



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:39 AM GMT

PDB ID : 3MM9
Title : Dissimilatory sulfite reductase nitrite complex
Authors : Parey, K.; Warkentin, E.; Kroneck, P.M.H.; Ermler, U.
Deposited on : 2010-04-19
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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

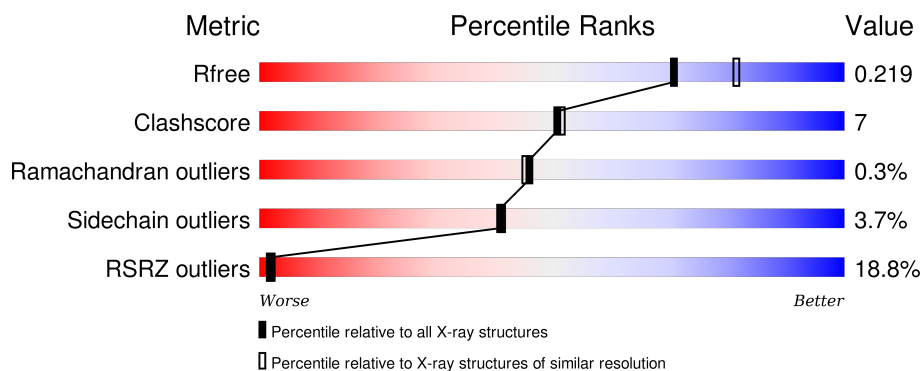
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	418	<div> <div>8%</div> <div>89%</div> <div>11%</div> </div>
1	D	418	<div> <div>27%</div> <div>82%</div> <div>17%</div> <div>.</div> </div>
2	B	366	<div> <div>6%</div> <div>85%</div> <div>13%</div> <div>..</div> </div>
2	E	366	<div> <div>34%</div> <div>73%</div> <div>23%</div> <div>..</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	NO2	A	590	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 13261 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.

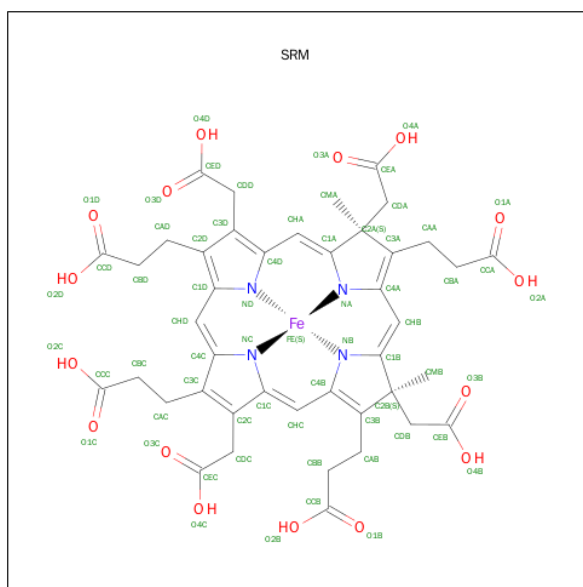
- Molecule 1 is a protein called Sulfite reductase, dissimilatory-type subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	417	Total	C	N	O	S	0	0	0
			3330	2134	557	613	26			
1	D	417	Total	C	N	O	S	0	0	0
			3330	2134	557	613	26			

- Molecule 2 is a protein called Sulfite reductase, dissimilatory-type subunit beta.

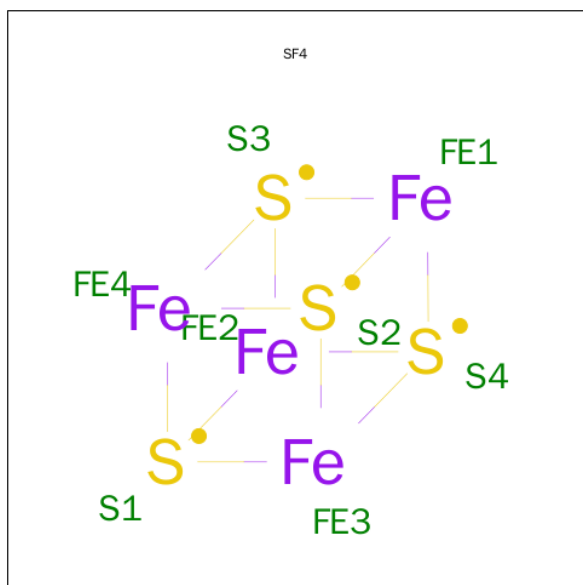
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	363	Total	C	N	O	S	0	1	0
			2907	1865	492	527	23			
2	E	363	Total	C	N	O	S	0	0	0
			2901	1862	491	526	22			

- Molecule 3 is SIROHEME (three-letter code: SRM) (formula: $C_{42}H_{42}FeN_4O_{16}$).



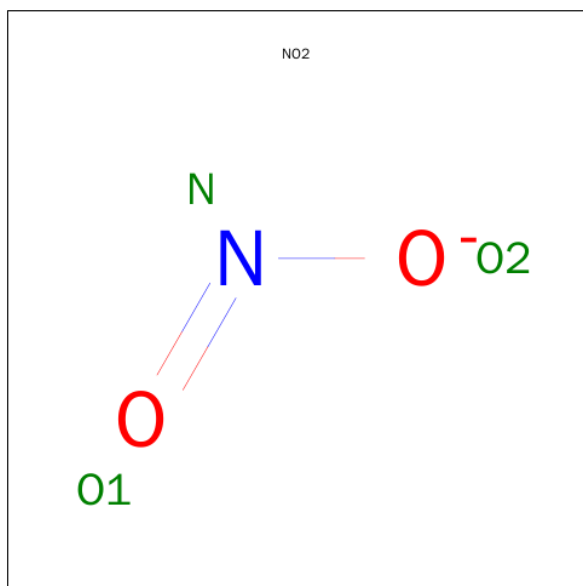
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Fe	N	O	0	0
			63	42	1	4	16		
3	B	1	Total	C	Fe	N	O	0	0
			63	42	1	4	16		
3	D	1	Total	C	Fe	N	O	0	0
			63	42	1	4	16		
3	E	1	Total	C	Fe	N	O	0	0
			63	42	1	4	16		

- Molecule 4 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Fe	S	0	0
			8	4	4		
4	A	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		
4	D	1	Total	Fe	S	0	0
			8	4	4		
4	D	1	Total	Fe	S	0	0
			8	4	4		
4	E	1	Total	Fe	S	0	0
			8	4	4		
4	E	1	Total	Fe	S	0	0
			8	4	4		

- Molecule 5 is NITRITE ION (three-letter code: NO2) (formula: NO₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	N	O	0	0
			3	1	2		

