



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:58 PM GMT

PDB ID : 4NBH
Title : Carbazole-bound Oxygenase with Gln282 replaced by Tyr and ferredoxin complex of carbazole 1,9a-dioxygenase
Authors : Ashikawa, Y.; Usami, Y.; Inoue, K.; Nojiri, H.
Deposited on : 2013-10-23
Resolution : 2.15 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

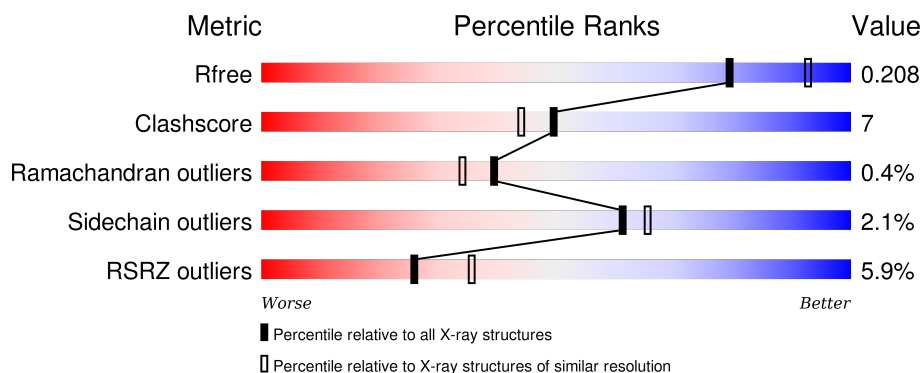
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	1045 (2.16-2.16)
Clashscore	102246	1152 (2.16-2.16)
Ramachandran outliers	100387	1131 (2.16-2.16)
Sidechain outliers	100360	1131 (2.16-2.16)
RSRZ outliers	91569	1050 (2.16-2.16)

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>2%</div> <div>81%</div> <div>18%</div> <div>.</div> </div>
1	B	392	<div> <div>5%</div> <div>81%</div> <div>18%</div> <div>..</div> </div>
1	C	392	<div> <div>2%</div> <div>79%</div> <div>20%</div> <div>.</div> </div>
2	D	115	<div> <div>29%</div> <div>77%</div> <div>13%</div> <div>10%</div> </div>
2	E	115	<div> <div>6%</div> <div>83%</div> <div>14%</div> <div>.</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
5	9CA	B	503	-	-	-	X
5	9CA	C	503	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12842 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	388	Total	C	N	O	S	0	0	0
			3131	2003	533	582	13			
1	B	390	Total	C	N	O	S	0	0	0
			3151	2015	539	584	13			
1	C	388	Total	C	N	O	S	0	0	0
			3131	2003	533	582	13			

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	282	TYR	GLN	ENGINEERED MUTATION	UNP Q84II6
A	385	LEU	-	EXPRESSION TAG	UNP Q84II6
A	386	GLU	-	EXPRESSION TAG	UNP Q84II6
A	387	HIS	-	EXPRESSION TAG	UNP Q84II6
A	388	HIS	-	EXPRESSION TAG	UNP Q84II6
A	389	HIS	-	EXPRESSION TAG	UNP Q84II6
A	390	HIS	-	EXPRESSION TAG	UNP Q84II6
A	391	HIS	-	EXPRESSION TAG	UNP Q84II6
A	392	HIS	-	EXPRESSION TAG	UNP Q84II6
B	282	TYR	GLN	ENGINEERED MUTATION	UNP Q84II6
B	385	LEU	-	EXPRESSION TAG	UNP Q84II6
B	386	GLU	-	EXPRESSION TAG	UNP Q84II6
B	387	HIS	-	EXPRESSION TAG	UNP Q84II6
B	388	HIS	-	EXPRESSION TAG	UNP Q84II6
B	389	HIS	-	EXPRESSION TAG	UNP Q84II6
B	390	HIS	-	EXPRESSION TAG	UNP Q84II6
B	391	HIS	-	EXPRESSION TAG	UNP Q84II6
B	392	HIS	-	EXPRESSION TAG	UNP Q84II6
C	282	TYR	GLN	ENGINEERED MUTATION	UNP Q84II6
C	385	LEU	-	EXPRESSION TAG	UNP Q84II6
C	386	GLU	-	EXPRESSION TAG	UNP Q84II6
C	387	HIS	-	EXPRESSION TAG	UNP Q84II6
C	388	HIS	-	EXPRESSION TAG	UNP Q84II6

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Chain	Residue	Modelled	Actual	Comment	Reference
C	389	HIS	-	EXPRESSION TAG	UNP Q84II6
C	390	HIS	-	EXPRESSION TAG	UNP Q84II6
C	391	HIS	-	EXPRESSION TAG	UNP Q84II6
C	392	HIS	-	EXPRESSION TAG	UNP Q84II6

- Molecule 2 is a protein called Ferredoxin CarAc.

