



# wwPDB X-ray Structure Validation Summary Report i

Feb 28, 2014 – 11:23 AM GMT

PDB ID : 4J9A  
Title : Engineered Digoxigenin binder DIG10.3  
Authors : Stoddard, B.L.; Doyle, L.A.  
Deposited on : 2013-02-15  
Resolution : 3.20 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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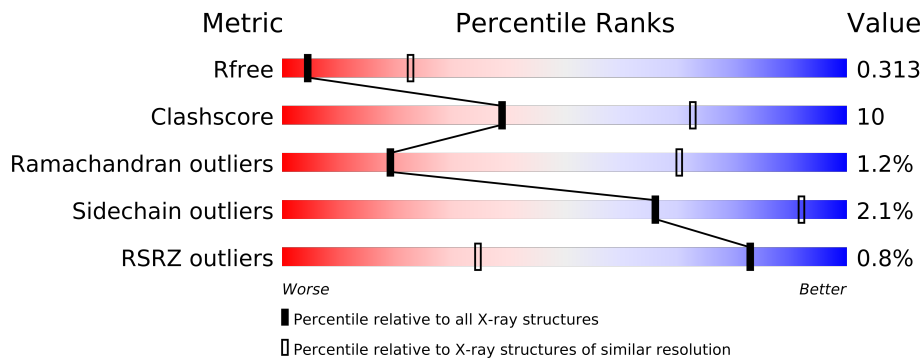
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 3.20 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))
$R_{free}$	66092	1824 (3.30-3.10)
Clashscore	79885	1078 (3.26-3.14)
Ramachandran outliers	78287	1059 (3.26-3.14)
Sidechain outliers	78261	1058 (3.26-3.14)
RSRZ outliers	66119	1825 (3.30-3.10)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	137	
1	B	137	
1	C	137	
1	D	137	
1	E	137	
1	F	137	
1	G	137	
1	H	137	
1	I	137	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7297 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Engineered Digoxigenin binder protein DIG10.3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	122	Total	C	N	O	S	0	0	0
			906	595	146	163	2			
1	B	121	Total	C	N	O	S	0	0	0
			826	543	137	144	2			
1	C	122	Total	C	N	O	S	0	0	0
			812	526	139	146	1			
1	D	124	Total	C	N	O	S	0	0	0
			820	531	141	146	2			
1	E	111	Total	C	N	O	S	0	0	0
			731	477	126	127	1			
1	F	123	Total	C	N	O	S	0	0	0
			800	514	141	144	1			
1	G	105	Total	C	N	O		0	0	0
			657	421	117	119				
1	H	113	Total	C	N	O	S	0	0	0
			746	488	126	131	1			
1	I	111	Total	C	N	O		0	0	0
			747	483	128	136				

There are 234 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	VAL	LEU	ENGINEERED MUTATION	UNP Q9HYR3
A	10	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
A	23	SER	CYS	ENGINEERED MUTATION	UNP Q9HYR3
A	34	TYR	PHE	ENGINEERED MUTATION	UNP Q9HYR3
A	37	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
A	41	TYR	TRP	ENGINEERED MUTATION	UNP Q9HYR3
A	61	TYR	HIS	ENGINEERED MUTATION	UNP Q9HYR3
A	62	MET	LEU	ENGINEERED MUTATION	UNP Q9HYR3
A	64	ILE	VAL	ENGINEERED MUTATION	UNP Q9HYR3
A	90	LEU	ALA	ENGINEERED MUTATION	UNP Q9HYR3
A	92	ALA	VAL	ENGINEERED MUTATION	UNP Q9HYR3