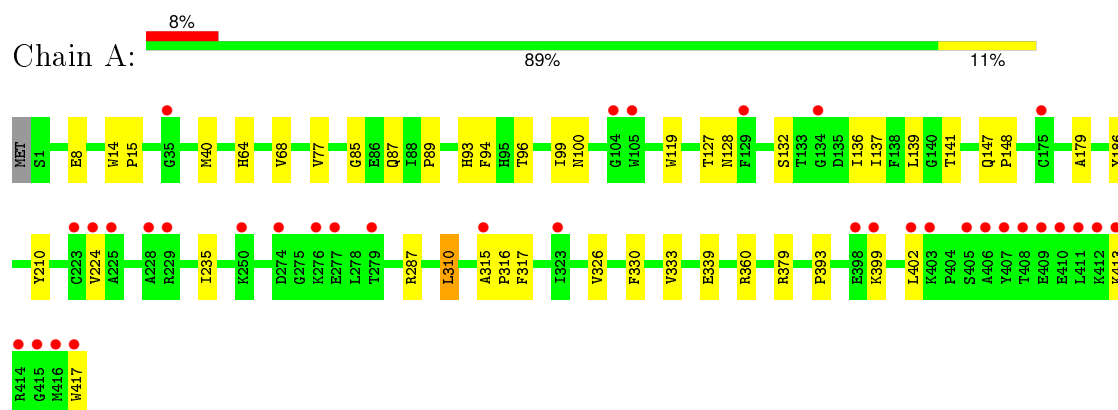
- Molecule 6 is water.

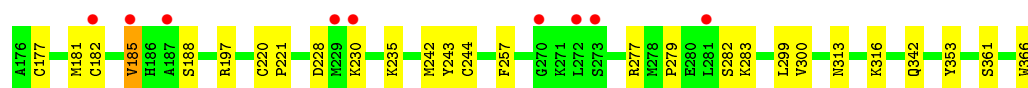
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	199	Total	O	0	0
			199	199		
6	B	226	Total	O	0	0
			226	226		
6	D	31	Total	O	0	0
			31	31		
6	E	18	Total	O	0	0
			18	18		

3 Residue-property plots

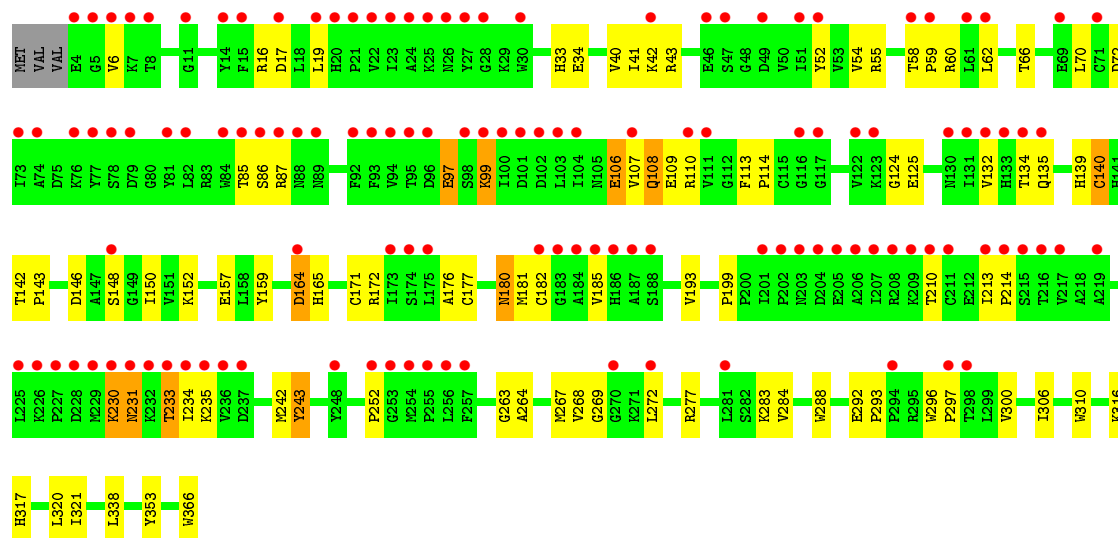
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). 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: Sulfite reductase, dissimilatory-type subunit alpha





- Molecule 2: Sulfite reductase, dissimilatory-type subunit beta



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	94.96Å 69.09Å 145.55Å 90.00° 107.46° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 47.46 – 2.10	Depositor EDS
% Data completeness (in resolution range)	90.7 (20.00-2.10) 90.6 (47.46-2.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.75 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.6.0046	Depositor
R, R_{free}	0.181 , 0.219 0.181 , 0.219	Depositor DCC
R_{free} test set	4773 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	34.1	Xtriage
Anisotropy	0.478	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.3	EDS
Estimated twinning fraction	0.019 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 95500 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13261	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, NO2, SRM

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	0.80	0/3417	0.74	2/4610 (0.0%)
1	D	0.65	4/3417 (0.1%)	0.63	0/4610
2	B	0.86	0/2990	0.81	4/4066 (0.1%)
2	E	0.69	3/2984 (0.1%)	0.67	1/4058 (0.0%)
All	All	0.75	7/12808 (0.1%)	0.71	7/17344 (0.0%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	99	LYS	CD-CE	13.18	1.84	1.51
1	D	23	LYS	CD-CE	11.96	1.81	1.51
1	D	117	ASP	CG-OD2	7.48	1.42	1.25
1	D	117	ASP	CG-OD1	5.71	1.38	1.25
2	E	106	GLU	CG-CD	5.50	1.60	1.51
1	D	113	ARG	NE-CZ	5.32	1.40	1.33
2	E	107	VAL	C-O	5.13	1.33	1.23

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	172	ARG	NE-CZ-NH2	-7.46	116.57	120.30
2	B	108	GLN	CA-CB-CG	5.83	126.23	113.40
1	A	287	ARG	NE-CZ-NH2	-5.63	117.48	120.30
2	B	60	ARG	NE-CZ-NH2	-5.32	117.64	120.30
2	B	197	ARG	NE-CZ-NH1	-5.25	117.67	120.30
1	A	360	ARG	NE-CZ-NH1	5.07	122.84	120.30
2	E	72	ASP	CB-CG-OD2	-5.02	113.78	118.30

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	3330	0	3276	27	0
1	D	3330	0	3276	51	0
2	B	2907	0	2840	37	0
2	E	2901	0	2838	65	0
3	A	63	0	34	6	0
3	B	63	0	34	3	0
3	D	63	0	34	10	0
3	E	63	0	34	12	0
4	A	16	0	0	0	0
4	B	16	0	0	0	0
4	D	16	0	0	1	0
4	E	16	0	0	1	0
5	A	3	0	0	0	0
6	A	199	0	0	1	0
6	B	226	0	0	1	0
6	D	31	0	0	1	0
6	E	18	0	0	6	0
All	All	13261	0	12366	174	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 7.