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	112	Total	C	N	O	S	0	0	0
			844	529	148	160	7			
2	F	104	Total	C	N	O	S	0	0	0
			768	483	129	149	7			

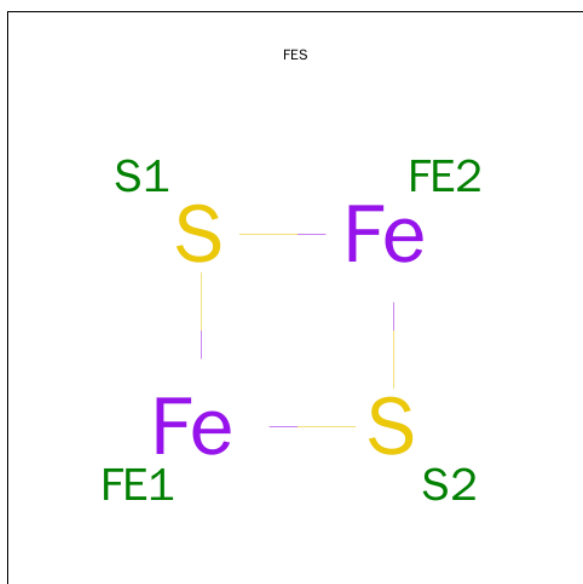
There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	108	LEU	-	EXPRESSION TAG	UNP Q8GI16
D	109	GLU	-	EXPRESSION TAG	UNP Q8GI16
D	110	HIS	-	EXPRESSION TAG	UNP Q8GI16
D	111	HIS	-	EXPRESSION TAG	UNP Q8GI16
D	112	HIS	-	EXPRESSION TAG	UNP Q8GI16
D	113	HIS	-	EXPRESSION TAG	UNP Q8GI16
D	114	HIS	-	EXPRESSION TAG	UNP Q8GI16
D	115	HIS	-	EXPRESSION TAG	UNP Q8GI16
E	108	LEU	-	EXPRESSION TAG	UNP Q8GI16
E	109	GLU	-	EXPRESSION TAG	UNP Q8GI16
E	110	HIS	-	EXPRESSION TAG	UNP Q8GI16
E	111	HIS	-	EXPRESSION TAG	UNP Q8GI16
E	112	HIS	-	EXPRESSION TAG	UNP Q8GI16
E	113	HIS	-	EXPRESSION TAG	UNP Q8GI16
E	114	HIS	-	EXPRESSION TAG	UNP Q8GI16
E	115	HIS	-	EXPRESSION TAG	UNP Q8GI16
F	108	LEU	-	EXPRESSION TAG	UNP Q8GI16
F	109	GLU	-	EXPRESSION TAG	UNP Q8GI16
F	110	HIS	-	EXPRESSION TAG	UNP Q8GI16
F	111	HIS	-	EXPRESSION TAG	UNP Q8GI16
F	112	HIS	-	EXPRESSION TAG	UNP Q8GI16
F	113	HIS	-	EXPRESSION TAG	UNP Q8GI16
F	114	HIS	-	EXPRESSION TAG	UNP Q8GI16
F	115	HIS	-	EXPRESSION TAG	UNP Q8GI16

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

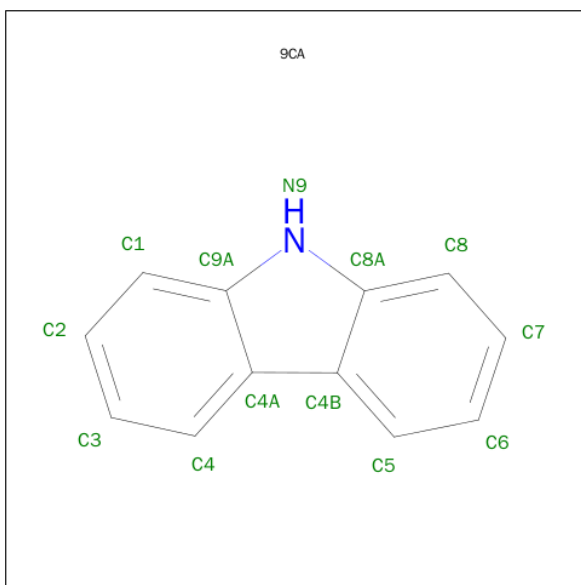
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Fe	0	0
			1	1		
3	A	1	Total	Fe	0	0
			1	1		
3	C	1	Total	Fe	0	0
			1	1		

- 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	0	0
			4	2	2		
4	B	1	Total	Fe	S	0	0
			4	2	2		
4	C	1	Total	Fe	S	0	0
			4	2	2		
4	D	1	Total	Fe	S	0	0
			4	2	2		
4	E	1	Total	Fe	S	0	0
			4	2	2		
4	F	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 5 is 9H-CARBAZOLE (three-letter code: 9CA) (formula: C₁₂H₉N).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	N	0	0
			13	12	1		
5	C	1	Total	C	N	0	0
			13	12	1		