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Chain	Residue	Modelled	Actual	Comment	Reference
A	99	TYR	GLN	ENGINEERED MUTATION	UNP Q9HYR3
A	103	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
A	105	TRP	LEU	ENGINEERED MUTATION	UNP Q9HYR3
A	117	LEU	ASP	ENGINEERED MUTATION	UNP Q9HYR3
A	119	PHE	TRP	ENGINEERED MUTATION	UNP Q9HYR3
A	124	VAL	HIS	ENGINEERED MUTATION	UNP Q9HYR3
A	127	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
A	130	LEU	GLY	ENGINEERED MUTATION	UNP Q9HYR3
A	131	GLU	VAL	ENGINEERED MUTATION	UNP Q9HYR3
A	132	HIS	-	EXPRESSION TAG	UNP Q9HYR3
A	133	HIS	-	EXPRESSION TAG	UNP Q9HYR3
A	134	HIS	-	EXPRESSION TAG	UNP Q9HYR3
A	135	HIS	-	EXPRESSION TAG	UNP Q9HYR3
A	136	HIS	-	EXPRESSION TAG	UNP Q9HYR3
A	137	HIS	-	EXPRESSION TAG	UNP Q9HYR3
B	7	VAL	LEU	ENGINEERED MUTATION	UNP Q9HYR3
B	10	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
B	23	SER	CYS	ENGINEERED MUTATION	UNP Q9HYR3
B	34	TYR	PHE	ENGINEERED MUTATION	UNP Q9HYR3
B	37	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
B	41	TYR	TRP	ENGINEERED MUTATION	UNP Q9HYR3
B	61	TYR	HIS	ENGINEERED MUTATION	UNP Q9HYR3
B	62	MET	LEU	ENGINEERED MUTATION	UNP Q9HYR3
B	64	ILE	VAL	ENGINEERED MUTATION	UNP Q9HYR3
B	90	LEU	ALA	ENGINEERED MUTATION	UNP Q9HYR3
B	92	ALA	VAL	ENGINEERED MUTATION	UNP Q9HYR3
B	99	TYR	GLN	ENGINEERED MUTATION	UNP Q9HYR3
B	103	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
B	105	TRP	LEU	ENGINEERED MUTATION	UNP Q9HYR3
B	117	LEU	ASP	ENGINEERED MUTATION	UNP Q9HYR3
B	119	PHE	TRP	ENGINEERED MUTATION	UNP Q9HYR3
B	124	VAL	HIS	ENGINEERED MUTATION	UNP Q9HYR3
B	127	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
B	130	LEU	GLY	ENGINEERED MUTATION	UNP Q9HYR3
B	131	GLU	VAL	ENGINEERED MUTATION	UNP Q9HYR3
B	132	HIS	-	EXPRESSION TAG	UNP Q9HYR3
B	133	HIS	-	EXPRESSION TAG	UNP Q9HYR3
B	134	HIS	-	EXPRESSION TAG	UNP Q9HYR3
B	135	HIS	-	EXPRESSION TAG	UNP Q9HYR3
B	136	HIS	-	EXPRESSION TAG	UNP Q9HYR3
B	137	HIS	-	EXPRESSION TAG	UNP Q9HYR3
C	7	VAL	LEU	ENGINEERED MUTATION	UNP Q9HYR3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	10	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
C	23	SER	CYS	ENGINEERED MUTATION	UNP Q9HYR3
C	34	TYR	PHE	ENGINEERED MUTATION	UNP Q9HYR3
C	37	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
C	41	TYR	TRP	ENGINEERED MUTATION	UNP Q9HYR3
C	61	TYR	HIS	ENGINEERED MUTATION	UNP Q9HYR3
C	62	MET	LEU	ENGINEERED MUTATION	UNP Q9HYR3
C	64	ILE	VAL	ENGINEERED MUTATION	UNP Q9HYR3
C	90	LEU	ALA	ENGINEERED MUTATION	UNP Q9HYR3
C	92	ALA	VAL	ENGINEERED MUTATION	UNP Q9HYR3
C	99	TYR	GLN	ENGINEERED MUTATION	UNP Q9HYR3
C	103	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
C	105	TRP	LEU	ENGINEERED MUTATION	UNP Q9HYR3
C	117	LEU	ASP	ENGINEERED MUTATION	UNP Q9HYR3
C	119	PHE	TRP	ENGINEERED MUTATION	UNP Q9HYR3
C	124	VAL	HIS	ENGINEERED MUTATION	UNP Q9HYR3
C	127	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
C	130	LEU	GLY	ENGINEERED MUTATION	UNP Q9HYR3
C	131	GLU	VAL	ENGINEERED MUTATION	UNP Q9HYR3
C	132	HIS	-	EXPRESSION TAG	UNP Q9HYR3
C	133	HIS	-	EXPRESSION TAG	UNP Q9HYR3
C	134	HIS	-	EXPRESSION TAG	UNP Q9HYR3
C	135	HIS	-	EXPRESSION TAG	UNP Q9HYR3
C	136	HIS	-	EXPRESSION TAG	UNP Q9HYR3
C	137	HIS	-	EXPRESSION TAG	UNP Q9HYR3
D	7	VAL	LEU	ENGINEERED MUTATION	UNP Q9HYR3
D	10	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
D	23	SER	CYS	ENGINEERED MUTATION	UNP Q9HYR3
D	34	TYR	PHE	ENGINEERED MUTATION	UNP Q9HYR3
D	37	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
D	41	TYR	TRP	ENGINEERED MUTATION	UNP Q9HYR3
D	61	TYR	HIS	ENGINEERED MUTATION	UNP Q9HYR3
D	62	MET	LEU	ENGINEERED MUTATION	UNP Q9HYR3
D	64	ILE	VAL	ENGINEERED MUTATION	UNP Q9HYR3
D	90	LEU	ALA	ENGINEERED MUTATION	UNP Q9HYR3
D	92	ALA	VAL	ENGINEERED MUTATION	UNP Q9HYR3
D	99	TYR	GLN	ENGINEERED MUTATION	UNP Q9HYR3
D	103	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
D	105	TRP	LEU	ENGINEERED MUTATION	UNP Q9HYR3
D	117	LEU	ASP	ENGINEERED MUTATION	UNP Q9HYR3
D	119	PHE	TRP	ENGINEERED MUTATION	UNP Q9HYR3
D	124	VAL	HIS	ENGINEERED MUTATION	UNP Q9HYR3