All (174) 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:23:LYS:CE	1:D:23:LYS:CD	1.81	1.57
2:E:99:LYS:CE	2:E:99:LYS:CD	1.84	1.55
1:D:218:GLY:HA3	6:D:462:HOH:O	1.60	1.01
1:D:25:ALA:HB2	1:D:44:ALA:HB3	1.44	0.96
2:E:230:LYS:HB2	2:E:231:ASN:HB2	1.53	0.89
2:B:181:MET:HG2	2:B:185:VAL:CG2	2.03	0.87
2:E:85:THR:HB	3:E:570:SRM:HAB2	1.56	0.86
3:D:580:SRM:HMB1	3:D:580:SRM:HBB2	1.58	0.85
2:E:134:THR:HB	4:E:585:SF4:S4	2.18	0.84
3:E:570:SRM:HBD2	3:E:570:SRM:HDD2	1.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:PHE:O	2:B:139:HIS:HE1	1.61	0.84
1:D:128:ASN:HB2	1:D:137:ILE:HB	1.61	0.81
2:B:181:MET:HG2	2:B:185:VAL:HG21	1.61	0.81
4:D:575:SF4:S4	6:E:465:HOH:O	2.38	0.81
1:A:147:GLN:HB3	1:A:148:PRO:HD3	1.66	0.78
2:E:230:LYS:CB	2:E:231:ASN:HB2	2.14	0.77
3:A:580:SRM:O2A	2:B:139:HIS:HD2	1.68	0.75
1:D:235:ILE:HD12	1:D:310:LEU:HD22	1.69	0.74
2:B:85:THR:HB	3:B:570:SRM:HAB1	1.68	0.74
2:E:52:TYR:CE1	2:E:97:GLU:HB3	2.26	0.71
1:D:211:LYS:NZ	3:D:580:SRM:HDD2	2.05	0.70
2:E:99:LYS:CE	2:E:99:LYS:CG	2.69	0.70
2:B:181:MET:HG2	2:B:185:VAL:HG23	1.74	0.68
2:E:125:GLU:HB3	2:E:165:HIS:HB3	1.75	0.67
1:A:235:ILE:HD12	1:A:310:LEU:HD22	1.77	0.66
3:D:580:SRM:CMB	3:D:580:SRM:HBB2	2.26	0.65
2:E:55:ARG:HH22	3:E:570:SRM:HBA2	1.61	0.65
1:D:66:GLY:H	1:D:81:TYR:HE1	1.44	0.64
2:E:140:CYS:HB3	6:E:376:HOH:O	1.98	0.63
1:D:23:LYS:CE	1:D:23:LYS:CG	2.75	0.62
2:E:230:LYS:CA	2:E:231:ASN:HB2	2.29	0.62
2:B:313:ASN:HB3	6:B:490:HOH:O	2.00	0.61
1:D:127:THR:C	1:D:128:ASN:HD22	2.04	0.61
2:E:106:GLU:O	2:E:110:ARG:HG3	2.02	0.60
1:A:339:GLU:OE2	1:A:379:ARG:NH2	2.35	0.60
1:D:129:PHE:HB2	2:E:62:LEU:HD12	1.85	0.59
3:A:580:SRM:O2A	2:B:139:HIS:CD2	2.52	0.59
2:E:146:ASP:O	2:E:150:ILE:HD12	2.02	0.59
2:E:199:PRO:HA	6:E:474:HOH:O	2.03	0.58
1:D:211:LYS:HZ3	3:D:580:SRM:HDD2	1.68	0.58
1:A:127:THR:O	2:B:61:LEU:HD12	2.04	0.57
1:D:128:ASN:OD1	2:E:60:ARG:NH1	2.38	0.57
3:E:570:SRM:O4D	3:E:570:SRM:HHA	2.06	0.56
1:D:57:ASP:HB3	1:D:59:LYS:HG2	1.87	0.56
2:E:124:GLY:HA3	2:E:316:LYS:HD2	1.87	0.56
1:D:45:ARG:HG2	1:D:49:LYS:HE2	1.88	0.56
2:E:108:GLN:HE22	2:E:114:PRO:HA	1.71	0.55
2:E:134:THR:CG2	2:E:182:CYS:HB2	2.36	0.55
2:E:296:TRP:N	2:E:297:PRO:CD	2.69	0.55
2:E:41:ILE:HD11	2:E:55:ARG:HH21	1.71	0.55
1:D:178:PRO:HG3	1:D:187:ASP:HA	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:253:ALA:HB2	1:D:258:ILE:HD12	1.89	0.55
2:E:267:MET:HG2	2:E:284:VAL:HG22	1.88	0.55
2:E:272:LEU:HB2	3:E:570:SRM:CCC	2.37	0.54
1:A:393:PRO:HG3	2:E:181:MET:HE1	1.89	0.54
2:E:66:THR:O	2:E:70:LEU:HG	2.08	0.54
1:A:186:TYR:CD1	1:A:333:VAL:HG11	2.43	0.54
1:D:99:ILE:HB	1:D:136:ILE:HB	1.89	0.54
1:A:315:ALA:HB1	1:A:316:PRO:HD2	1.90	0.53
1:D:23:LYS:CD	1:D:23:LYS:NZ	2.67	0.53
2:B:157:GLU:HG3	2:B:300:VAL:HG11	1.89	0.53
1:D:14:TRP:O	2:E:152:LYS:NZ	2.35	0.52
1:A:14:TRP:CD2	1:A:15:PRO:HD2	2.45	0.52
1:D:147:GLN:HB3	1:D:148:PRO:HD3	1.92	0.52
1:A:310:LEU:HD12	1:A:326:VAL:HA	1.91	0.52
3:D:580:SRM:HHB	3:D:580:SRM:HBA1	1.92	0.52
1:D:25:ALA:CB	1:D:44:ALA:HB3	2.30	0.52
2:B:82:LEU:HD23	2:B:82:LEU:N	2.25	0.52
2:E:87:ARG:CZ	2:E:172:ARG:HD2	2.40	0.52
1:D:133:THR:H	3:D:580:SRM:HAB2	1.75	0.51
1:A:96:THR:HG23	2:B:139:HIS:NE2	2.25	0.51
2:E:243:TYR:HA	6:E:474:HOH:O	2.09	0.51
1:D:131:GLY:HA3	3:D:580:SRM:HBB1	1.93	0.51
2:E:176:ALA:HB2	2:E:185:VAL:HG21	1.92	0.51
2:E:40:VAL:HG13	2:E:54:VAL:HG22	1.93	0.51
2:E:193:VAL:HG21	2:E:267:MET:SD	2.51	0.50
1:A:40:MET:SD	1:A:141:THR:HA	2.52	0.50
2:E:58:THR:HG22	2:E:113:PHE:CD2	2.47	0.49
2:E:233:THR:OG1	2:E:234:ILE:N	2.45	0.49
2:E:142:THR:N	2:E:143:PRO:HD3	2.27	0.49
1:D:112:LEU:HA	1:D:115:LEU:HD12	1.94	0.49
2:B:181:MET:CG	2:B:185:VAL:HG21	2.38	0.49
2:E:86:SER:OG	3:E:570:SRM:HAB1	2.13	0.49
2:E:134:THR:HG21	2:E:182:CYS:HB2	1.95	0.49
3:A:580:SRM:CMB	3:A:580:SRM:CBB	2.90	0.48
2:B:142:THR:HA	2:B:257:PHE:HZ	1.78	0.48
1:D:55:TYR:CD1	2:E:293:PRO:HB3	2.49	0.48
1:A:330:PHE:HB2	2:B:366:TRP:CH2	2.49	0.48
1:D:399:LYS:HB2	1:D:417:TRP:CZ2	2.48	0.48
1:D:82:SER:HB3	1:D:91:VAL:O	2.14	0.47