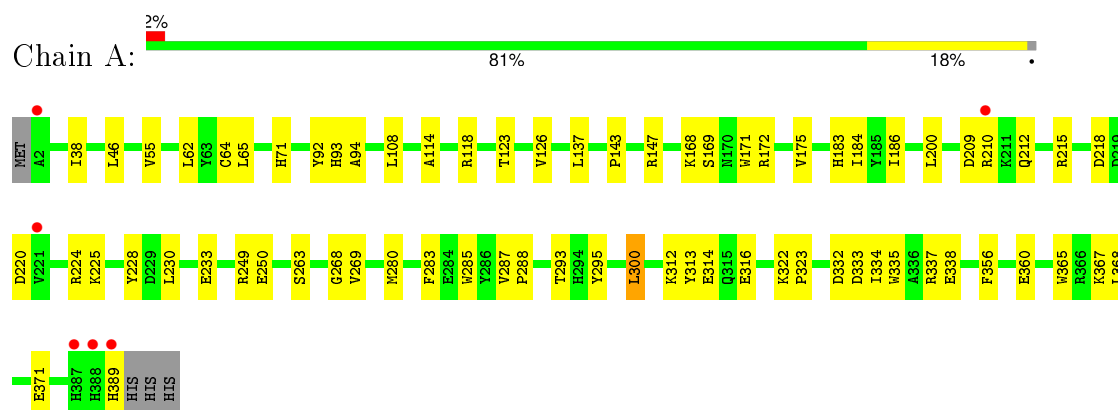
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	330	Total	O	0	0
			330	330		
6	B	263	Total	O	0	0
			263	263		
6	C	278	Total	O	0	0
			278	278		
6	D	30	Total	O	0	0
			30	30		
6	E	46	Total	O	0	0
			46	46		
6	F	49	Total	O	0	0
			49	49		

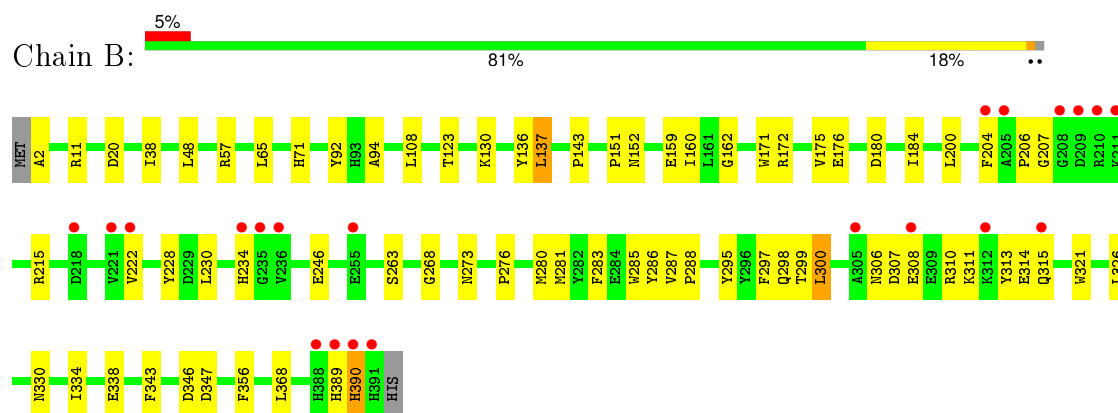
3 Residue-property plots

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.

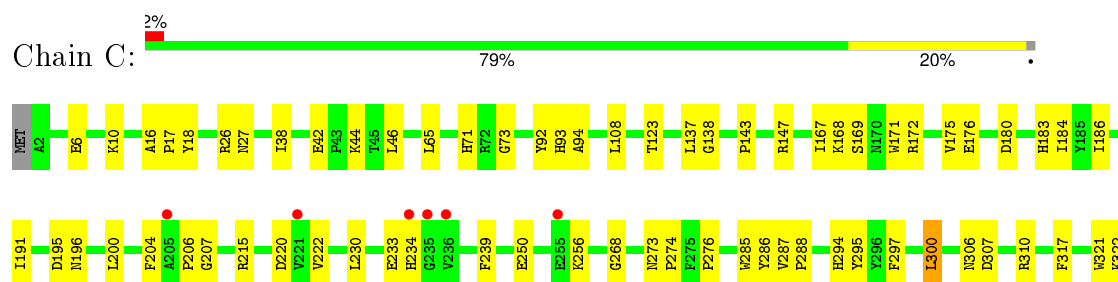
- Molecule 1: Terminal oxygenase component of carbazole



- Molecule 1: Terminal oxygenase component of carbazole

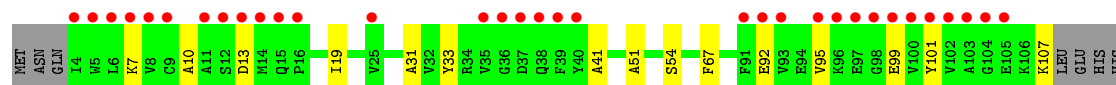
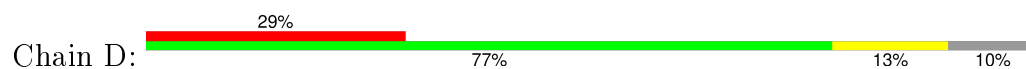