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Chain	Residue	Modelled	Actual	Comment	Reference
D	127	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
D	130	LEU	GLY	ENGINEERED MUTATION	UNP Q9HYR3
D	131	GLU	VAL	ENGINEERED MUTATION	UNP Q9HYR3
D	132	HIS	-	EXPRESSION TAG	UNP Q9HYR3
D	133	HIS	-	EXPRESSION TAG	UNP Q9HYR3
D	134	HIS	-	EXPRESSION TAG	UNP Q9HYR3
D	135	HIS	-	EXPRESSION TAG	UNP Q9HYR3
D	136	HIS	-	EXPRESSION TAG	UNP Q9HYR3
D	137	HIS	-	EXPRESSION TAG	UNP Q9HYR3
E	7	VAL	LEU	ENGINEERED MUTATION	UNP Q9HYR3
E	10	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
E	23	SER	CYS	ENGINEERED MUTATION	UNP Q9HYR3
E	34	TYR	PHE	ENGINEERED MUTATION	UNP Q9HYR3
E	37	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
E	41	TYR	TRP	ENGINEERED MUTATION	UNP Q9HYR3
E	61	TYR	HIS	ENGINEERED MUTATION	UNP Q9HYR3
E	62	MET	LEU	ENGINEERED MUTATION	UNP Q9HYR3
E	64	ILE	VAL	ENGINEERED MUTATION	UNP Q9HYR3
E	90	LEU	ALA	ENGINEERED MUTATION	UNP Q9HYR3
E	92	ALA	VAL	ENGINEERED MUTATION	UNP Q9HYR3
E	99	TYR	GLN	ENGINEERED MUTATION	UNP Q9HYR3
E	103	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
E	105	TRP	LEU	ENGINEERED MUTATION	UNP Q9HYR3
E	117	LEU	ASP	ENGINEERED MUTATION	UNP Q9HYR3
E	119	PHE	TRP	ENGINEERED MUTATION	UNP Q9HYR3
E	124	VAL	HIS	ENGINEERED MUTATION	UNP Q9HYR3
E	127	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
E	130	LEU	GLY	ENGINEERED MUTATION	UNP Q9HYR3
E	131	GLU	VAL	ENGINEERED MUTATION	UNP Q9HYR3
E	132	HIS	-	EXPRESSION TAG	UNP Q9HYR3
E	133	HIS	-	EXPRESSION TAG	UNP Q9HYR3
E	134	HIS	-	EXPRESSION TAG	UNP Q9HYR3
E	135	HIS	-	EXPRESSION TAG	UNP Q9HYR3
E	136	HIS	-	EXPRESSION TAG	UNP Q9HYR3
E	137	HIS	-	EXPRESSION TAG	UNP Q9HYR3
F	7	VAL	LEU	ENGINEERED MUTATION	UNP Q9HYR3
F	10	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
F	23	SER	CYS	ENGINEERED MUTATION	UNP Q9HYR3
F	34	TYR	PHE	ENGINEERED MUTATION	UNP Q9HYR3
F	37	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
F	41	TYR	TRP	ENGINEERED MUTATION	UNP Q9HYR3
F	61	TYR	HIS	ENGINEERED MUTATION	UNP Q9HYR3