1:D:211:LYS:HZ1	3:D:580:SRM:HDD2	1.79	0.47
3:E:570:SRM:HAC2	3:E:570:SRM:HCD1	1.60	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:142:ARG:HG2	1:D:142:ARG:HH11	1.78	0.47
1:A:99:ILE:HB	1:A:136:ILE:HB	1.96	0.47
2:E:58:THR:HG22	2:E:113:PHE:CE2	2.51	0.46
2:E:263:GLY:HA3	2:E:288:TRP:NE1	2.30	0.46
1:A:77:VAL:HG13	1:A:96:THR:O	2.16	0.46
1:D:14:TRP:CD2	1:D:15:PRO:HD2	2.50	0.46
2:B:134:THR:OG1	2:B:177:CYS:SG	2.69	0.46
3:E:570:SRM:O2A	3:E:570:SRM:HMA3	2.15	0.46
2:E:210:THR:OG1	2:E:252:PRO:HG2	2.16	0.46
1:D:96:THR:HG23	2:E:139:HIS:CE1	2.50	0.46
1:A:402:LEU:HD12	1:A:417:TRP:HH2	1.80	0.46
1:D:151:GLU:HG2	2:E:6:VAL:HG22	1.96	0.46
2:B:124:GLY:HA3	2:B:316:LYS:HD3	1.98	0.45
2:E:16:ARG:HA	2:E:19:LEU:HD12	1.98	0.45
1:D:316:PRO:HG3	1:D:321:ALA:HB2	1.98	0.45
2:B:119:TRP:HB2	2:B:126:TYR:CD2	2.51	0.45
1:D:288:CYS:O	1:D:289:MET:HB2	2.17	0.45
1:D:59:LYS:HE3	1:D:61:HIS:CE1	2.51	0.45
3:A:580:SRM:C4C	2:B:182[B]:CYS:HA	2.46	0.45
1:D:37:ASP:O	1:D:121:LYS:HG3	2.16	0.45
2:E:34:GLU:O	2:E:42:LYS:HB3	2.16	0.45
1:D:80:ARG:NH2	3:D:580:SRM:O3A	2.49	0.45
1:A:128:ASN:HD22	2:B:61:LEU:HA	1.81	0.45
1:A:315:ALA:HB1	1:A:316:PRO:CD	2.47	0.45
1:D:317:PHE:HE2	2:E:180:ASN:HD22	1.65	0.44
2:E:157:GLU:HG3	2:E:300:VAL:HG11	1.99	0.44
2:E:134:THR:HG22	2:E:182:CYS:HB2	1.97	0.44
2:E:264:ALA:O	2:E:288:TRP:HA	2.18	0.44
2:B:181:MET:CG	2:B:185:VAL:CG2	2.89	0.44
3:D:580:SRM:CBB	3:D:580:SRM:CMB	2.91	0.44
1:D:80:ARG:HA	1:D:80:ARG:HD3	1.85	0.44
2:B:146:ASP:O	2:B:150:ILE:HD12	2.18	0.44
3:A:580:SRM:CCA	2:B:139:HIS:HD2	2.31	0.43
1:A:393:PRO:CG	2:E:181:MET:HE1	2.48	0.43
1:A:119:TRP:CH2	1:A:141:THR:HB	2.54	0.43
2:E:33:HIS:HB3	2:E:43:ARG:NH1	2.33	0.43
1:D:36:LYS:O	1:D:38:VAL:N	2.51	0.43
1:A:94:PHE:O	2:B:139:HIS:CE1	2.53	0.43
2:E:316:LYS:HG2	2:E:317:HIS:CD2	2.53	0.43
2:E:306:ILE:HD11	2:E:338:LEU:HD11	2.01	0.43
2:E:85:THR:CB	3:E:570:SRM:HAB2	2.40	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:570:SRM:HDD2	3:E:570:SRM:CBD	2.40	0.43
1:D:330:PHE:HB2	2:E:366:TRP:CH2	2.53	0.43
2:B:228:ASP:HB2	2:B:235:LYS:HG3	2.00	0.42
1:D:248:ALA:O	1:D:251:GLU:HB3	2.20	0.42
1:D:129:PHE:HA	1:D:130:HIS:HA	1.73	0.42
2:B:142:THR:N	2:B:143:PRO:CD	2.83	0.42
1:D:235:ILE:CD1	1:D:310:LEU:HD22	2.46	0.42
2:B:175:LEU:HD23	2:B:175:LEU:C	2.40	0.42
3:A:580:SRM:HMB3	3:A:580:SRM:HBB2	2.01	0.42
1:D:310:LEU:HD12	1:D:326:VAL:HA	2.01	0.42
2:E:320:LEU:HD23	2:E:320:LEU:C	2.39	0.42
1:A:96:THR:HG22	1:A:139:LEU:HA	2.02	0.42
2:B:220:CYS:HA	2:B:221:PRO:HD3	1.90	0.42
2:E:164:ASP:HB2	6:E:375:HOH:O	2.20	0.42
1:D:186:TYR:CD1	1:D:333:VAL:HG11	2.55	0.42
2:B:279:PRO:HD2	2:B:361:SER:HB2	2.01	0.42
1:A:85:GLY:O	1:A:89:PRO:HA	2.19	0.41
2:E:140:CYS:CB	6:E:376:HOH:O	2.64	0.41
2:E:59:PRO:HD3	2:E:113:PHE:CZ	2.55	0.41
1:A:179:ALA:O	2:B:23:ILE:HG23	2.19	0.41
2:E:213:ILE:HB	2:E:214:PRO:HD3	2.03	0.41
2:B:170:MET:CE	3:B:570:SRM:HBD1	2.51	0.41
1:A:8:GLU:OE1	6:A:511:HOH:O	2.20	0.41
2:E:292:GLU:O	2:E:293:PRO:C	2.60	0.41
2:B:299:LEU:C	2:B:299:LEU:HD23	2.41	0.41
2:B:133:HIS:CG	2:B:151:VAL:HG21	2.56	0.41
1:D:139:LEU:HD13	2:E:135:GLN:HE22	1.86	0.41
2:E:171:CYS:HB2	2:E:310:TRP:CH2	2.56	0.41
3:E:570:SRM:CBA	3:E:570:SRM:CHB	2.97	0.41
1:D:45:ARG:HH11	1:D:45:ARG:HG3	1.85	0.41
2:B:342:GLN:HG2	1:D:371:ARG:HG3	2.03	0.41
2:B:164:ASP:HB3	2:B:166:LYS:HG3	2.03	0.41
1:D:271:ILE:HD11	1:D:278:LEU:HD21	2.02	0.41
3:B:570:SRM:C1A	3:B:570:SRM:HBA1	2.51	0.41
1:A:317:PHE:CZ	2:B:244:CYS:HB2	2.56	0.41
2:E:106:GLU:HG2	2:E:110:ARG:HD2	2.02	0.40
3:E:570:SRM:HHA	3:E:570:SRM:CED	2.51	0.40
2:E:269:GLY:O	2:E:321:ILE:HB	2.22	0.40
1:A:128:ASN:HB2	1:A:137:ILE:HB	2.03	0.40
2:B:353:TYR:HA	2:E:353:TYR:HA	2.04	0.40
1:D:101:GLN:HA	1:D:102:PRO:HD3	1.96	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	415/418 (99%)	402 (97%)	13 (3%)	0	100	100
1	D	415/418 (99%)	386 (93%)	28 (7%)	1 (0%)	52	53
2	B	362/366 (99%)	347 (96%)	14 (4%)	1 (0%)	46	45
2	E	361/366 (99%)	322 (89%)	37 (10%)	2 (1%)	30	24
All	All	1553/1568 (99%)	1457 (94%)	92 (6%)	4 (0%)	46	45