- Molecule 1: Terminal oxygenase component of carbazole

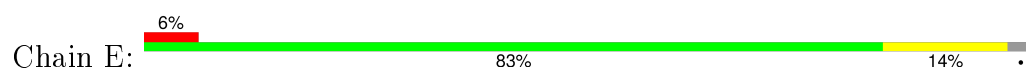




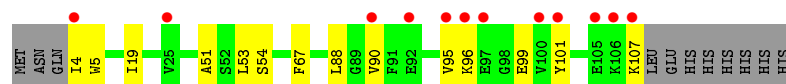
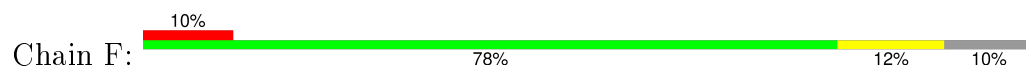
• Molecule 2: Ferredoxin CarAc



• Molecule 2: Ferredoxin CarAc



• Molecule 2: Ferredoxin CarAc



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	98.18 Å 89.95 Å 105.19 Å 90.00° 104.29° 90.00°	Depositor
Resolution (Å)	40.92 – 2.15 40.92 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.6 (40.92-2.15) 99.8 (40.92-2.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.35 (at 2.16 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.183 , 0.211 0.183 , 0.208	Depositor DCC
R_{free} test set	4844 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	24.6	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 96320 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12842	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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: 9CA, 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	0.33	0/3217	0.61	0/4368
1	B	0.30	0/3239	0.58	0/4398
1	C	0.31	0/3217	0.59	0/4368
2	D	0.30	0/784	0.55	0/1066
2	E	0.30	0/865	0.57	0/1176
2	F	0.32	0/784	0.59	0/1066
All	All	0.31	0/12106	0.59	0/16442