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Chain	Residue	Modelled	Actual	Comment	Reference
F	62	MET	LEU	ENGINEERED MUTATION	UNP Q9HYR3
F	64	ILE	VAL	ENGINEERED MUTATION	UNP Q9HYR3
F	90	LEU	ALA	ENGINEERED MUTATION	UNP Q9HYR3
F	92	ALA	VAL	ENGINEERED MUTATION	UNP Q9HYR3
F	99	TYR	GLN	ENGINEERED MUTATION	UNP Q9HYR3
F	103	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
F	105	TRP	LEU	ENGINEERED MUTATION	UNP Q9HYR3
F	117	LEU	ASP	ENGINEERED MUTATION	UNP Q9HYR3
F	119	PHE	TRP	ENGINEERED MUTATION	UNP Q9HYR3
F	124	VAL	HIS	ENGINEERED MUTATION	UNP Q9HYR3
F	127	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
F	130	LEU	GLY	ENGINEERED MUTATION	UNP Q9HYR3
F	131	GLU	VAL	ENGINEERED MUTATION	UNP Q9HYR3
F	132	HIS	-	EXPRESSION TAG	UNP Q9HYR3
F	133	HIS	-	EXPRESSION TAG	UNP Q9HYR3
F	134	HIS	-	EXPRESSION TAG	UNP Q9HYR3
F	135	HIS	-	EXPRESSION TAG	UNP Q9HYR3
F	136	HIS	-	EXPRESSION TAG	UNP Q9HYR3
F	137	HIS	-	EXPRESSION TAG	UNP Q9HYR3
G	7	VAL	LEU	ENGINEERED MUTATION	UNP Q9HYR3
G	10	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
G	23	SER	CYS	ENGINEERED MUTATION	UNP Q9HYR3
G	34	TYR	PHE	ENGINEERED MUTATION	UNP Q9HYR3
G	37	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
G	41	TYR	TRP	ENGINEERED MUTATION	UNP Q9HYR3
G	61	TYR	HIS	ENGINEERED MUTATION	UNP Q9HYR3
G	62	MET	LEU	ENGINEERED MUTATION	UNP Q9HYR3
G	64	ILE	VAL	ENGINEERED MUTATION	UNP Q9HYR3
G	90	LEU	ALA	ENGINEERED MUTATION	UNP Q9HYR3
G	92	ALA	VAL	ENGINEERED MUTATION	UNP Q9HYR3
G	99	TYR	GLN	ENGINEERED MUTATION	UNP Q9HYR3
G	103	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
G	105	TRP	LEU	ENGINEERED MUTATION	UNP Q9HYR3
G	117	LEU	ASP	ENGINEERED MUTATION	UNP Q9HYR3
G	119	PHE	TRP	ENGINEERED MUTATION	UNP Q9HYR3
G	124	VAL	HIS	ENGINEERED MUTATION	UNP Q9HYR3
G	127	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
G	130	LEU	GLY	ENGINEERED MUTATION	UNP Q9HYR3
G	131	GLU	VAL	ENGINEERED MUTATION	UNP Q9HYR3
G	132	HIS	-	EXPRESSION TAG	UNP Q9HYR3
G	133	HIS	-	EXPRESSION TAG	UNP Q9HYR3
G	134	HIS	-	EXPRESSION TAG	UNP Q9HYR3