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	37	ASP
2	E	159	TYR
2	E	231	ASN
2	B	142	THR

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	353/354 (100%)	342 (97%)	11 (3%)	47	50
1	D	353/354 (100%)	342 (97%)	11 (3%)	47	50
2	B	315/317 (99%)	305 (97%)	10 (3%)	46	48

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	314/317 (99%)	296 (94%)	18 (6%)	25	22
All	All	1335/1342 (100%)	1285 (96%)	50 (4%)	41	41

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

Mol	Chain	Res	Type
1	A	64	HIS
1	A	68	VAL
1	A	87	GLN
1	A	93	HIS
1	A	100	ASN
1	A	132	SER
1	A	210	TYR
1	A	224	VAL
1	A	310	LEU
1	A	399	LYS
1	A	413	LYS
2	B	97	GLU
2	B	108	GLN
2	B	185	VAL
2	B	188	SER
2	B	230	LYS
2	B	242	MET
2	B	243	TYR
2	B	277	ARG
2	B	282	SER
2	B	283	LYS
1	D	100	ASN
1	D	144	GLU
1	D	210	TYR
1	D	224	VAL
1	D	247	GLU
1	D	276	LYS
1	D	299	LEU
1	D	310	LEU
1	D	339	GLU
1	D	399	LYS
1	D	413	LYS
2	E	17	ASP
2	E	97	GLU
2	E	108	GLN
2	E	109	GLU

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Mol	Chain	Res	Type
2	E	132	VAL
2	E	140	CYS
2	E	148	SER
2	E	164	ASP
2	E	177	CYS
2	E	180	ASN
2	E	230	LYS
2	E	233	THR
2	E	235	LYS
2	E	242	MET
2	E	243	TYR
2	E	268	VAL
2	E	277	ARG
2	E	283	LYS

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

Mol	Chain	Res	Type
1	A	50	GLN
1	A	100	ASN
2	B	139	HIS
1	D	50	GLN
1	D	100	ASN
2	E	108	GLN
2	E	135	GLN
2	E	180	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

13 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	SF4	A	575	1	0,12,12	0.00	-	0,24,24	0.00	-
4	SF4	A	576	1	0,12,12	0.00	-	0,24,24	0.00	-
3	SRM	A	580	2,5	29,70,70	2.11	8 (27%)	29,112,112	4.08	11 (37%)
5	NO2	A	590	3	2,2,2	1.33	0	1,1,1	0.47	0
3	SRM	B	570	1	29,70,70	2.33	8 (27%)	29,112,112	4.70	18 (62%)
4	SF4	B	585	2	0,12,12	0.00	-	0,24,24	0.00	-
4	SF4	B	586	2	0,12,12	0.00	-	0,24,24	0.00	-
4	SF4	D	575	1,6	0,12,12	0.00	-	0,24,24	0.00	-
4	SF4	D	576	1	0,12,12	0.00	-	0,24,24	0.00	-
3	SRM	D	580	-	29,70,70	2.19	8 (27%)	29,112,112	3.96	14 (48%)
3	SRM	E	570	1	29,70,70	2.74	10 (34%)	29,112,112	4.57	16 (55%)
4	SF4	E	585	2	0,12,12	0.00	-	0,24,24	0.00	-
4	SF4	E	586	2	0,12,12	0.00	-	0,24,24	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
4	SF4	A	575	1	-	0/0/48/48	0/6/5/5
4	SF4	A	576	1	-	0/0/48/48	0/6/5/5
3	SRM	A	580	2,5	-	0/22/126/126	0/0/8/8
5	NO2	A	590	3	-	0/0/0/0	0/0/0/0
3	SRM	B	570	1	-	0/22/126/126	0/0/8/8
4	SF4	B	585	2	-	0/0/48/48	0/6/5/5
4	SF4	B	586	2	-	0/0/48/48	0/6/5/5
4	SF4	D	575	1,6	-	0/0/48/48	0/6/5/5
4	SF4	D	576	1	-	0/0/48/48	0/6/5/5
3	SRM	D	580	-	-	0/22/126/126	0/0/8/8
3	SRM	E	570	1	-	0/22/126/126	0/0/8/8