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	3131	0	3031	44	0
1	B	3151	0	3045	48	0
1	C	3131	0	3031	48	0
2	D	768	0	745	7	0
2	E	844	0	805	8	0
2	F	768	0	745	11	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	1	0
4	B	4	0	0	0	0
4	C	4	0	0	1	0
4	D	4	0	0	0	0
4	E	4	0	0	1	0
4	F	4	0	0	0	0
5	B	13	0	9	1	0
5	C	13	0	9	0	0
6	A	330	0	0	3	0
6	B	263	0	0	4	0
6	C	278	0	0	3	0
6	D	30	0	0	0	0
6	E	46	0	0	0	0
6	F	49	0	0	2	0
All	All	12842	0	11420	165	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 (165) 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:B:2:ALA:HB1	6:B:779:HOH:O	1.44	1.13
1:A:280:MET:HE1	1:A:300:LEU:HD13	1.66	0.78
1:C:6:GLU:O	1:C:10:LYS:HG2	1.88	0.74
1:C:65:LEU:HD23	1:C:123:THR:HG22	1.69	0.74
1:A:65:LEU:HD23	1:A:123:THR:HG22	1.72	0.72
1:C:220:ASP:OD1	1:C:222:VAL:HG22	1.92	0.68
1:B:230:LEU:HA	6:B:799:HOH:O	1.95	0.66
1:A:118:ARG:HD2	6:A:765:HOH:O	1.95	0.65
1:B:2:ALA:HB3	1:B:20:ASP:OD2	1.97	0.64
1:A:280:MET:HE3	1:A:313:TYR:HE1	1.61	0.64
1:B:38:ILE:HG23	1:B:57:ARG:HH21	1.63	0.63
1:B:65:LEU:HD23	1:B:123:THR:HG22	1.79	0.63
1:A:220:ASP:HB2	1:A:224:ARG:HB2	1.81	0.63
1:C:306:ASN:O	1:C:310:ARG:HG3	2.00	0.62
1:C:38:ILE:HD12	1:C:44:LYS:HD3	1.81	0.62
1:C:94:ALA:HB1	1:C:108:LEU:HB2	1.83	0.61
1:A:94:ALA:HB1	1:A:108:LEU:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:ARG:HB2	1:B:230:LEU:HD11	1.84	0.59
1:B:48:LEU:HD23	1:B:137:LEU:HD23	1.82	0.59
1:B:215:ARG:HB3	1:B:228:TYR:HB2	1.85	0.59
1:A:287:VAL:HB	1:A:295:TYR:HB2	1.84	0.59
1:A:38:ILE:HD13	1:A:62:LEU:HD22	1.83	0.59
1:C:333:ASP:O	1:C:337:ARG:HG3	2.03	0.58
2:F:96:LYS:HG3	6:F:321:HOH:O	2.04	0.58
1:B:283:PHE:HB2	1:B:299:THR:OG1	2.05	0.57
2:D:51:ALA:HB2	2:D:67:PHE:CG	2.40	0.56
2:F:53:LEU:CD1	2:F:88:LEU:HD11	2.35	0.56
2:F:4:ILE:HG23	2:F:5:TRP:H	1.71	0.56
1:A:333:ASP:O	1:A:337:ARG:HG3	2.06	0.56
1:A:114:ALA:O	1:A:118:ARG:HD3	2.07	0.55
1:A:230:LEU:HB3	1:A:233:GLU:HG3	1.88	0.55
2:D:92:GLU:HG2	2:D:107:LYS:HE2	1.88	0.55
2:D:19:ILE:HG21	2:D:54:SER:HA	1.89	0.55
1:B:306:ASN:OD1	1:B:308:GLU:HB2	2.06	0.55
1:B:326:LEU:O	1:B:330:ASN:HB2	2.06	0.55
2:F:107:LYS:HB2	2:F:107:LYS:NZ	2.22	0.55
1:A:184:ILE:HD11	1:A:200:LEU:CD1	2.36	0.55
1:A:280:MET:HE1	1:A:300:LEU:CD1	2.34	0.54
1:B:287:VAL:HB	1:B:295:TYR:HB2	1.90	0.54
1:B:334:ILE:O	1:B:338:GLU:HG3	2.08	0.54
1:A:209:ASP:OD1	1:A:212:GLN:HG3	2.08	0.54
1:B:276:PRO:HD2	1:B:300:LEU:HD21	1.90	0.53
1:B:11:ARG:HH21	1:C:388:HIS:CE1	2.26	0.53
2:E:47:THR:HG23	2:E:88:LEU:HD23	1.91	0.53
1:A:367:LYS:O	1:A:371:GLU:HG3	2.09	0.53
1:A:312:LYS:O	1:A:316:GLU:HG3	2.09	0.52
1:B:280:MET:HE3	1:B:313:TYR:CE1	2.45	0.52
2:E:19:ILE:HG21	2:E:54:SER:HA	1.92	0.52
1:A:280:MET:CE	1:A:313:TYR:HE1	2.21	0.51
1:B:280:MET:HE3	1:B:313:TYR:HE1	1.75	0.51
1:A:215:ARG:HD2	6:A:687:HOH:O	2.09	0.51
1:C:94:ALA:CB	1:C:108:LEU:HB2	2.41	0.51
1:C:360:GLU:HG3	6:C:627:HOH:O	2.10	0.51
1:C:184:ILE:HD11	1:C:200:LEU:CD1	2.40	0.51
1:B:184:ILE:HD11	1:B:200:LEU:CD1	2.41	0.51
2:E:10:ALA:HB3	2:E:13:ASP:OD2	2.10	0.51
1:C:171:TRP:CE2	1:C:172:ARG:HG3	2.46	0.51
1:A:171:TRP:CE2	1:A:172:ARG:HG3	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:ARG:HG3	1:A:250:GLU:N	2.27	0.50
1:C:285:TRP:HB2	1:C:297:PHE:HB3	1.94	0.50
2:D:31:ALA:O	2:D:41:ALA:HA	2.12	0.50
1:C:176:GLU:O	1:C:180:ASP:HB2	2.11	0.49
5:B:503:9CA:H1	6:B:738:HOH:O	2.11	0.49
1:A:94:ALA:CB	1:A:108:LEU:HB2	2.42	0.49
2:D:10:ALA:HB3	2:D:13:ASP:OD2	2.11	0.49
1:C:276:PRO:CD	1:C:300:LEU:HD21	2.43	0.49
1:C:143:PRO:HG3	1:C:147:ARG:CZ	2.42	0.49
2:E:51:ALA:HB2	2:E:67:PHE:CG	2.47	0.49
1:B:273:ASN:OD1	1:B:281:MET:HG3	2.13	0.49
2:E:5:TRP:CZ3	2:E:94:GLU:HG2	2.48	0.48
1:B:280:MET:CE	1:B:300:LEU:HD22	2.42	0.48
1:B:222:VAL:HG12	1:B:222:VAL:O	2.12	0.48
1:B:171:TRP:CG	1:B:288:PRO:HG3	2.49	0.48
1:C:93:HIS:HB2	4:C:502:FES:S1	2.53	0.48
1:B:204:PHE:O	1:B:206:PRO:HD3	2.14	0.47
1:A:218:ASP:O	1:A:225:LYS:HD3	2.15	0.47
1:A:93:HIS:HB2	4:A:502:FES:S1	2.54	0.47
1:B:176:GLU:O	1:B:180:ASP:HB2	2.14	0.47
1:A:218:ASP:OD1	1:A:218:ASP:O	2.33	0.47
1:A:228:TYR:CD1	1:A:263:SER:HB3	2.49	0.47
2:F:51:ALA:HB2	2:F:67:PHE:CG	2.49	0.47