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Chain	Residue	Modelled	Actual	Comment	Reference
G	135	HIS	-	EXPRESSION TAG	UNP Q9HYR3
G	136	HIS	-	EXPRESSION TAG	UNP Q9HYR3
G	137	HIS	-	EXPRESSION TAG	UNP Q9HYR3
H	7	VAL	LEU	ENGINEERED MUTATION	UNP Q9HYR3
H	10	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
H	23	SER	CYS	ENGINEERED MUTATION	UNP Q9HYR3
H	34	TYR	PHE	ENGINEERED MUTATION	UNP Q9HYR3
H	37	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
H	41	TYR	TRP	ENGINEERED MUTATION	UNP Q9HYR3
H	61	TYR	HIS	ENGINEERED MUTATION	UNP Q9HYR3
H	62	MET	LEU	ENGINEERED MUTATION	UNP Q9HYR3
H	64	ILE	VAL	ENGINEERED MUTATION	UNP Q9HYR3
H	90	LEU	ALA	ENGINEERED MUTATION	UNP Q9HYR3
H	92	ALA	VAL	ENGINEERED MUTATION	UNP Q9HYR3
H	99	TYR	GLN	ENGINEERED MUTATION	UNP Q9HYR3
H	103	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
H	105	TRP	LEU	ENGINEERED MUTATION	UNP Q9HYR3
H	117	LEU	ASP	ENGINEERED MUTATION	UNP Q9HYR3
H	119	PHE	TRP	ENGINEERED MUTATION	UNP Q9HYR3
H	124	VAL	HIS	ENGINEERED MUTATION	UNP Q9HYR3
H	127	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
H	130	LEU	GLY	ENGINEERED MUTATION	UNP Q9HYR3
H	131	GLU	VAL	ENGINEERED MUTATION	UNP Q9HYR3
H	132	HIS	-	EXPRESSION TAG	UNP Q9HYR3
H	133	HIS	-	EXPRESSION TAG	UNP Q9HYR3
H	134	HIS	-	EXPRESSION TAG	UNP Q9HYR3
H	135	HIS	-	EXPRESSION TAG	UNP Q9HYR3
H	136	HIS	-	EXPRESSION TAG	UNP Q9HYR3
H	137	HIS	-	EXPRESSION TAG	UNP Q9HYR3
I	7	VAL	LEU	ENGINEERED MUTATION	UNP Q9HYR3
I	10	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3
I	23	SER	CYS	ENGINEERED MUTATION	UNP Q9HYR3
I	34	TYR	PHE	ENGINEERED MUTATION	UNP Q9HYR3
I	37	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
I	41	TYR	TRP	ENGINEERED MUTATION	UNP Q9HYR3
I	61	TYR	HIS	ENGINEERED MUTATION	UNP Q9HYR3
I	62	MET	LEU	ENGINEERED MUTATION	UNP Q9HYR3
I	64	ILE	VAL	ENGINEERED MUTATION	UNP Q9HYR3
I	90	LEU	ALA	ENGINEERED MUTATION	UNP Q9HYR3
I	92	ALA	VAL	ENGINEERED MUTATION	UNP Q9HYR3
I	99	TYR	GLN	ENGINEERED MUTATION	UNP Q9HYR3
I	103	ALA	SER	ENGINEERED MUTATION	UNP Q9HYR3

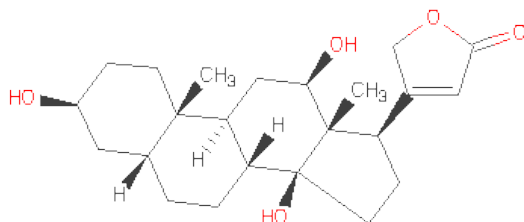
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Chain	Residue	Modelled	Actual	Comment	Reference
I	105	TRP	LEU	ENGINEERED MUTATION	UNP Q9HYR3
I	117	LEU	ASP	ENGINEERED MUTATION	UNP Q9HYR3
I	119	PHE	TRP	ENGINEERED MUTATION	UNP Q9HYR3
I	124	VAL	HIS	ENGINEERED MUTATION	UNP Q9HYR3
I	127	PRO	ALA	ENGINEERED MUTATION	UNP Q9HYR3
I	130	LEU	GLY	ENGINEERED MUTATION	UNP Q9HYR3
I	131	GLU	VAL	ENGINEERED MUTATION	UNP Q9HYR3
I	132	HIS	-	EXPRESSION TAG	UNP Q9HYR3
I	133	HIS	-	EXPRESSION TAG	UNP Q9HYR3
I	134	HIS	-	EXPRESSION TAG	UNP Q9HYR3
I	135	HIS	-	EXPRESSION TAG	UNP Q9HYR3
I	136	HIS	-	EXPRESSION TAG	UNP Q9HYR3
I	137	HIS	-	EXPRESSION TAG	UNP Q9HYR3