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SF4	E	585	2	-	0/0/48/48	0/6/5/5
4	SF4	E	586	2	-	0/0/48/48	0/6/5/5

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	570	SRM	C1B-NB	-5.58	1.29	1.38
3	E	570	SRM	C4A-NA	-5.29	1.29	1.39
3	E	570	SRM	C4C-NC	-5.18	1.29	1.36
3	B	570	SRM	C1B-NB	-5.14	1.30	1.38
3	E	570	SRM	C1C-NC	-4.85	1.30	1.36
3	B	570	SRM	C4C-NC	-4.48	1.30	1.36
3	B	570	SRM	C4A-NA	-4.09	1.31	1.39
3	B	570	SRM	C1C-NC	-3.72	1.31	1.36
3	A	580	SRM	C4A-NA	-3.72	1.32	1.39
3	D	580	SRM	C4A-NA	-3.50	1.32	1.39
3	D	580	SRM	C1A-NA	-3.11	1.33	1.38
3	E	570	SRM	CHC-C4B	-2.62	1.33	1.39
3	B	570	SRM	CDA-C2A	-2.41	1.52	1.56
3	E	570	SRM	C4B-NB	-2.27	1.34	1.39
3	E	570	SRM	C1A-NA	-2.25	1.34	1.38
3	A	580	SRM	CDA-C2A	-2.21	1.52	1.56
3	A	580	SRM	C1A-NA	-2.20	1.34	1.38
3	D	580	SRM	C4B-NB	-2.17	1.35	1.39
3	A	580	SRM	FE-NA	2.46	2.05	1.95
3	D	580	SRM	CAD-C2D	2.75	1.56	1.52
3	E	570	SRM	CAD-C2D	2.93	1.57	1.52
3	D	580	SRM	FE-NA	3.08	2.08	1.95
3	A	580	SRM	FE-NB	3.09	2.08	1.95
3	A	580	SRM	CAD-C2D	3.38	1.57	1.52
3	D	580	SRM	FE-NB	3.52	2.09	1.95
3	B	570	SRM	CAA-C3A	3.65	1.57	1.51
3	B	570	SRM	C3C-C2C	3.86	1.49	1.37
3	D	580	SRM	C3C-C2C	4.01	1.49	1.37
3	A	580	SRM	C3C-C2C	4.03	1.49	1.37
3	E	570	SRM	C3C-C2C	4.22	1.50	1.37
3	B	570	SRM	C3D-C2D	5.26	1.51	1.39
3	A	580	SRM	C3D-C2D	6.32	1.53	1.39
3	E	570	SRM	C3D-C2D	7.01	1.55	1.39
3	D	580	SRM	C3D-C2D	7.03	1.55	1.39

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	580	SRM	CAB-C3B-C2B	-16.14	105.28	123.46
3	B	570	SRM	CAA-C3A-C2A	-12.81	109.04	123.46
3	E	570	SRM	CAA-C3A-C2A	-10.83	111.27	123.46
3	D	580	SRM	CDD-C3D-C4D	-9.72	111.54	127.34
3	B	570	SRM	CBC-CAC-C3C	-8.95	96.48	112.53
3	D	580	SRM	CAB-C3B-C2B	-8.90	113.44	123.46
3	E	570	SRM	CDC-C2C-C1C	-8.56	113.56	127.38
3	B	570	SRM	C4A-NA-C1A	-8.15	102.48	106.90
3	B	570	SRM	CAB-C3B-C2B	-7.88	114.59	123.46
3	E	570	SRM	CAC-C3C-C4C	-7.46	118.91	127.01
3	E	570	SRM	C4A-NA-C1A	-7.40	102.88	106.90
3	B	570	SRM	CEC-CDC-C2C	-6.92	103.08	116.31
3	E	570	SRM	CAD-C2D-C1D	-6.50	119.95	127.01
3	D	580	SRM	CAD-C2D-C1D	-6.22	120.25	127.01
3	E	570	SRM	CAC-C3C-C2C	-5.98	114.50	129.38
3	E	570	SRM	CEC-CDC-C2C	-4.54	107.63	116.31
3	B	570	SRM	C3B-C4B-NB	-4.04	105.60	110.09
3	D	580	SRM	CAA-C3A-C2A	-4.02	118.94	123.46
3	A	580	SRM	C2A-CDA-CEA	-3.98	109.28	115.45
3	D	580	SRM	CAD-C2D-C3D	-3.98	119.48	129.38
3	E	570	SRM	CHB-C4A-C3A	-3.97	116.46	125.48
3	A	580	SRM	CAC-CBC-CCC	-3.68	106.00	112.75
3	A	580	SRM	C4B-NB-C1B	-3.63	104.93	106.90
3	B	570	SRM	CHB-C4A-C3A	-3.38	117.79	125.48
3	D	580	SRM	C4B-NB-C1B	-3.18	105.17	106.90
3	E	570	SRM	CBC-CAC-C3C	-3.17	106.85	112.53
3	B	570	SRM	CDD-C3D-C4D	-2.83	122.74	127.34
3	E	570	SRM	C4B-NB-C1B	-2.71	105.43	106.90
3	E	570	SRM	CDD-C3D-C4D	-2.69	122.97	127.34
3	B	570	SRM	CAC-C3C-C2C	-2.47	123.24	129.38
3	D	580	SRM	C3A-C4A-NA	-2.44	107.38	110.09
3	B	570	SRM	CAD-C2D-C3D	-2.40	123.40	129.38
3	D	580	SRM	CAC-CBC-CCC	-2.28	108.57	112.75
3	B	570	SRM	CMA-C2A-CDA	-2.24	107.10	109.76
3	D	580	SRM	CBC-CAC-C3C	-2.22	108.54	112.53
3	A	580	SRM	CAD-C2D-C1D	-2.11	124.72	127.01
3	E	570	SRM	C2B-CDB-CEB	2.23	118.91	115.45
3	B	570	SRM	CAA-CBA-CCA	2.26	116.88	112.75
3	A	580	SRM	C3B-C4B-NB	2.27	112.61	110.09
3	B	570	SRM	C2B-CDB-CEB	2.35	119.09	115.45
3	B	570	SRM	CAD-C2D-C1D	2.37	129.58	127.01
3	D	580	SRM	CAC-C3C-C4C	2.43	129.64	127.01
3	A	580	SRM	CED-CDD-C3D	2.67	121.41	116.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	570	SRM	CHC-C4B-NB	2.88	129.31	123.70
3	D	580	SRM	C3B-C4B-NB	3.22	113.66	110.09
3	B	570	SRM	CED-CDD-C3D	3.61	123.21	116.31
3	A	580	SRM	CMA-C2A-CDA	3.98	114.50	109.76
3	E	570	SRM	CAB-CBB-CCB	4.03	120.13	112.75
3	A	580	SRM	CAC-C3C-C4C	4.85	132.27	127.01
3	E	570	SRM	CMB-C2B-CDB	5.10	115.83	109.76
3	D	580	SRM	CBD-CAD-C2D	5.29	122.01	112.53
3	E	570	SRM	CBD-CAD-C2D	5.41	122.23	112.53
3	D	580	SRM	CMA-C2A-CDA	5.66	116.50	109.76
3	A	580	SRM	CBD-CAD-C2D	6.45	124.09	112.53
3	B	570	SRM	CBD-CAD-C2D	7.47	125.91	112.53
3	B	570	SRM	C3A-C4A-NA	7.63	118.57	110.09
3	A	580	SRM	C4A-NA-C1A	8.04	111.27	106.90
3	E	570	SRM	C3A-C4A-NA	8.19	119.19	110.09
3	D	580	SRM	C4A-NA-C1A	9.55	112.08	106.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 33 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	580	SRM	6	0
3	B	570	SRM	3	0
4	D	575	SF4	1	0
3	D	580	SRM	10	0
3	E	570	SRM	12	0
4	E	585	SF4	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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	417/418 (99%)	0.37	35 (8%) 14 19	21, 34, 73, 133	0
1	D	417/418 (99%)	1.37	112 (26%) 1 1	29, 87, 142, 181	0
2	B	363/366 (99%)	0.20	21 (5%) 26 34	20, 32, 45, 79	0
2	E	363/366 (99%)	1.79	126 (34%) 0 1	34, 91, 137, 178	0
All	All	1560/1568 (99%)	0.93	294 (18%) 2 2	20, 52, 133, 181	0