2:E:96:LYS:O	2:E:97:GLU:HB2	2.15	0.47
1:C:196:ASN:O	1:C:256:LYS:HD2	2.16	0.46
1:B:276:PRO:CD	1:B:300:LEU:HD21	2.44	0.46
1:B:311:LYS:O	1:B:315:GLN:HG3	2.15	0.46
1:C:230:LEU:HB3	1:C:233:GLU:HG3	1.98	0.46
1:A:143:PRO:HG3	1:A:147:ARG:CZ	2.46	0.45
1:A:64:CYS:HB2	1:A:126:VAL:CG2	2.46	0.45
2:F:19:ILE:HG21	2:F:54:SER:HA	1.98	0.45
1:C:346:ASP:O	1:C:347:ASP:HB2	2.17	0.45
2:F:107:LYS:HB2	2:F:107:LYS:HZ2	1.82	0.45
2:F:99:GLU:HB3	2:F:101:TYR:HE1	1.82	0.45
1:B:171:TRP:CE2	1:B:172:ARG:HG3	2.51	0.45
1:C:183:HIS:O	1:C:186:ILE:HG12	2.17	0.45
1:A:215:ARG:HB2	1:A:230:LEU:HD11	1.99	0.45
1:C:363:VAL:HG12	1:C:367:LYS:HE2	1.98	0.45
1:C:38:ILE:CD1	1:C:44:LYS:HD3	2.46	0.44
1:C:287:VAL:HB	1:C:295:TYR:HB2	1.99	0.44
1:A:184:ILE:HD11	1:A:200:LEU:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:VAL:HG11	1:A:365:TRP:CE2	2.52	0.44
2:D:7:LYS:HG3	2:D:101:TYR:HE1	1.81	0.44
1:C:27:ASN:HA	1:C:138:GLY:HA3	1.99	0.44
2:F:90:VAL:HG13	6:F:345:HOH:O	2.17	0.44
1:C:239:PHE:O	1:C:250:GLU:HA	2.17	0.44
1:C:167:ILE:HB	1:C:294:HIS:CE1	2.53	0.44
1:C:273:ASN:HA	1:C:274:PRO:HA	1.86	0.44
1:A:334:ILE:O	1:A:338:GLU:HG3	2.18	0.44
1:B:159:GLU:HG2	1:B:313:TYR:HD2	1.83	0.44
1:B:215:ARG:NH2	6:B:836:HOH:O	2.52	0.43
1:A:38:ILE:CD1	1:A:55:VAL:HG12	2.48	0.43
1:C:168:LYS:HE2	6:C:794:HOH:O	2.18	0.43
1:A:108:LEU:N	1:A:108:LEU:HD12	2.33	0.43
1:C:171:TRP:CG	1:C:288:PRO:HG3	2.53	0.43
1:A:332:ASP:HA	1:A:335:TRP:NE1	2.34	0.43
1:B:94:ALA:HB1	1:B:108:LEU:HB2	2.01	0.43
2:D:95:VAL:HA	2:D:99:GLU:O	2.19	0.43
1:A:287:VAL:HA	1:A:288:PRO:HD3	1.89	0.43
2:F:4:ILE:HG23	2:F:5:TRP:N	2.34	0.43
2:F:95:VAL:HA	2:F:99:GLU:O	2.19	0.43
1:B:321:TRP:HA	1:B:321:TRP:CE3	2.54	0.42
1:B:310:ARG:O	1:B:314:GLU:HG3	2.19	0.42
1:B:343:PHE:CG	1:C:73:GLY:HA3	2.55	0.42
1:A:168:LYS:HA	1:A:293:THR:HG22	2.01	0.42
1:A:322:LYS:HB3	1:A:323:PRO:HD3	2.02	0.42
1:B:38:ILE:HG23	1:B:57:ARG:NH2	2.31	0.42
1:A:183:HIS:O	1:A:186:ILE:HG12	2.19	0.42
1:C:215:ARG:HB2	1:C:230:LEU:HD11	2.02	0.42
1:A:64:CYS:HB2	1:A:126:VAL:HG21	2.01	0.42
1:C:204:PHE:O	1:C:206:PRO:HD3	2.19	0.42
1:B:151:PRO:O	1:B:152:ASN:HB2	2.19	0.42
1:B:280:MET:HE2	1:B:300:LEU:HD22	2.01	0.42
1:C:276:PRO:HD3	1:C:300:LEU:HD21	2.02	0.42
1:C:42:GLU:HB3	1:C:44:LYS:HZ2	1.84	0.42
1:C:317:PHE:HA	1:C:321:TRP:HB2	2.02	0.42
1:C:230:LEU:HA	6:C:873:HOH:O	2.20	0.42
1:C:108:LEU:N	1:C:108:LEU:HD12	2.34	0.41
1:B:389:HIS:HB3	1:B:390:HIS:H	1.59	0.41
1:B:207:GLY:HA3	1:B:234:HIS:O	2.19	0.41
1:C:322:LYS:HB3	1:C:323:PRO:HD3	2.02	0.41
1:A:312:LYS:HE2	1:A:316:GLU:OE2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:276:PRO:HD2	1:C:300:LEU:HD21	2.03	0.41
1:B:285:TRP:HB2	1:B:297:PHE:HB3	2.02	0.41
1:C:184:ILE:HD11	1:C:200:LEU:HD11	2.01	0.41
1:B:162:GLY:HA3	1:B:298:GLN:O	2.20	0.41
2:E:68:HIS:HB2	4:E:201:FES:S2	2.60	0.41
1:A:322:LYS:HB3	1:A:323:PRO:CD	2.51	0.41
1:C:322:LYS:HB3	1:C:323:PRO:CD	2.49	0.41
1:C:207:GLY:HA3	1:C:234:HIS:O	2.21	0.41
1:B:2:ALA:HB3	1:B:20:ASP:CG	2.41	0.41
1:B:390:HIS:O	1:B:390:HIS:ND1	2.54	0.41
1:B:65:LEU:CD2	1:B:123:THR:HG22	2.49	0.41
1:A:269:VAL:HB	1:A:285:TRP:CD1	2.55	0.41
1:A:210:ARG:HG3	1:A:360:GLU:OE2	2.21	0.41
1:C:16:ALA:HB3	1:C:17:PRO:HD3	2.03	0.41
1:A:389:HIS:HB2	6:A:918:HOH:O	2.21	0.41
1:B:228:TYR:CD1	1:B:263:SER:HB3	2.56	0.40
1:B:175:VAL:HG22	1:B:286:TYR:CD2	2.56	0.40
1:C:18:TYR:CE2	1:C:366:ARG:HG2	2.56	0.40
2:E:31:ALA:O	2:E:41:ALA:HA	2.22	0.40
1:B:136:TYR:CE1	1:B:143:PRO:HD2	2.56	0.40
1:B:346:ASP:O	1:B:347:ASP:HB2	2.22	0.40
1:C:191:ILE:O	1:C:195:ASP:HB2	2.21	0.40
1:B:130:LYS:HB3	1:B:160:ILE:HB	2.03	0.40
1:C:175:VAL:HG22	1:C:286:TYR:CD2	2.56	0.40
1:C:26:ARG:O	1:C:27:ASN:HB2	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	386/392 (98%)	369 (96%)	15 (4%)	2 (0%)	34 26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	388/392 (99%)	361 (93%)	25 (6%)	2 (0%)	34	26
1	C	386/392 (98%)	367 (95%)	17 (4%)	2 (0%)	34	26
2	D	102/115 (89%)	96 (94%)	6 (6%)	0	100	100
2	E	110/115 (96%)	105 (96%)	5 (4%)	0	100	100
2	F	102/115 (89%)	99 (97%)	3 (3%)	0	100	100
All	All	1474/1521 (97%)	1397 (95%)	71 (5%)	6 (0%)	39	34