- Molecule 2 is DIGOXIGENIN (three-letter code: DOG) (formula:  $C_{23}H_{34}O_5$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			28	23	5		
2	B	1	Total	C	O	0	0
			28	23	5		
2	C	1	Total	C	O	0	0
			28	23	5		
2	D	1	Total	C	O	0	0
			28	23	5		
2	E	1	Total	C	O	0	0
			28	23	5		

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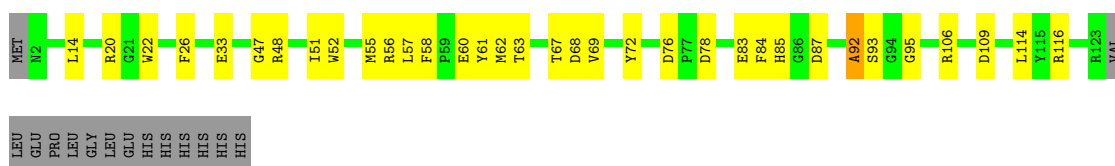
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	F	1	Total	C	O	0	0
			28	23	5		
2	G	1	Total	C	O	0	0
			28	23	5		
2	H	1	Total	C	O	0	0
			28	23	5		
2	I	1	Total	C	O	0	0
			28	23	5		

### 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: Engineered Digoxigenin binder protein DIG10.3

Chain A: 



- Molecule 1: Engineered Digoxigenin binder protein DIG10.3

Chain B: 



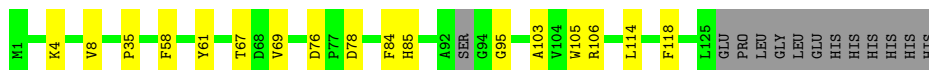
- Molecule 1: Engineered Digoxigenin binder protein DIG10.3

Chain C: 



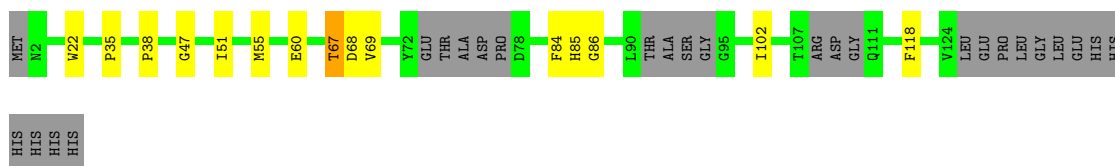
- Molecule 1: Engineered Digoxigenin binder protein DIG10.3

Chain D: 



- Molecule 1: Engineered Digoxigenin binder protein DIG10.3

Chain E: 



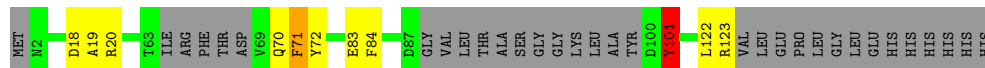
- Molecule 1: Engineered Digoxigenin binder protein DIG10.3

Chain F: 



- Molecule 1: Engineered Digoxigenin binder protein DIG10.3

Chain G:



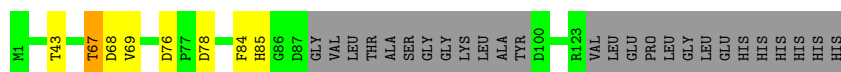
- Molecule 1: Engineered Digoxigenin binder protein DIG10.3

Chain H:



- Molecule 1: Engineered Digoxigenin binder protein DIG10.3

Chain I:



