



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:32 AM GMT

PDB ID : 2DE6
Title : The reduced complex between oxygenase and ferredoxin in carbazole 1,9a-dioxygenase
Authors : Ashikawa, Y.; Nojiri, H.
Deposited on : 2006-02-08
Resolution : 1.80 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

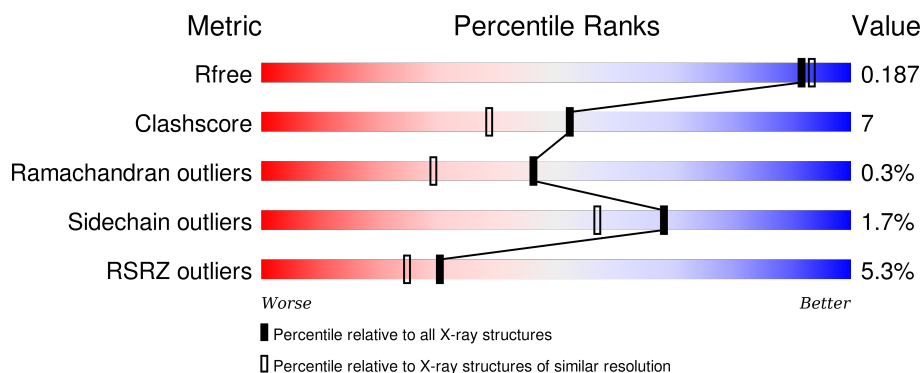
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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	392	<div> <div>3%</div> <div>85%</div> <div>14%</div> <div>.</div> </div>
1	B	392	<div> <div>3%</div> <div>82%</div> <div>17%</div> <div>..</div> </div>
1	C	392	<div> <div>3%</div> <div>81%</div> <div>18%</div> <div>.</div> </div>
2	D	115	<div> <div>28%</div> <div>79%</div> <div>11%</div> <div>10%</div> </div>
2	E	115	<div> <div>7%</div> <div>81%</div> <div>11%</div> <div>8%</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	115	

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
4	FES	B	401	-	-	-	X
4	FES	E	201	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13231 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 terminal oxygenase component of carbazole.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	389	Total	C	N	O	S	0	0	0
			3136	2004	535	583	14			
1	B	390	Total	C	N	O	S	0	0	0
			3146	2010	538	584	14			
1	C	389	Total	C	N	O	S	0	0	0
			3136	2004	535	583	14			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	385	LEU	-	EXPRESSION TAG	GB 28201207
A	386	GLU	-	EXPRESSION TAG	GB 28201207
A	387	HIS	-	EXPRESSION TAG	GB 28201207
A	388	HIS	-	EXPRESSION TAG	GB 28201207
A	389	HIS	-	EXPRESSION TAG	GB 28201207
A	390	HIS	-	EXPRESSION TAG	GB 28201207
A	391	HIS	-	EXPRESSION TAG	GB 28201207
A	392	HIS	-	EXPRESSION TAG	GB 28201207
B	385	LEU	-	EXPRESSION TAG	GB 28201207
B	386	GLU	-	EXPRESSION TAG	GB 28201207
B	387	HIS	-	EXPRESSION TAG	GB 28201207
B	388	HIS	-	EXPRESSION TAG	GB 28201207
B	389	HIS	-	EXPRESSION TAG	GB 28201207
B	390	HIS	-	EXPRESSION TAG	GB 28201207
B	391	HIS	-	EXPRESSION TAG	GB 28201207
B	392	HIS	-	EXPRESSION TAG	GB 28201207
C	385	LEU	-	EXPRESSION TAG	GB 28201207
C	386	GLU	-	EXPRESSION TAG	GB 28201207
C	387	HIS	-	EXPRESSION TAG	GB 28201207
C	388	HIS	-	EXPRESSION TAG	GB 28201207
C	389	HIS	-	EXPRESSION TAG	GB 28201207
C	390	HIS	-	EXPRESSION TAG	GB 28201207
C	391	HIS	-	EXPRESSION TAG	GB 28201207

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Chain	Residue	Modelled	Actual	Comment	Reference
C	392	HIS	-	EXPRESSION TAG	GB 28201207

- Molecule 2 is a protein called ferredoxin component of carbazole.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	104	Total	C	N	O	S	0	0	0
			768	483	129	149	7			
2	E	106	Total	C	N	O	S	0	0	0
			785	494	132	152	7			
2	F	104	Total	C	N	O	S	0	0	0
			768	483	129	149	7			