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	268	GLY
1	B	268	GLY
1	C	268	GLY
1	C	71	HIS
1	A	71	HIS
1	B	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	335/339 (99%)	326 (97%)	9 (3%)	52	53
1	B	337/339 (99%)	329 (98%)	8 (2%)	57	60
1	C	335/339 (99%)	327 (98%)	8 (2%)	57	60
2	D	82/93 (88%)	81 (99%)	1 (1%)	78	83
2	E	90/93 (97%)	89 (99%)	1 (1%)	80	85
2	F	82/93 (88%)	82 (100%)	0	100	100
All	All	1261/1296 (97%)	1234 (98%)	27 (2%)	61	65

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	LEU
1	A	92	TYR
1	A	137	LEU
1	A	169	SER
1	A	283	PHE
1	A	300	LEU
1	A	314	GLU
1	A	356	PHE
1	A	368	LEU
1	B	92	TYR
1	B	137	LEU
1	B	246	GLU
1	B	300	LEU
1	B	307	ASP
1	B	356	PHE
1	B	368	LEU
1	B	390	HIS
1	C	46	LEU
1	C	92	TYR
1	C	137	LEU
1	C	169	SER
1	C	300	LEU
1	C	307	ASP
1	C	356	PHE
1	C	368	LEU
2	D	33	TYR
2	E	6	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	165	GLN
1	B	165	GLN
1	C	165	GLN
1	C	388	HIS
2	E	112	HIS

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 ⓘ

Of 11 ligands modelled in this entry, 3 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	FES	A	502	1	0,4,4	0.00	-	0,4,4	0.00	-
4	FES	B	502	1	0,4,4	0.00	-	0,4,4	0.00	-
5	9CA	B	503	-	15,15,15	1.26	1 (6%)	20,21,21	0.44	0
4	FES	C	502	1	0,4,4	0.00	-	0,4,4	0.00	-
5	9CA	C	503	-	15,15,15	1.26	1 (6%)	20,21,21	0.44	0
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	502	1	-	0/0/4/4	0/1/1/1
4	FES	B	502	1	-	0/0/4/4	0/1/1/1
5	9CA	B	503	-	-	0/0/0/0	0/3/3/3
4	FES	C	502	1	-	0/0/4/4	0/1/1/1
5	9CA	C	503	-	-	0/0/0/0	0/3/3/3
4	FES	D	201	2	-	0/0/4/4	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	503	9CA	C4B-C4A	-2.13	1.39	1.45
5	C	503	9CA	C4B-C4A	-2.11	1.39	1.45