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	132.79Å 90.99Å 110.08Å 90.00° 92.68° 90.00°	Depositor
Resolution (Å)	45.54 – 3.20 45.50 – 3.20	Depositor EDS
% Data completeness (in resolution range)	97.5 (45.54-3.20) 97.5 (45.50-3.20)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.84 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.262 , 0.317 0.263 , 0.313	Depositor DCC
$R_{free}$ test set	1082 reflections (5.39%)	DCC
Wilson B-factor (Å <sup>2</sup> )	86.5	Xtriage
Anisotropy	0.609	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 117.9	EDS
Estimated twinning fraction	0.020 for -h,-k,l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	2 of 21172 reflections (0.009%)	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	7297	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.77% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DOG

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	0.57	0/939	0.73	0/1290
1	B	0.59	0/857	0.68	0/1181
1	C	0.49	0/844	0.64	0/1167
1	D	0.53	0/847	0.69	0/1167
1	E	0.55	0/756	0.66	0/1041
1	F	0.51	0/826	0.67	0/1141
1	G	0.52	0/677	0.73	2/935 (0.2%)
1	H	0.53	0/772	0.66	0/1067
1	I	0.54	0/773	0.68	0/1071
All	All	0.54	0/7291	0.68	2/10060 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	101	TYR	CB-CG-CD1	7.64	125.58	121.00
1	G	101	TYR	CB-CG-CD2	-6.31	117.21	121.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	906	0	762	29	0
1	B	826	0	613	12	0
1	C	812	0	572	10	0
1	D	820	0	605	12	0
1	E	731	0	507	22	0
1	F	800	0	566	11	0
1	G	657	0	439	9	0
1	H	746	0	535	14	0
1	I	747	0	547	7	0
2	A	28	0	34	1	0
2	B	28	0	34	0	0
2	C	28	0	34	0	0
2	D	28	0	34	1	0
2	E	28	0	34	3	0
2	F	28	0	34	2	0
2	G	28	0	34	3	0
2	H	28	0	34	4	0
2	I	28	0	34	0	0
All	All	7297	0	5452	123	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 10.

The worst 5 of 123 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:35:PRO:HG2	1:E:118:PHE:CE1	1.71	1.25
1:A:60:GLU:OE1	1:B:92:ALA:HB2	1.58	1.02
1:E:35:PRO:HG2	1:E:118:PHE:HE1	1.26	0.99
1:E:35:PRO:CG	1:E:118:PHE:HE1	1.80	0.94
1:A:26:PHE:O	1:A:48:ARG:NH1	2.01	0.94

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	120/137 (88%)	113 (94%)	5 (4%)	2 (2%)	14	62
1	B	117/137 (85%)	108 (92%)	6 (5%)	3 (3%)	8	47
1	C	120/137 (88%)	113 (94%)	5 (4%)	2 (2%)	14	62
1	D	120/137 (88%)	115 (96%)	4 (3%)	1 (1%)	27	77
1	E	103/137 (75%)	100 (97%)	3 (3%)	0	100	100
1	F	119/137 (87%)	114 (96%)	4 (3%)	1 (1%)	27	77
1	G	99/137 (72%)	89 (90%)	8 (8%)	2 (2%)	11	56
1	H	107/137 (78%)	99 (92%)	7 (6%)	1 (1%)	25	76
1	I	107/137 (78%)	103 (96%)	4 (4%)	0	100	100
All	All	1012/1233 (82%)	954 (94%)	46 (4%)	12 (1%)	19	70

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	19	ALA
1	H	109	ASP
1	A	95	GLY
1	B	95	GLY
1	C	95	GLY

### 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	74/116 (64%)	72 (97%)	2 (3%)	57	90
1	B	52/116 (45%)	51 (98%)	1 (2%)	69	93
1	C	48/116 (41%)	47 (98%)	1 (2%)	66	92
1	D	50/116 (43%)	50 (100%)	0	100	100
1	E	40/116 (34%)	39 (98%)	1 (2%)	60	90
1	F	46/116 (40%)	45 (98%)	1 (2%)	64	91
1	G	32/116 (28%)	31 (97%)	1 (3%)	52	88
1	H	43/116 (37%)	43 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	48/116 (41%)	46 (96%)	2 (4%)	40	82
All	All	433/1044 (42%)	424 (98%)	9 (2%)	66	92

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	67	THR
1	I	67	THR
1	G	101	TYR
1	B	39	PRO
1	F	122	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