All (294) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	417	TRP	10.9
2	E	4	GLU	10.6
1	D	33	ALA	9.6
2	E	207	ILE	9.1
2	E	234	ILE	8.6
2	E	184	ALA	8.0
1	D	132	SER	7.7
1	D	131	GLY	7.6
2	E	77	TYR	7.6
2	E	205	GLU	7.2
1	D	1	SER	6.9
2	E	183	GLY	6.7
2	E	233	THR	6.7
1	D	72	GLY	6.7
1	D	5	LEU	6.6
2	E	23	ILE	6.6
1	D	40	MET	6.3
2	E	232	LYS	6.2
1	D	129	PHE	6.0
2	E	214	PRO	6.0
2	E	86	SER	5.9

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Mol	Chain	Res	Type	RSRZ
1	D	67	ILE	5.9
1	D	130	HIS	5.9
1	A	415	GLY	5.8
2	E	272	LEU	5.8
2	E	88	ASN	5.8
1	A	416	MET	5.8
2	E	253	GLY	5.7
2	E	116	GLY	5.4
2	E	78	SER	5.4
1	D	9	LEU	5.3
2	E	21	PRO	5.3
2	E	256	LEU	5.2
1	D	225	ALA	5.1
1	A	414	ARG	5.1
1	D	228	ALA	5.0
2	E	100	ILE	5.0
2	E	236	VAL	5.0
2	E	229	MET	4.9
1	A	411	LEU	4.9
1	A	407	TYR	4.9
2	E	182	CYS	4.9
1	D	71	VAL	4.9
2	E	185	VAL	4.8
2	E	27	TYR	4.8
2	E	87	ARG	4.8
2	E	204	ASP	4.8
2	E	217	VAL	4.8
1	A	413	LYS	4.8
1	D	224	VAL	4.8
2	E	93	PHE	4.7
2	E	5	GLY	4.7
1	D	70	VAL	4.7
2	E	213	ILE	4.6
2	E	132	VAL	4.6
1	D	154	GLY	4.6
2	E	103	LEU	4.6
1	D	134	GLY	4.6
2	E	211	CYS	4.5
2	E	6	VAL	4.5
2	E	210	THR	4.5
2	E	201	ILE	4.4
2	E	104	ILE	4.4

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Mol	Chain	Res	Type	RSRZ
1	D	263	VAL	4.4
2	E	230	LYS	4.3
2	E	133	HIS	4.3
2	E	122	VAL	4.3
2	B	272	LEU	4.3
2	E	208	ARG	4.3
2	E	85	THR	4.3
1	D	36	LYS	4.3
2	E	202	PRO	4.2
2	E	227	PRO	4.2
1	D	254	SER	4.2
2	E	20	HIS	4.2
2	E	131	ILE	4.2
1	A	406	ALA	4.1
2	E	175	LEU	4.1
1	D	88	ILE	4.1
2	B	4	GLU	4.1
2	E	22	VAL	4.1
1	D	115	LEU	4.1
2	E	94	VAL	4.1
2	E	216	THR	4.1
1	D	28	MET	4.0
1	A	408	THR	4.0
2	E	71	CYS	4.0
1	A	224	VAL	4.0
2	E	209	LYS	4.0
1	D	127	THR	4.0
1	D	207	MET	3.9
2	E	188	SER	3.9
1	D	249	VAL	3.9
2	E	46	GLU	3.9
2	E	231	ASN	3.9
2	E	225	LEU	3.8
2	E	25	LYS	3.8
2	E	235	LYS	3.8
2	E	111	VAL	3.8
1	D	137	ILE	3.8
1	D	323	ILE	3.8
1	D	32	ALA	3.7
2	E	76	LYS	3.7
2	E	92	PHE	3.7
1	D	229	ARG	3.7