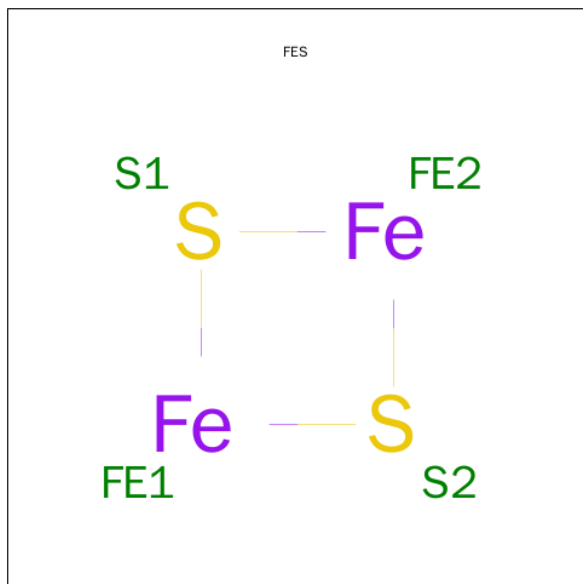
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	108	LEU	-	EXPRESSION TAG	GB 27228521
D	109	GLU	-	EXPRESSION TAG	GB 27228521
D	110	HIS	-	EXPRESSION TAG	GB 27228521
D	111	HIS	-	EXPRESSION TAG	GB 27228521
D	112	HIS	-	EXPRESSION TAG	GB 27228521
D	113	HIS	-	EXPRESSION TAG	GB 27228521
D	114	HIS	-	EXPRESSION TAG	GB 27228521
D	115	HIS	-	EXPRESSION TAG	GB 27228521
E	108	LEU	-	EXPRESSION TAG	GB 27228521
E	109	GLU	-	EXPRESSION TAG	GB 27228521
E	110	HIS	-	EXPRESSION TAG	GB 27228521
E	111	HIS	-	EXPRESSION TAG	GB 27228521
E	112	HIS	-	EXPRESSION TAG	GB 27228521
E	113	HIS	-	EXPRESSION TAG	GB 27228521
E	114	HIS	-	EXPRESSION TAG	GB 27228521
E	115	HIS	-	EXPRESSION TAG	GB 27228521
F	108	LEU	-	EXPRESSION TAG	GB 27228521
F	109	GLU	-	EXPRESSION TAG	GB 27228521
F	110	HIS	-	EXPRESSION TAG	GB 27228521
F	111	HIS	-	EXPRESSION TAG	GB 27228521
F	112	HIS	-	EXPRESSION TAG	GB 27228521
F	113	HIS	-	EXPRESSION TAG	GB 27228521
F	114	HIS	-	EXPRESSION TAG	GB 27228521
F	115	HIS	-	EXPRESSION TAG	GB 27228521

- Molecule 3 is FE (II) ION (three-letter code: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Fe 1 1	0	0
3	A	1	Total Fe 1 1	0	0
3	C	1	Total Fe 1 1	0	0

- Molecule 4 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Fe S 4 2 2	0	0
4	B	1	Total Fe S 4 2 2	0	0
4	C	1	Total Fe S 4 2 2	0	0
4	D	1	Total Fe S 4 2 2	0	0
4	E	1	Total Fe S 4 2 2	0	0
4	F	1	Total Fe S 4 2 2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	411	Total O 411 411	0	0

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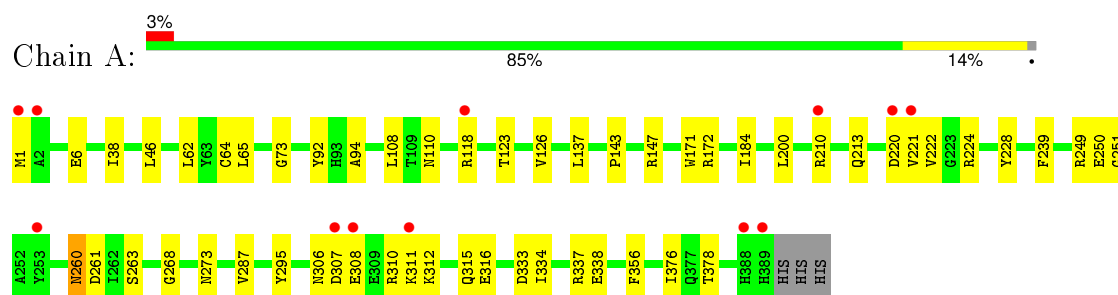
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	413	Total 413	O 413	0	0
5	C	397	Total 397	O 397	0	0
5	D	63	Total 63	O 63	0	0
5	E	86	Total 86	O 86	0	0
5	F	95	Total 95	O 95	0	0