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	502	FES	1	0
5	B	503	9CA	1	0
4	C	502	FES	1	0
4	E	201	FES	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	388/392 (98%)	-0.15	6 (1%) 76 82	11, 21, 38, 48	0
1	B	390/392 (99%)	0.14	21 (5%) 29 40	12, 26, 46, 53	0
1	C	388/392 (98%)	0.01	9 (2%) 64 72	14, 25, 41, 47	0
2	D	104/115 (90%)	1.25	33 (31%) 1 1	17, 37, 48, 54	0
2	E	112/115 (97%)	0.20	7 (6%) 23 32	20, 32, 44, 48	0
2	F	104/115 (90%)	0.41	12 (11%) 6 11	18, 32, 44, 51	0
All	All	1486/1521 (97%)	0.13	88 (5%) 26 36	11, 26, 45, 54	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	221	VAL	6.3
1	B	389	HIS	5.6
2	D	98	GLY	5.3
1	C	235	GLY	5.3
2	F	25	VAL	5.0
2	D	101	TYR	4.9
2	D	95	VAL	4.6
2	D	37	ASP	4.5
1	C	221	VAL	4.3
1	C	388	HIS	4.3
2	D	6	LEU	4.3
2	F	107	LYS	4.2
2	D	93	VAL	4.2
2	F	4	ILE	4.2
1	B	210	ARG	4.2
1	A	221	VAL	4.2
1	A	389	HIS	4.2
2	D	104	GLY	4.1
2	D	12	SER	4.0

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Mol	Chain	Res	Type	RSRZ
2	D	4	ILE	4.0
1	C	389	HIS	3.9
1	B	390	HIS	3.9
1	B	235	GLY	3.9
2	D	92	GLU	3.8
2	D	5	TRP	3.8
1	A	388	HIS	3.8
1	B	391	HIS	3.7
2	D	25	VAL	3.7
2	D	105	GLU	3.7
2	F	95	VAL	3.6
1	B	209	ASP	3.5
2	D	7	LYS	3.5
1	C	387	HIS	3.4
2	D	39	PHE	3.4
2	E	114	HIS	3.3
2	D	38	GLN	3.2
2	D	97	GLU	3.2
1	B	234	HIS	3.1
2	D	9	CYS	3.1
2	E	113	HIS	3.1
1	B	305	ALA	3.0
1	C	234	HIS	3.0
1	B	312	LYS	3.0
1	C	236	VAL	3.0
2	D	40	TYR	3.0
2	D	100	VAL	3.0
2	E	110	HIS	3.0
2	D	36	GLY	3.0
2	D	35	VAL	3.0
2	D	96	LYS	3.0
1	B	222	VAL	2.9
1	B	205	ALA	2.9
1	A	387	HIS	2.8
2	F	105	GLU	2.8
2	D	11	ALA	2.8
2	D	91	PHE	2.8
2	F	106	LYS	2.7
2	D	103	ALA	2.7
1	B	208	GLY	2.7
2	D	8	VAL	2.7
2	E	37	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
2	F	96	LYS	2.6
1	B	315	GLN	2.6
2	D	15	GLN	2.6
1	C	205	ALA	2.5
2	D	13	ASP	2.5
1	B	204	PHE	2.5
2	E	25	VAL	2.5
2	F	90	VAL	2.5
1	B	308	GLU	2.5
2	D	102	VAL	2.5
2	D	99	GLU	2.4
2	F	92	GLU	2.4
1	B	211	LYS	2.4
1	B	236	VAL	2.3
2	D	14	MET	2.3
1	A	2	ALA	2.3
1	B	218	ASP	2.3
1	A	210	ARG	2.3
2	E	112	HIS	2.3
2	E	97	GLU	2.3
2	D	16	PRO	2.2
1	B	388	HIS	2.2
1	C	255	GLU	2.2
2	F	100	VAL	2.1
1	B	255	GLU	2.1
2	F	101	TYR	2.1
2	F	97	GLU	2.1

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	9CA	C	503	13/13	0.84	0.24	4.09	36,39,41,41	0
5	9CA	B	503	13/13	0.89	0.20	2.44	39,40,42,42	0
4	FES	D	201	4/4	0.99	0.09	-0.39	16,19,19,20	0
4	FES	E	201	4/4	0.99	0.09	-0.40	18,19,20,21	0
4	FES	A	502	4/4	1.00	0.11	-0.51	15,17,17,20	0
3	FE2	A	501	1/1	1.00	0.11	-0.57	19,19,19,19	0
4	FES	C	502	4/4	0.99	0.09	-0.70	20,24,26,27	0
3	FE2	B	501	1/1	0.99	0.09	-1.91	37,37,37,37	0
4	FES	F	201	4/4	0.99	0.05	-1.98	18,18,18,21	0
3	FE2	C	501	1/1	0.99	0.05	-2.67	27,27,27,27	0
4	FES	B	502	4/4	0.99	0.10	-5.19	11,12,13,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.