C1C	-2.60	124.07	128.36
4	B	401	HEC	CMC-C2C-C1C	-2.55	124.15	128.36
4	A	802	HEC	CBC-CAC-C3C	-2.49	121.83	127.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	401	HEC	CBC-CAC-C3C	-2.46	121.88	127.35
4	B	401	HEC	CBC-CAC-C3C	-2.46	121.89	127.35
4	D	401	HEC	CBC-CAC-C3C	-2.40	122.02	127.35
4	C	401	HEC	CMC-C2C-C1C	-2.29	124.57	128.36
4	C	401	HEC	CMD-C2D-C3D	2.01	129.43	125.24
4	A	802	HEC	CMD-C2D-C3D	2.01	129.43	125.24
4	B	401	HEC	CMD-C2D-C3D	2.01	129.45	125.24
4	B	402	HEC	CAD-CBD-CGD	2.06	116.53	112.75
4	D	401	HEC	CMD-C2D-C3D	2.09	129.60	125.24
4	C	402	HEC	CAD-CBD-CGD	2.13	116.66	112.75
4	A	802	HEC	CAD-CBD-CGD	2.52	117.36	112.75
4	D	401	HEC	CAA-C2A-C1A	2.62	129.86	127.01
4	B	401	HEC	CAA-C2A-C1A	2.64	129.88	127.01
4	C	401	HEC	CAA-C2A-C1A	2.72	129.96	127.01
4	B	401	HEC	CAD-CBD-CGD	2.74	117.76	112.75
4	C	401	HEC	CAD-CBD-CGD	2.77	117.83	112.75
4	A	802	HEC	CAA-C2A-C1A	2.83	130.09	127.01
4	D	401	HEC	CAD-CBD-CGD	2.87	118.01	112.75

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 74 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	802	HEC	8	0
4	A	803	HEC	9	0
4	B	401	HEC	8	0
4	B	402	HEC	9	0
4	C	401	HEC	9	0
4	C	402	HEC	10	0
4	D	401	HEC	9	0
4	D	402	HEC	12	0

5.7 Other polymers (i)

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	297/328 (90%)	0.23	16 (5%)	29	28	30, 49, 76, 91	0
1	B	308/328 (93%)	0.21	19 (6%)	24	23	27, 43, 73, 93	0
1	C	307/328 (93%)	0.08	10 (3%)	50	50	27, 42, 72, 80	0
1	D	298/328 (90%)	0.16	14 (4%)	35	34	31, 43, 73, 89	0
All	All	1210/1312 (92%)	0.17	59 (4%)	33	32	27, 45, 74, 93	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	118	MET	6.2
1	B	120	ASN	5.9
1	B	326	HIS	5.8
1	B	229	PRO	5.4
1	C	120	ASN	5.2
1	B	22	GLN	5.0
1	C	27	ASN	4.9
1	D	326	HIS	4.8
1	A	120	ASN	4.5
1	A	21	PRO	4.3
1	D	289	ASP	4.2
1	B	119	ASN	4.1
1	C	326	HIS	4.0
1	B	106	ALA	3.9
1	D	102	PRO	3.6
1	B	233	LYS	3.2
1	C	28	THR	3.2
1	D	22	GLN	3.1
1	A	145	GLY	3.1
1	D	106	ALA	2.9
1	B	121	THR	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	242	ALA	2.8
1	D	320	GLN	2.8
1	A	29	VAL	2.7
1	B	129	VAL	2.7
1	B	243	ASP	2.6
1	B	228	LEU	2.6
1	A	326	HIS	2.6
1	A	119	ASN	2.6
1	D	108	ALA	2.6
1	B	27	ASN	2.6
1	B	285	ALA	2.6
1	A	157	LEU	2.6
1	D	319	ALA	2.5
1	D	149	PRO	2.5
1	C	119	ASN	2.5
1	A	75	GLY	2.5
1	D	148	ASP	2.4
1	C	230	ALA	2.4
1	C	325	GLU	2.3
1	C	244	ASP	2.3
1	B	146	GLN	2.3
1	A	146	GLN	2.3
1	B	28	THR	2.3
1	C	145	GLY	2.3
1	A	107	GLN	2.3
1	A	20	ALA	2.3
1	B	107	GLN	2.2
1	A	101	ALA	2.2
1	D	144	PRO	2.2
1	D	280	ASN	2.2
1	A	290	THR	2.2
1	A	284	GLY	2.2
1	A	181	ASP	2.2
1	D	181	ASP	2.1
1	B	21	PRO	2.1
1	D	147	LYS	2.0
1	A	123	GLU	2.0
1	C	286	THR	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	CA	C	601	1/1	0.94	0.19	3.05	45,45,45,45	0
2	CA	B	501	1/1	0.96	0.20	2.02	40,40,40,40	0
2	CA	D	701	1/1	0.94	0.19	1.40	53,53,53,53	0
4	HEC	D	402	43/43	0.94	0.20	1.06	34,39,50,53	0
4	HEC	B	402	43/43	0.94	0.20	0.96	32,42,48,53	0
4	HEC	A	802	43/43	0.93	0.20	0.78	43,47,54,60	0
4	HEC	C	402	43/43	0.94	0.19	0.76	33,39,46,49	0
4	HEC	D	401	43/43	0.94	0.21	0.73	36,41,49,52	0
4	HEC	B	401	43/43	0.95	0.18	0.41	31,35,40,42	0
4	HEC	A	803	43/43	0.94	0.18	0.20	38,44,50,53	0
4	HEC	C	401	43/43	0.96	0.17	-0.21	34,39,50,55	0
2	CA	A	401	1/1	0.97	0.08	-3.50	46,46,46,46	0
3	ZN	B	802	1/1	0.97	0.04	-4.25	52,52,52,52	0
3	ZN	A	801	1/1	0.99	0.03	-4.33	44,44,44,44	0
3	ZN	D	702	1/1	0.93	0.10	-	83,83,83,83	0
3	ZN	A	402	1/1	0.98	0.06	-	67,67,67,67	0
3	ZN	C	602	1/1	0.98	0.04	-	72,72,72,72	0
3	ZN	B	504	1/1	0.96	0.04	-	66,66,66,66	0
3	ZN	B	502	1/1	0.93	0.08	-	83,83,83,83	0
3	ZN	B	503	1/1	0.94	0.04	-	74,74,74,74	0

6.5 Other polymers (i)

There are no such residues in this entry.