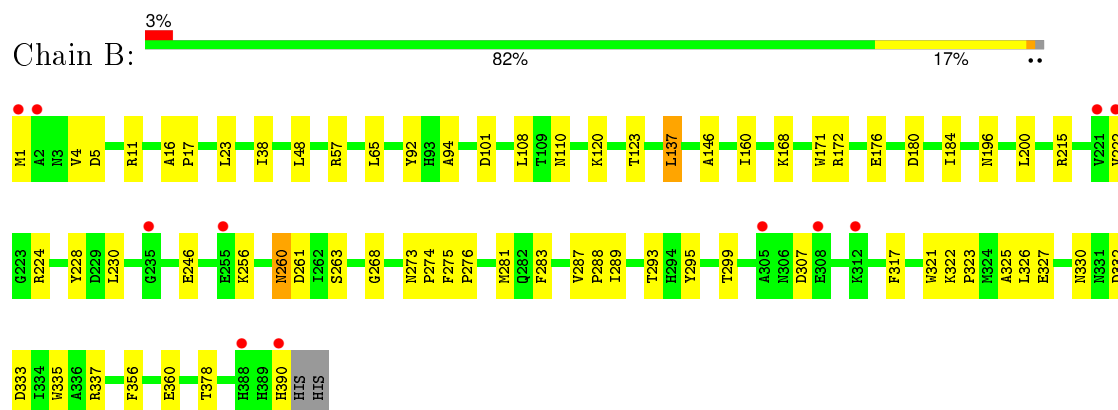
3 Residue-property plots

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 ($RSRZ > 2$). 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.

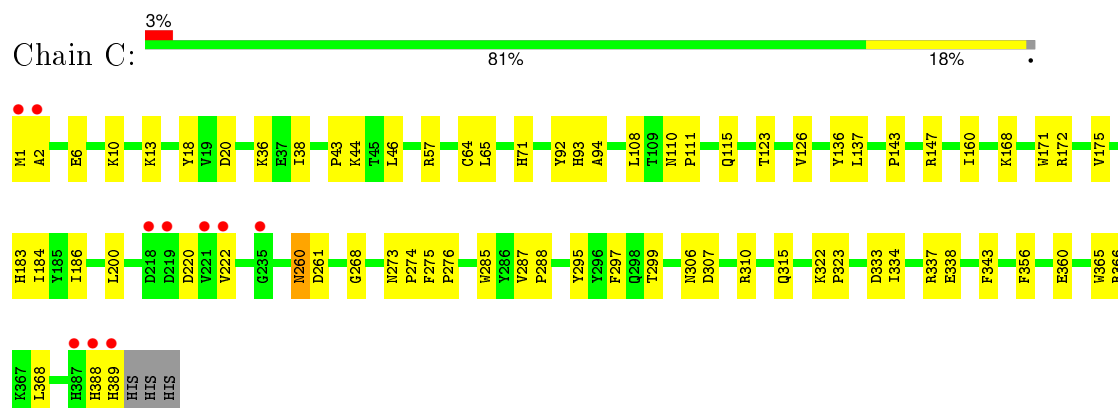
- Molecule 1: terminal oxygenase component of carbazole



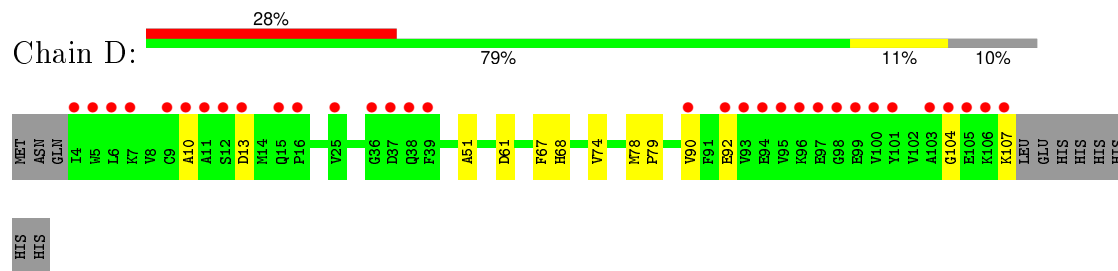
- Molecule 1: terminal oxygenase component of carbazole



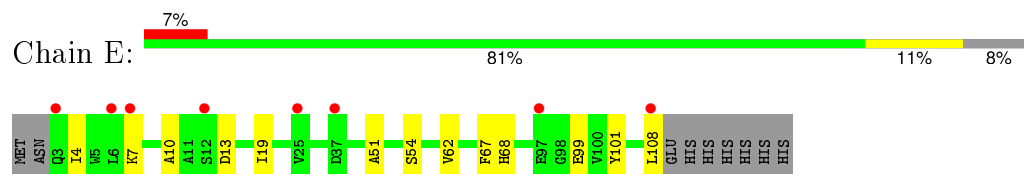
- Molecule 1: terminal oxygenase component of carbazole