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Mol	Chain	Res	Type	RSRZ
2	E	102	ASP	3.7
1	D	244	VAL	3.6
1	D	157	GLU	3.6
1	D	259	GLU	3.6
2	E	215	SER	3.6
1	D	136	ILE	3.5
2	E	219	ALA	3.5
1	D	145	TYR	3.5
1	D	151	GLU	3.5
2	E	51	ILE	3.5
1	D	298	ALA	3.5
1	A	412	LYS	3.4
1	D	417	TRP	3.4
2	E	42	LYS	3.4
2	E	123	LYS	3.4
1	D	274	ASP	3.4
1	D	4	PRO	3.4
1	D	64	HIS	3.4
2	E	298	THR	3.4
2	E	73	ILE	3.4
2	E	173	ILE	3.4
2	E	98	SER	3.4
1	D	34	GLU	3.4
1	D	89	PRO	3.4
2	E	26	ASN	3.4
1	A	409	GLU	3.4
1	D	105	TRP	3.3
2	E	254	MET	3.3
2	E	174	SER	3.3
1	D	275	GLY	3.3
1	D	74	GLY	3.3
1	A	323	ILE	3.3
1	D	2	GLU	3.3
1	D	31	ALA	3.3
1	D	117	ASP	3.2
2	E	294	PRO	3.2
1	D	86	GLU	3.2
2	E	95	THR	3.2
1	D	47	LEU	3.2
2	E	62	LEU	3.2
1	A	410	GLU	3.2
1	D	69	SER	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	48	LEU	3.2
1	D	49	LYS	3.2
2	E	206	ALA	3.2
1	D	273	TRP	3.2
1	D	81	TYR	3.2
1	D	333	VAL	3.1
1	D	257	ASP	3.1
2	B	229	MET	3.1
1	D	276	LYS	3.1
1	D	21	ILE	3.1
2	E	8	THR	3.1
2	E	134	THR	3.1
1	D	35	GLY	3.1
2	E	252	PRO	3.1
2	E	24	ALA	3.0
1	A	276	LYS	3.0
2	E	96	ASP	3.0
2	B	182[A]	CYS	3.0
2	E	47	SER	3.0
1	D	45	ARG	3.0
2	B	90	VAL	3.0
2	E	248	TYR	3.0
2	E	186	HIS	3.0
1	D	332	GLU	2.9
2	E	7	LYS	2.9
1	D	54	SER	2.9
2	B	281	LEU	2.9
2	E	61	LEU	2.9
1	D	226	SER	2.9
1	D	227	LYS	2.9
1	D	146	LEU	2.9
2	E	82	LEU	2.9
2	B	131	ILE	2.9
1	D	144	GLU	2.9
2	E	84	TRP	2.9
1	D	160	PHE	2.9
2	E	99	LYS	2.9
1	D	7	ASP	2.9
2	B	132	VAL	2.8
1	A	250	LYS	2.8
2	E	89	ASN	2.8
1	D	56	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	272	LYS	2.7
1	D	111	ALA	2.7
1	D	223	CYS	2.7
2	B	86	SER	2.7
2	E	203	ASN	2.7
1	D	313	GLY	2.7
2	E	52	TYR	2.7
2	E	81	TYR	2.7
1	D	30	LYS	2.7
2	B	230	LYS	2.7
2	E	69	GLU	2.7
1	D	110	LYS	2.7
1	A	405	SER	2.7
1	D	8	GLU	2.7
1	A	105	TRP	2.7
2	E	30	TRP	2.7
1	D	258	ILE	2.6
2	E	228	ASP	2.6
1	D	222	ASP	2.6
1	A	228	ALA	2.6
1	A	277	GLU	2.6
1	A	129	PHE	2.6
1	A	274	ASP	2.6
1	D	58	LYS	2.6
1	D	83	ASP	2.6
1	A	225	ALA	2.6
1	A	399	LYS	2.6
2	E	226	LYS	2.5
1	D	251	GLU	2.5
1	A	398	GLU	2.5
1	A	35	GLY	2.5
1	D	24	THR	2.5
2	E	28	GLY	2.5
2	E	58	THR	2.5
1	D	315	ALA	2.5
2	E	187	ALA	2.5
2	E	15	PHE	2.5
1	D	260	ASN	2.5
2	E	237	ASP	2.5
1	D	53	ILE	2.5
1	A	315	ALA	2.4
2	E	79	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	138	PHE	2.4
1	A	229	ARG	2.4
1	D	26	GLU	2.4
1	D	73	TYR	2.4
2	E	49	ASP	2.4
1	D	133	THR	2.4
2	E	107	VAL	2.4
1	A	223	CYS	2.4
1	D	38	VAL	2.3
2	E	130	ASN	2.3
2	E	14	TYR	2.3
1	D	178	PRO	2.3
1	D	206	PRO	2.3
1	D	18	VAL	2.3
2	E	164	ASP	2.3
2	E	117	GLY	2.3
1	D	338	ASP	2.3
2	E	17	ASP	2.3
1	A	279	THR	2.3
2	B	187	ALA	2.3
2	B	129	SER	2.3
1	D	112	LEU	2.3
1	D	279	THR	2.3
2	B	58	THR	2.2
2	E	255	PRO	2.2
2	E	135	GLN	2.2
2	B	85	THR	2.2
1	D	255	TRP	2.2
2	B	84	TRP	2.2
2	E	19	LEU	2.2
2	E	281	LEU	2.2
1	D	43	GLY	2.2
1	A	403	LYS	2.2
1	D	94	PHE	2.2
2	B	174	SER	2.2
2	B	270	GLY	2.2
2	B	185	VAL	2.2
2	E	74	ALA	2.2
2	E	11	GLY	2.2
1	D	304	GLU	2.2
1	D	128	ASN	2.2
2	E	59	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
2	E	148	SER	2.1
2	E	110	ARG	2.1
1	D	107	TYR	2.1
1	A	134	GLY	2.1
2	B	134	THR	2.1
1	A	402	LEU	2.1
2	E	257	PHE	2.1
2	B	273	SER	2.1
2	B	87	ARG	2.1
2	E	270	GLY	2.1
1	D	99	ILE	2.1
1	D	195	LEU	2.1
1	D	106	PHE	2.1
1	D	150	PHE	2.0
1	A	104	GLY	2.0
1	D	122	TRP	2.0
1	D	200	GLN	2.0
1	D	322	VAL	2.0
2	E	297	PRO	2.0
1	A	175	CYS	2.0
2	E	101	ASP	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	NO2	A	590	3/3	0.95	0.27	3.16	30,30,33,34	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	SRM	D	580	63/63	0.89	0.25	0.06	71,95,121,130	0
3	SRM	B	570	63/63	0.97	0.20	0.02	19,24,29,31	0
3	SRM	E	570	63/63	0.91	0.21	-0.12	61,78,91,100	0
3	SRM	A	580	63/63	0.96	0.16	-0.61	22,30,43,56	0
4	SF4	B	585	8/8	0.92	0.13	-0.75	24,28,32,33	8
4	SF4	A	576	8/8	0.98	0.08	-1.18	33,35,36,37	0
4	SF4	B	586	8/8	0.98	0.06	-1.33	30,31,32,33	0
4	SF4	A	575	8/8	0.98	0.11	-1.41	24,26,27,29	0
4	SF4	E	585	8/8	0.92	0.09	-1.58	83,86,90,91	8
4	SF4	E	586	8/8	0.97	0.07	-1.63	69,73,76,76	0
4	SF4	D	575	8/8	0.98	0.06	-1.84	75,77,82,85	0
4	SF4	D	576	8/8	0.96	0.04	-3.47	54,57,60,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.