9 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
2	DOG	A	201	-	32,32,32	1.68	5 (15%)	53,53,53	1.23	6 (11%)
2	DOG	B	201	-	32,32,32	1.21	4 (12%)	53,53,53	1.33	5 (9%)
2	DOG	C	201	-	32,32,32	1.24	2 (6%)	53,53,53	1.18	6 (11%)
2	DOG	D	201	-	32,32,32	1.33	3 (9%)	53,53,53	1.27	6 (11%)
2	DOG	E	201	-	32,32,32	0.99	2 (6%)	53,53,53	1.63	8 (15%)
2	DOG	F	201	-	32,32,32	1.12	2 (6%)	53,53,53	1.59	10 (18%)
2	DOG	G	201	-	32,32,32	1.42	4 (12%)	53,53,53	1.52	10 (18%)
2	DOG	H	201	-	32,32,32	1.24	3 (9%)	53,53,53	1.50	12 (22%)
2	DOG	I	201	-	32,32,32	1.16	3 (9%)	53,53,53	1.32	7 (13%)

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
2	DOG	A	201	-	-	0/4/81/81	0/1/5/5
2	DOG	B	201	-	-	0/4/81/81	0/1/5/5
2	DOG	C	201	-	-	0/4/81/81	0/1/5/5
2	DOG	D	201	-	-	0/4/81/81	0/1/5/5
2	DOG	E	201	-	-	0/4/81/81	0/1/5/5
2	DOG	F	201	-	-	0/4/81/81	0/1/5/5
2	DOG	G	201	-	-	0/4/81/81	0/1/5/5
2	DOG	H	201	-	-	0/4/81/81	0/1/5/5
2	DOG	I	201	-	-	0/4/81/81	0/1/5/5

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	201	DOG	C14-C13	-6.81	1.49	1.56
2	G	201	DOG	C14-C13	-5.32	1.51	1.56
2	D	201	DOG	C14-C13	-4.64	1.51	1.56
2	H	201	DOG	C14-C13	-4.51	1.52	1.56
2	C	201	DOG	C14-C13	-3.64	1.52	1.56

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	201	DOG	C15-C14-C13	5.15	108.23	103.44
2	B	201	DOG	C15-C14-C13	4.31	107.45	103.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	201	DOG	O14-C14-C8	-3.96	101.80	108.43
2	D	201	DOG	O14-C14-C8	-3.94	101.82	108.43
2	E	201	DOG	C9-C11-C12	-3.88	109.29	114.35

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	122/137 (89%)	-0.22	0 100 100	38, 57, 78, 94	0
1	B	121/137 (88%)	-0.20	0 100 100	48, 68, 96, 123	0
1	C	122/137 (89%)	-0.23	0 100 100	50, 73, 96, 129	0
1	D	124/137 (90%)	-0.27	0 100 100	46, 64, 87, 95	0
1	E	111/137 (81%)	-0.21	0 100 100	53, 79, 99, 107	0
1	F	123/137 (89%)	-0.23	0 100 100	52, 76, 94, 110	0
1	G	105/137 (76%)	-0.19	0 100 100	52, 84, 111, 124	0
1	H	113/137 (82%)	-0.06	0 100 100	54, 78, 109, 117	0
1	I	111/137 (81%)	-0.17	0 100 100	45, 71, 107, 146	0
All	All	1052/1233 (85%)	-0.20	0 83 100	38, 73, 101, 146	0

There are no RSRZ outliers to report.

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	DOG	G	201	28/28	0.37	1.70	51,63,78,86	0
2	DOG	D	201	28/28	0.32	1.59	43,49,58,65	0
2	DOG	E	201	28/28	0.28	1.01	58,71,78,79	0
2	DOG	F	201	28/28	0.38	0.72	53,63,68,73	0
2	DOG	A	201	28/28	0.29	0.58	43,49,59,74	0
2	DOG	B	201	28/28	0.29	0.36	52,57,61,67	0
2	DOG	I	201	28/28	0.30	0.13	51,61,74,75	0
2	DOG	C	201	28/28	0.25	-0.45	47,52,61,63	0
2	DOG	H	201	28/28	0.27	-0.72	53,68,79,85	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.