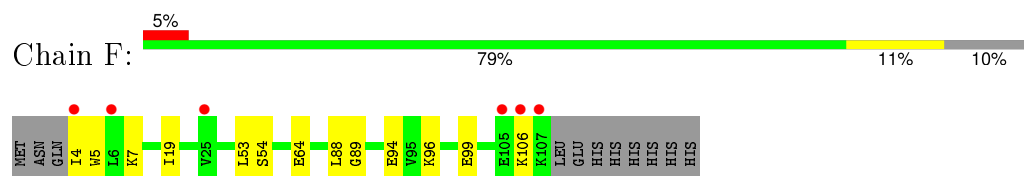
- Molecule 2: ferredoxin component of carbazole



- Molecule 2: ferredoxin component of carbazole



- Molecule 2: ferredoxin component of carbazole



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	98.22Å 90.01Å 105.52Å 90.00° 104.14° 90.00°	Depositor
Resolution (Å)	47.63 – 1.80 47.88 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.6 (47.63-1.80) 99.6 (47.88-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 1.79Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.187 , 0.214 0.188 , 0.187	Depositor DCC
R_{free} test set	8258 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	21.2	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 53.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 164386 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13231	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% 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: FE2, FES

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	0.31	0/3221	0.61	0/4372
1	B	0.29	0/3232	0.60	0/4387
1	C	0.29	0/3221	0.59	0/4372
2	D	0.28	0/784	0.56	0/1066
2	E	0.29	0/801	0.57	0/1089
2	F	0.30	0/784	0.61	0/1066
All	All	0.30	0/12043	0.59	0/16352

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 [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	3136	0	3042	35	0
1	B	3146	0	3049	49	0
1	C	3136	0	3042	45	0
2	D	768	0	745	9	0
2	E	785	0	764	15	0
2	F	768	0	745	8	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	4	0	0	0	0
4	B	4	0	0	0	0
4	C	4	0	0	1	0
4	D	4	0	0	1	0
4	E	4	0	0	1	0
4	F	4	0	0	0	0
5	A	411	0	0	2	0
5	B	413	0	0	7	0
5	C	397	0	0	7	0
5	D	63	0	0	1	0
5	E	86	0	0	1	0
5	F	95	0	0	0	0
All	All	13231	0	11387	156	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 (156) 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:65:LEU:HD23	1:C:123:THR:HG22	1.59	0.83
1:A:65:LEU:HD23	1:A:123:THR:HG22	1.64	0.79
1:B:322:LYS:HB3	1:B:323:PRO:HD3	1.68	0.73
1:A:118:ARG:HG3	5:A:909:HOH:O	1.87	0.73
1:C:6:GLU:O	1:C:10:LYS:HG2	1.91	0.71
1:B:281:MET:HE3	1:B:283:PHE:HZ	1.56	0.70
1:B:101:ASP:O	1:B:120:LYS:HE3	1.94	0.67
1:A:1:MET:H1	1:A:376:ILE:CG2	2.08	0.67
2:F:89:GLY:HA3	2:F:106:LYS:HE2	1.75	0.66
1:A:210:ARG:HA	1:A:213:GLN:HG2	1.79	0.65
1:B:65:LEU:HD23	1:B:123:THR:HG22	1.77	0.65
1:A:1:MET:N	1:A:378:THR:HG22	2.11	0.64
1:B:281:MET:HE3	1:B:283:PHE:CZ	2.32	0.64
1:A:184:ILE:HD11	1:A:200:LEU:CD1	2.27	0.64
1:C:360:GLU:HG3	5:C:566:HOH:O	1.96	0.64
1:B:360:GLU:HG3	5:B:568:HOH:O	1.98	0.63
1:A:94:ALA:HB1	1:A:108:LEU:HB2	1.81	0.63
1:A:249:ARG:HG3	1:A:250:GLU:N	2.15	0.62
2:D:90:VAL:HG23	2:D:107:LYS:HG2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2:ALA:HA	5:C:817:HOH:O	2.00	0.61
2:F:94:GLU:HG2	2:F:96:LYS:HE3	1.80	0.61
1:C:220:ASP:OD1	1:C:222:VAL:HG22	2.01	0.60
2:E:7:LYS:HE3	2:E:99:GLU:OE2	2.01	0.60
1:B:94:ALA:HB1	1:B:108:LEU:HB2	1.84	0.60
1:A:1:MET:H1	1:A:376:ILE:HG21	1.65	0.60
1:A:1:MET:H2	1:A:378:THR:HG22	1.67	0.59
1:C:94:ALA:HB1	1:C:108:LEU:HB2	1.85	0.58
1:C:43:PRO:HG2	5:C:855:HOH:O	2.04	0.57
1:B:287:VAL:HB	1:B:295:TYR:HB2	1.87	0.56
2:E:4:ILE:N	2:E:4:ILE:HD12	2.21	0.56
1:B:222:VAL:HG12	1:B:222:VAL:O	2.06	0.56
2:E:108:LEU:HD21	5:E:266:HOH:O	2.06	0.55
1:A:94:ALA:CB	1:A:108:LEU:HB2	2.36	0.55
1:A:312:LYS:O	1:A:316:GLU:HG3	2.06	0.55
1:A:239:PHE:O	1:A:251:GLY:N	2.37	0.54
1:B:317:PHE:HA	1:B:321:TRP:HB2	1.89	0.54
1:B:94:ALA:CB	1:B:108:LEU:HB2	2.37	0.54
2:E:10:ALA:HA	2:E:99:GLU:OE1	2.08	0.54
1:A:287:VAL:HB	1:A:295:TYR:HB2	1.89	0.53
1:B:38:ILE:HG23	1:B:57:ARG:HH21	1.74	0.53
1:C:168:LYS:HE2	5:C:896:HOH:O	2.08	0.53
2:D:92:GLU:HG2	2:D:107:LYS:HE2	1.90	0.53
1:C:333:ASP:O	1:C:337:ARG:HG3	2.08	0.53
1:C:287:VAL:HB	1:C:295:TYR:HB2	1.91	0.52
1:A:261:ASP:HB3	1:A:273:ASN:O	2.09	0.52
1:C:38:ILE:HA	1:C:44:LYS:HZ3	1.74	0.52
1:B:333:ASP:O	1:B:337:ARG:HG3	2.10	0.51
1:B:1:MET:HB3	1:B:378:THR:HG21	1.93	0.51
1:B:11:ARG:HH21	1:C:388:HIS:CE1	2.28	0.51
1:B:120:LYS:HE2	5:B:630:HOH:O	2.11	0.51
1:B:215:ARG:HB3	1:B:228:TYR:HB2	1.94	0.50
2:D:10:ALA:HB3	2:D:13:ASP:OD2	2.11	0.50
1:C:261:ASP:HB3	1:C:273:ASN:O	2.10	0.50
1:A:307:ASP:HA	1:A:310:ARG:HD2	1.94	0.50
1:C:1:MET:SD	1:C:1:MET:N	2.84	0.49
1:C:111:PRO:HG3	5:C:623:HOH:O	2.11	0.49
1:C:260:ASN:C	1:C:260:ASN:HD22	2.14	0.49
1:C:93:HIS:HB2	4:C:401:FES:S1	2.52	0.49
1:C:1:MET:HA	1:C:20:ASP:OD2	2.13	0.49
2:F:19:ILE:HG21	2:F:54:SER:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:260:ASN:HD22	1:B:260:ASN:H	1.61	0.49
1:B:260:ASN:ND2	1:B:260:ASN:H	2.11	0.48
1:C:171:TRP:CG	1:C:288:PRO:HG3	2.49	0.48
1:B:171:TRP:CG	1:B:288:PRO:HG3	2.49	0.48
1:A:171:TRP:CE2	1:A:172:ARG:HG3	2.49	0.48
1:B:172:ARG:O	1:B:176:GLU:HG3	2.14	0.48
1:C:334:ILE:O	1:C:338:GLU:HG3	2.14	0.48
1:C:94:ALA:CB	1:C:108:LEU:HB2	2.44	0.48
1:B:168:LYS:HE2	5:B:912:HOH:O	2.14	0.47
1:C:13:LYS:NZ	2:F:64:GLU:OE2	2.45	0.47
1:A:6:GLU:HG3	5:A:707:HOH:O	2.14	0.47
2:F:53:LEU:CD1	2:F:88:LEU:HD11	2.45	0.47
2:E:4:ILE:H	2:E:4:ILE:HD12	1.81	0.46
1:C:38:ILE:HG23	1:C:57:ARG:HH21	1.80	0.46
2:F:7:LYS:HB2	2:F:7:LYS:NZ	2.29	0.46
1:B:390:HIS:HA	5:B:828:HOH:O	2.15	0.46
1:C:389:HIS:NE2	2:E:62:VAL:HG21	2.30	0.46
1:B:171:TRP:CE2	1:B:172:ARG:HG3	2.50	0.46
2:E:19:ILE:HG21	2:E:54:SER:HA	1.98	0.46
1:C:184:ILE:HD11	1:C:200:LEU:CD1	2.45	0.46
1:A:65:LEU:CD2	1:A:123:THR:HG22	2.41	0.46
1:B:261:ASP:HB3	1:B:273:ASN:O	2.15	0.46
2:D:51:ALA:HB2	2:D:67:PHE:CG	2.51	0.46
2:F:7:LYS:HE3	2:F:99:GLU:HG2	1.97	0.46
1:B:283:PHE:HB2	1:B:299:THR:OG1	2.16	0.46
1:B:215:ARG:HB2	1:B:230:LEU:HD11	1.98	0.46
1:C:306:ASN:O	1:C:310:ARG:HG3	2.16	0.46
1:B:321:TRP:O	1:B:325:ALA:HB3	2.16	0.45
2:D:104:GLY:HA2	5:D:251:HOH:O	2.15	0.45
1:B:273:ASN:OD1	1:B:281:MET:HG2	2.16	0.45
1:C:171:TRP:CE2	1:C:172:ARG:HG3	2.51	0.45
1:B:289:ILE:HB	1:B:293:THR:OG1	2.16	0.45
1:B:23:LEU:HG	5:B:628:HOH:O	2.17	0.45
1:B:326:LEU:O	1:B:330:ASN:HB2	2.17	0.45
1:B:260:ASN:N	1:B:260:ASN:HD22	2.15	0.45
1:A:184:ILE:HD11	1:A:200:LEU:HD11	1.97	0.45
1:A:311:LYS:O	1:A:315:GLN:HG3	2.16	0.45
1:A:143:PRO:HG3	1:A:147:ARG:CZ	2.47	0.44
1:A:260:ASN:C	1:A:260:ASN:HD22	2.20	0.44
1:A:222:VAL:HG23	1:A:224:ARG:HG3	1.98	0.44
1:B:160:ILE:HG23	1:B:299:THR:HB	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:36:LYS:HE3	5:C:881:HOH:O	2.17	0.44
1:A:220:ASP:OD1	1:A:221:VAL:N	2.46	0.44
1:C:183:HIS:O	1:C:186:ILE:HG12	2.18	0.44
1:C:65:LEU:CD2	1:C:123:THR:HG22	2.40	0.44
1:C:64:CYS:HB2	1:C:126:VAL:CG2	2.48	0.44
2:F:4:ILE:HG13	2:F:5:TRP:N	2.33	0.44
1:C:315:GLN:HG3	5:C:886:HOH:O	2.17	0.44
2:E:51:ALA:HB2	2:E:67:PHE:CG	2.53	0.43
1:A:1:MET:H3	1:A:378:THR:CG2	2.31	0.43
1:B:196:ASN:O	1:B:256:LYS:HD2	2.18	0.43
2:E:10:ALA:HB3	2:E:13:ASP:OD2	2.18	0.43
2:E:68:HIS:HB2	4:E:201:FES:S1	2.59	0.43
1:C:285:TRP:HB2	1:C:297:PHE:HB3	2.01	0.43
1:B:332:ASP:HA	1:B:335:TRP:NE1	2.34	0.43
1:B:176:GLU:O	1:B:180:ASP:HB2	2.19	0.43
1:B:146:ALA:CB	1:B:222:VAL:HG11	2.48	0.43
1:B:4:VAL:HG12	1:B:5:ASP:N	2.34	0.42
2:D:61:ASP:O	2:D:74:VAL:HG22	2.18	0.42
1:B:184:ILE:HD11	1:B:200:LEU:CD1	2.49	0.42
2:E:4:ILE:H	2:E:4:ILE:CD1	2.31	0.42
1:C:136:TYR:CE1	1:C:143:PRO:HD2	2.54	0.42
1:C:389:HIS:CD2	2:E:62:VAL:HG21	2.55	0.42
1:B:322:LYS:O	1:B:327:GLU:HG3	2.20	0.42
5:B:808:HOH:O	1:C:115:GLN:HG2	2.20	0.42
1:A:228:TYR:CD1	1:A:263:SER:HB3	2.54	0.42
1:A:333:ASP:O	1:A:337:ARG:HG3	2.20	0.42
1:B:16:ALA:HB3	1:B:17:PRO:HD3	2.01	0.42
1:A:306:ASN:OD1	1:A:308:GLU:HB2	2.20	0.41
1:C:275:PHE:CG	1:C:276:PRO:HA	2.55	0.41
1:B:287:VAL:HA	1:B:288:PRO:HD3	1.95	0.41
1:B:275:PHE:CG	1:B:276:PRO:HA	2.55	0.41
2:E:99:GLU:OE1	2:E:99:GLU:HA	2.21	0.41
2:D:68:HIS:HB2	4:D:201:FES:S1	2.61	0.41
1:C:322:LYS:HB3	1:C:323:PRO:CD	2.50	0.41
1:C:18:TYR:CE2	1:C:366:ARG:HG2	2.55	0.41
1:B:224:ARG:NH2	5:B:839:HOH:O	2.52	0.41
1:C:160:ILE:HG23	1:C:299:THR:HB	2.03	0.41
1:B:38:ILE:HG23	1:B:38:ILE:O	2.20	0.41
1:C:273:ASN:HA	1:C:274:PRO:HA	1.94	0.41
1:B:273:ASN:HA	1:B:274:PRO:HA	1.89	0.41
2:E:99:GLU:HB3	2:E:101:TYR:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:ASP:HB2	1:A:224:ARG:HB2	2.03	0.41
1:A:334:ILE:O	1:A:338:GLU:HG3	2.21	0.41
1:A:73:GLY:HA3	1:C:343:PHE:CG	2.56	0.41
2:D:51:ALA:HB2	2:D:67:PHE:CD2	2.56	0.41
2:E:4:ILE:N	2:E:4:ILE:CD1	2.84	0.40
1:A:38:ILE:HD13	1:A:62:LEU:HD22	2.02	0.40
1:B:228:TYR:CD1	1:B:263:SER:HB3	2.57	0.40
1:C:64:CYS:HB2	1:C:126:VAL:HG21	2.03	0.40
1:C:175:VAL:HG11	1:C:365:TRP:CE2	2.56	0.40
1:A:1:MET:N	1:A:378:THR:CG2	2.81	0.40
2:D:78:MET:HA	2:D:79:PRO:HD3	1.96	0.40
1:A:64:CYS:HB2	1:A:126:VAL:HG21	2.02	0.40
1:B:48:LEU:HD23	1:B:137:LEU:HD23	2.02	0.40
1:C:143:PRO:HG3	1:C:147:ARG:CZ	2.52	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	387/392 (99%)	368 (95%)	18 (5%)	1 (0%)	46	29
1	B	388/392 (99%)	368 (95%)	19 (5%)	1 (0%)	46	29
1	C	387/392 (99%)	369 (95%)	16 (4%)	2 (0%)	34	17
2	D	102/115 (89%)	99 (97%)	3 (3%)	0	100	100
2	E	104/115 (90%)	101 (97%)	3 (3%)	0	100	100
2	F	102/115 (89%)	99 (97%)	3 (3%)	0	100	100
All	All	1470/1521 (97%)	1404 (96%)	62 (4%)	4 (0%)	46	29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	268	GLY
1	C	268	GLY
1	A	268	GLY
1	C	71	HIS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	336/339 (99%)	330 (98%)	6 (2%)	66	54
1	B	337/339 (99%)	330 (98%)	7 (2%)	61	47
1	C	336/339 (99%)	328 (98%)	8 (2%)	57	41
2	D	82/93 (88%)	82 (100%)	0	100	100
2	E	84/93 (90%)	84 (100%)	0	100	100
2	F	82/93 (88%)	82 (100%)	0	100	100
All	All	1257/1296 (97%)	1236 (98%)	21 (2%)	68	57

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	LEU
1	A	92	TYR
1	A	110	ASN
1	A	137	LEU
1	A	260	ASN
1	A	356	PHE
1	B	92	TYR
1	B	110	ASN
1	B	137	LEU
1	B	246	GLU
1	B	260	ASN
1	B	307	ASP
1	B	356	PHE
1	C	46	LEU
1	C	92	TYR

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Mol	Chain	Res	Type
1	C	110	ASN
1	C	137	LEU
1	C	260	ASN
1	C	307	ASP
1	C	356	PHE
1	C	368	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	110	ASN
1	A	165	GLN
1	A	260	ASN
1	B	110	ASN
1	B	165	GLN
1	B	234	HIS
1	B	260	ASN
1	C	110	ASN
1	C	165	GLN
1	C	260	ASN
2	E	3	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 3 are monoatomic - leaving 6 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	FES	A	401	1	0,4,4	0.00	-	0,4,4	0.00	-
4	FES	B	401	1	0,4,4	0.00	-	0,4,4	0.00	-
4	FES	C	401	1	0,4,4	0.00	-	0,4,4	0.00	-
4	FES	D	201	2	0,4,4	0.00	-	0,4,4	0.00	-
4	FES	E	201	2	0,4,4	0.00	-	0,4,4	0.00	-
4	FES	F	201	2	0,4,4	0.00	-	0,4,4	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	FES	A	401	1	-	0/0/4/4	0/1/1/1
4	FES	B	401	1	-	0/0/4/4	0/1/1/1
4	FES	C	401	1	-	0/0/4/4	0/1/1/1
4	FES	D	201	2	-	0/0/4/4	0/1/1/1
4	FES	E	201	2	-	0/0/4/4	0/1/1/1
4	FES	F	201	2	-	0/0/4/4	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	401	FES	1	0
4	D	201	FES	1	0
4	E	201	FES	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	389/392 (99%)	-0.05	12 (3%)	52 47	12, 20, 33, 40	0
1	B	390/392 (99%)	-0.02	11 (2%)	56 51	12, 23, 34, 39	0
1	C	389/392 (99%)	-0.10	10 (2%)	59 54	14, 23, 32, 41	0
2	D	104/115 (90%)	1.20	32 (30%)	1 0	15, 30, 37, 39	0
2	E	106/115 (92%)	0.36	8 (7%)	17 13	20, 28, 34, 37	0
2	F	104/115 (90%)	0.18	6 (5%)	26 21	17, 26, 33, 38	0
All	All	1482/1521 (97%)	0.08	79 (5%)	30 25	12, 23, 34, 41	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1	MET	8.7
1	A	1	MET	8.0
2	D	95	VAL	7.1
1	B	1	MET	6.5
2	D	4	ILE	6.5
1	C	2	ALA	5.4
1	C	388	HIS	5.4
1	A	2	ALA	5.3
2	D	101	TYR	5.1
2	F	4	ILE	5.1
2	D	25	VAL	4.8
2	D	5	TRP	4.7
2	D	97	GLU	4.5
1	C	221	VAL	4.5
2	D	99	GLU	4.5
2	F	107	LYS	4.3
2	D	37	ASP	4.2
2	D	12	SER	4.2
2	D	98	GLY	4.2

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Mol	Chain	Res	Type	RSRZ
2	D	93	VAL	4.1
1	C	389	HIS	4.1
1	A	221	VAL	4.1
2	E	108	LEU	3.9
2	D	104	GLY	3.9
1	B	2	ALA	3.9
2	E	25	VAL	3.8
1	B	221	VAL	3.8
1	B	390	HIS	3.7
2	D	38	GLN	3.7
2	D	7	LYS	3.5
2	D	94	GLU	3.5
1	C	219	ASP	3.5
2	D	92	GLU	3.5
2	D	11	ALA	3.5
2	D	105	GLU	3.5
1	A	389	HIS	3.4
2	E	3	GLN	3.3
1	B	305	ALA	3.3
2	D	16	PRO	3.2
2	F	105	GLU	3.1
2	E	37	ASP	3.1
1	A	308	GLU	3.1
2	D	96	LYS	3.1
2	D	100	VAL	3.0
2	D	107	LYS	2.9
2	E	97	GLU	2.9
2	D	13	ASP	2.9
2	D	9	CYS	2.9
1	A	311	LYS	2.8
1	B	312	LYS	2.8
2	D	6	LEU	2.8
2	D	10	ALA	2.8
1	B	308	GLU	2.8
1	C	218	ASP	2.7
1	B	222	VAL	2.7
1	A	253	TYR	2.7
2	F	25	VAL	2.6
1	B	255	GLU	2.6
2	E	12	SER	2.6
2	F	106	LYS	2.5
2	D	36	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	210	ARG	2.5
2	D	90	VAL	2.5
2	D	39	PHE	2.4
2	F	6	LEU	2.4
2	E	6	LEU	2.4
1	A	220	ASP	2.4
1	A	118	ARG	2.3
1	A	307	ASP	2.3
1	B	235	GLY	2.3
1	B	388	HIS	2.2
2	D	103	ALA	2.2
1	A	388	HIS	2.2
1	C	387	HIS	2.2
1	C	222	VAL	2.1
2	E	7	LYS	2.1
1	C	235	GLY	2.1
2	D	15	GLN	2.1
2	D	106	LYS	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
4	FES	B	401	4/4	1.00	0.14	6.17	15,17,17,18	0
4	FES	E	201	4/4	1.00	0.10	2.36	21,22,22,22	0
4	FES	D	201	4/4	1.00	0.10	1.20	16,16,18,19	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	FES	C	401	4/4	0.98	0.11	0.96	17,18,21,22	0
4	FES	A	401	4/4	1.00	0.10	-0.12	13,14,15,16	0
4	FES	F	201	4/4	1.00	0.10	-0.29	16,17,17,18	0
3	FE2	B	501	1/1	0.99	0.08	-2.85	34,34,34,34	0
3	FE2	A	501	1/1	0.99	0.04	-3.92	29,29,29,29	0
3	FE2	C	501	1/1	0.99	0.04	-4.97	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.